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L18: Entry 3 of 9

File: USPT

Feb 16, 1999

DOCUMENT-IDENTIFIER: US 5871923 A

TITLE: Methods for screening for antimycotics

Detailed Description Paragraph Right (124):

A compound that inhibits termination may be toxic to the cell, and the increase in phosphatase expression could be canceled by a decrease in the number of living cells that are capable of translation. In order to provide a control for this, for each concentration of each test or control compound used, a parallel microtiter plate is prepared and incubated, however, this parallel plate is assayed for an external reductase either encoded or controlled by the FRE1 gene (Ferric Reductase of *Saccharomyces cerevisiae*: Molecular Characterization, Role in Iron Uptake, and Transcriptional Control by Iron, A. Dancis, D. G. Roman, G. J. Anderson, A. G. Hinnebusch, and R. D. Klausner, Proc. Natl. Acad. Sci. 89:3869-3873, 1992). An increase or decrease of more than three fold in the phosphatase:reductase ratio also indicates that the test compound interfered with translation termination. Furthermore, a decrease in the level of reductase expression indicates that the compound is toxic to the fungal cell.

Detailed Description Paragraph Right (133):

A compound that alters the frequency of frames-hifting may be toxic to the cell, and the increase in phosphatase expression could be canceled by a decrease in the number of living cells that are capable of translation. In order to provide a control for this, for each concentration of each test or control compound used, a parallel microtiter plate is prepared and incubated, however, this parallel plate is assayed for an external reductase either encoded or controlled by the FRE1 gene. An increase or decrease of more than three fold in the phosphatase:reductase ratio also indicates that the test compound interfered with frameshifting. Furthermore, a decrease in the level of reductase expression indicates that the compound is toxic to the fungal cell.

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L18: Entry 2 of 9

File: USPT

May 29, 2001

DOCUMENT-IDENTIFIER: US 6239264 B1

TITLE: Genomic DNA sequences of ashbya gossypii and uses thereof

Detailed Description Paragraph Table (10):

PAG1402RP YOR023c unknown function 1 PAG1402UP YOR161c unknown function 1 PAG1403RP YBR280c YBR280c:sim to SRM1p/PRP20p 1 Syntenie two genes covered by YJL068c:sim to human esterase D RP SRS;end of syntenie PAG1403UP YBR281c has beta-transducin (WD40) repeats 1 PAG1404RP YPL012w Lpa5p unknown function 1 syntenie 1 YPL014w LPA3 unknown function mito ribosomal S24 protein PAG1405RP 4 PAG1405UP YHR086W NAM8 protein essential for meiotic recombination 1 and suppressor of MT- splicing defects, has 3 RNA recognition domains PAG1406RP YHR007C ERG11 Cytochrome P450 L1 (14DM) (Lanosterol 1 14-alpha-demethylase) PAG1406UP YPL026c SHA3 Ser/Thr-protein kinase, suppressor of Htalp 1 mutations that cause aberrant transcription PAG1408RP MITO-Chimeric Plasmid DNA PAG1408UP YBR072w HSP26 YEAST HEAT SHOCK PROTEIN 26 1 expressed during entry to stationary phase and induced by osmostress PAG1409RP YPR154W YPR153W:unknown fubtion, gene may be 1 syntenie, two genes covered by spliced;YPR154w:protein with sim to RP-SRS; YPR153W several SH3 domain-containing proteins including myosin ID and IC heavy chains, human growth factor receptor-bound grb2 protein, C. elegans sex muscle abnormal protein 5 PAG1409UP YPR156c member of the major facilitator superfamily 1 YPR155c:NCA2:protein (MFS) mulitdrug resistance proteins family required for CTRL of MT 1 synthesis of ATP6 and ATP8;Hit no 1:YGR138C (putative drug transporter) neglegcted due to syntenie PAG1410RP YOR116c YOR116c: RPO31: RNA-POLIII largest 1 syntenie subunit PAG1410UP YOR117w: YOR117w: YTA1: Syntenie: subunit of 1 syntenie 26S proteasome complex and member of the ATPase family PAG1412RP YJR153w sim to polygalacturonases 1 PAG1412UP 4 PAG1413RP YDR150w NUM1 nuclear migration 1 syntenie ;should contain the N- term of NUM 1 PAG1413UP YDR152w unknown function 1 Syntenie YDR151c:CTH1:protein of the mammalian growth factor induced proteins, len 325 aa PAG1414RP YLR272c unknown function 1 PAG1414UP 4 PAG1415RP YGR271w seems to be an RNA-helicase related 1 just one gene on this plasmid protein; PAG1415UP YGR271w has sim to Yer172p; has A(P-loop) 1 UP-SRS covers 1917aa to 1676aa PAG1416RP YLR430w SEN1 positive effector of tRNA-splicing 1 codons 1790 up to 1971;C-term endonuclease, required for intron cleavage including terminator should be for all ten precursor tRNA families on this plasmid;syntenie PAG1416UP YLR432w protein highly similar to to PUR5p and 1 syntenie inosine-5'-monophosphate of human and E. coli, has sim to YML056c (which was actually hit no 1) PAG1417RP YPR183w Dolichol-phosphate mannosyltransferase 1 syntenie.SMX3:YPR182w: SnRNA associated protein PAG1417UP YPR181c SEC23 Protein transport protein 1 syntenie PAG1418RP YCL060c protein with sim to SDL1 L-serine 1 syntenie dehydratase PAG1418UP YCL061c unknown function 1 syntenie PAG1419RP YLR219w 2 PAG1419UP 4 PAG1420RP YJR107w sim to acylglycerol lipase 1 PAG1420UP YJR014w YJR014w: unknown 1 two genes covered by UP-SRS functionYGR198w:unknown function PAG1421RP YNL075w unknown function 1 PAG1421UP only sim with Ser/Thr rich sequences 4 PAG1422RP YGL091c NBP35 NBP35: nucleotide binding protein 1 syntenie (ATP/GTP) YGL092w NUP145 nuclear pore protein (nucleoporin) 1 PAG1422UP YGL092w NUP145 1 Hit no 1 to YGL172w corresponds to NUP49 and was disregarded due to syntenie PAG1423RP YDR189w: SLY1 SLY1: YDR189w: member of the SEC1- 1 syntenie family, involved in vesicle trafficking between the ER and Golgi PAG1423UP YDR191W HST4 sim to SIR2 1 has A(P-loop) PAG1424RP 4 PAG1424UP 4 PAG1425RP YLR187W YLR187W unknown function, sim to 1 YNL278w was hit no 5;gives YNL278W weak indication of syntenie or a probable homology region for chromosomal rearrangements PAG1425UP YNL279w probable membrane protein 1 weak syntenie PAG1426RP YDR196c unknown function, has A(P-loop) 1 two genes covered with RP-SRS YDR197w CBS2 CBS2:translational activator of COB mRNA,

non-essential PAG1426UP YDR194c MSS16 MSS16:MT RNA helicase of the DEAD 1 syntenie; neighboring-clone to box family required for splicing of group II SLY1 introns of COX1 and COB PAG1427RP YLR214W FRE1 ferric (and cupric) reductase, acts on ferric 1 syntenie; two genes with RP- iron chelates external to the cell SRS YLR215c unknown function 1 syntenie PAG1427UP YDL143w CCT4 Component of chaperonin containing T- 1 end of syntenie complex YLR215C 1 same gene sequenced with RP- SRS PAG1428RP YDL060w unknown function 1 syntenie, whole gene on plasmid PAG1428UP YDL060w unknown function 1 start of gene, syntenie. Two genes covered by UP-SRS YDL061c YS29B ribosomal protein 1 syntenie. Two genes covered by UP-SRS; identical to YLR388w PAG1429RP 4 PAG1429UP YBR260c protein with weak sim to human bcr (break 1 point cluster) protein PAG1430RP YLR213C YLR213C :unknown fnction, has WAP- 1 syntenie. End of syntenie type `four disulfide core` domain signature YDL144C unknown function 1 syntenie PAG1430UP YDL145c YDL145c: RET1: N-Term has 4 WD-beta 1 syntenie transducin repeats. Coatomer complex alpha chain PAG1431RP YHR178W protein with sim to transcription factors, has 1 Zn(2)-Cys(6) fungal-type binuclear cluster domain in the N-terminal region PAG1431UP YMR270C RRN9 component of the upstream activation factor 1 (UAF)-complex, involved in activation of RNA polymerase I promoter; non-essential PAG1432RP sim to proline rich sequences 4 PAG1432UP YDR330W Small region of similarity near C-terminus 1 to Undulin extracellular matrix glycoprotein PAG1433RP YBR141c unknown function 1 involved in maintenance of M dsRNA killer plasmid PAG1433UP YBR143c SUP45 SUP45:recessive omnipotent suppressor, 1 syntenie translational release factor eRF1 PAG1434RP 4 PAG1434UP YCR065w HCM1 HCM1 hom to forkhead. Has a 1 transcriptional activation domain of Drosophila fkh homeotic gene PAG1435UP 4 PAG1436RP YCR093w CDC39 nuclear protein that negatively affects basal 1 N-term up to aa570 on plasmid transcription from many promoters, mutants activate the pheromone response pathway at the level of the G-proteins PAG1436UP YKL215c protein with sim to Pseudomonas 1 hydantoinases hyuA-hyuB PAG1437RP YOR224C RPB8 RPB8:Shared subunit of RNA-POL I,II,III, 1 syntenie. Two genes with RP- essential SRS YOR226C protein with sim to nitrogen fixation 1 Hit no3 was proteins YPL135w:LPI10:protein with sim to H. influenza nitrogen fixation protein HIU32721-12 which was equally good as hit no 2. Taken this we reach syntenie to PAG1437UP PAG1437UP YPL133c LPI12 protein with sim to transcription factors, has 1 syntenie Zn(2)-Cys(6) fungal type binuclear cluster domain in the N-terminal region PAG1438RP YJR132w NMD5 Nam7p/Upflp interacting protein. Nam7p: 1 protein involved in decay of mRNA containing nonsense codons PAG1438UP YBR079c protein homologous to surface antigens 1 from trophoblast endothelial activated lymphocytes and P. falciparum PAG1439RP YGR276c unknown function 1

Detailed Description Paragraph Table (12):

has 1 identical to Zn(2)-Cys(6) fungal-type binuclear cluster domain in the N-terminal region PAG1470UP YNR043w ERG19 Mevalonate kinase, generates mevalonate- 1 identical to 5-phosphate from mevalonate, needed for 1155,1470,1527,1535,1546,1595 ARS-CEN plasmid stability (regulation of autonomous replication) PAG1471RP YHR096c HXT5 Highly similar to hexose transporters HXT2 1 syntenie due to the transporter and HXT4 (S. cerevisiae) genes ; continued syntenie with plasmid PAG1469RP/UP PAG1471UP YHR094C HXT1 HEX1:Hexokinase II, converts hexoses to 1 chosen due to syntenie, the other hexose phosphates in glycolysis and plays a hits(YJL214W:HXT8;YDR345C; regulatory role in glucose repression YLR081W) had no higher sim. PAG1472RP YDR016c unknown function 1 weak case of syntenie PAG1472UP YDR014w hypothetical protein 2 weak syntenie PAG1473RP YMR097c has ATP/GTP-binding site motif 1 syntenie PAG1473UP YMR094w CTF13 kinetochore proteinCbf3, subunit c 1 syntenie; YMR096w: len 297aa, sim to YFL059p and YNL333p.YMR095c: len 224aa, sim to YML334p PAG1474RP YOR070c unknown 1 PAG1474UP YKR081c unknown 1 PAG1475RP 4 PAG1475UP YPR190c RPC82 RNA-POL III, third largest subunit 1 YGR049w Similar to Scm4p (SCM4_YEAST), 1 possible Cdc4p-interacting protein. PAG1476RP YML091c RPM2 Ribonuclease P of MT, generates mature 1 tRNA molecules by cleaving their 5' ends PAG1476UP YML126c HMGS 3-hydroxy-3-methylglutaryl coenzyme A 1 located near TUB3/YML124c synthase, functions in mevalonate synthesis PAG1477RP YER093c unknown function 1 syntenie YNL116w unknown 1 PAG1477UP YER091c MET6 Homocysteine methyltransferase, 1 syntenie.YER092w:len methionine synthase; 5- 125:unknown methyltetrahydropteroyl triglutamate-- homocysteinemethyltransferase- PAG1478RP YER022w SRB4 component of RNA-POLIII holoenzyme and 1 syntenie Kornberg's mediator (SRB) subcomplex, required for basal transcription PAG1478UP YER021w SUN2 Component of 26S proteasome complex 1 syntenie PAG1479RP 4 PAG1479UP YJR091c JSN1 protein that when overexpressed can 1

almost all of the ORF on this suppress the hyperstable microtubule plasmid starting from codon 20 phenotype of tub2-150 PAG1480RP YMR167w MLH1 Mismatch repair protein and homolog of 1 syntenie; YMR168c:CBF3b, len E. coli MutL involved in repair of small 608aa YMR169c:ALD3, len insertions 506aa PAG1480UP YMR170c ALD2 Aldehyde dehydrogenase 1 syntenie PAG1482RP YLR214w FRE1 Ferric (and cupric) reductase, acts on ferric 1 syntenie iron chelates external to the cell PAG1482UP YLR215c unknown function 1 syntenie PAG1483RP YDL171c GLT1 Glutamate synthase, involved with 1 glutamine synthase in glutamate biosynthesis PAG1483UP YNR013c protein with sim to Pho87p and YJL198p, 1 member of the phosphate permease family, 12 TMD PAG1484RP YNR006w VPS27 protein involved in vacuolar sorting 1 PAG1484UP YPL256c CLN2 G1/S-specific cyclin, interacts with 1 CDC28p protein kinase to control the events at START PAG1485RP tRNA pre-tRNA-leu 1 redundant PAG1485UP YGL170c with sim to phosphoribulokinase precursor 2 (phosphopentokinase) PAG1486RP YNL161w SER/THR protein kinase of unknown 1 function; related protein from N. crassa is required for hyphal elongation, has sim to DBF2, DBF20, YPK1, YPK2, and TPK2, strong sim to CAMP-dependent protein kinases like cot-1 and human myotonic dystrophy kinase MDK PAG1486UP YHR142w unknown function, has 7 potential TMD 1 PAG1487RP YOR036w PEP12 PEP12:Syntaxin(t-SNARE) involved in 1 disturbed syntenie. Two genes Golgi to vacuole transport, len 288aa covered with RP-SRS YDR267C protein with sim to SEC13 and other 1 disturbed syntenie proteins with WD-40 repeats; has sim to transcription factors PAG1487UP YOR038c HIR2 HIR2:Histone transcription regulator, 1 disturbed syntenie required for periodic repression of 3 of the 4 histone gene loci and for autogenous repression of HTA1-HTB1 locus by H2A and H2B PAG1488RP YIR007w YIB7 sim to endoglucanases 1 PAG1488UP YOL027c unknown, sim to YPR125p 1 PAG1489RP YBR001c NTH2 alpha, alpha-trehalase, converts alpha, alpha- 1 CEN- trehalose to glucose, promoter contains the PLASMID, HISTONES:SYNTE stress-regulated CCCCT-elements (STRE) NIE common to stress-induced genes, repressors: glucose PAG1489UP YBL003c HTA2 Histone H2a 1 syntenie PAG1490RP YMR167w MLH1 mismatch repair protein and homolog of 1 syntenie:YMR170c:ALD5.YMR E. coli MUTL 169c:ALD3 YMR168c:CBF3B PAG1490UP YMR170c ALDS Aldehyde dehydrogenase 1 syntenie PAG1491RP 4 PAG1491UP YNL082w PMS1 protein required for mismatch repair, 2 homologous to MutL PAG1492RP YKR070w unknown function 1 two genes covered by RP-SRS YOR052c unknown function 1 two genes covered by RP-SRS PAG1492UP YLR292c SEC72 SEC72:Component of ER protein- 1 translocation complex that includes SEC61, 62, 66 and KAR2p PAG1493RP YPL243w SRP68 signal recognition particle subunit 1 syntenie PAG1493UP YPL246c unknown function 1 syntenie.YPL245w: has A(P- loop), len 454 YPL224c:len 339 PAG1494RP YOL095c HRE571 sim to S. aureus helicase pcrA 1 syntenie.YOL094c:RFC4:len323 aa, replication factorC PAG1494UP YOL093w unknown function 1 syntenie. End of syntenie YJL007 unknown function 1 syntenie. End of syntenie PAG1495RP YGL227w with sim to Dictyostelium non-receptor 1 tyrosine kinase U32174; contains WW(WWP) domain of about 40aa which is also found in dystrophin, Rsp5p, and Ess1p PAG1495UP 4 PAG1496RP YER020w GPA2 guanine nucleotide binding protein alpha 1 subunit involved in regulation of the cAMP pathway during mating PAG1496UP YJR109c CPA2 Carbamoylphosphat synthase, arginine 1 specific PAG1497RP YPL022w RAD1 component of the nucleotide excision 1 repairosome, homolog of human XPF xeroderma pigmentosum gene pRduct and the mammalian ERCC-4 protein, required for double-strand-break induced recombination PAG1497UP YPL016w ADR6 SWI1; Component of the SWI/SNF global 1 end of gene covered by RP-SRS transcription activator complex, acts to assist gene-specific activators PAG1499RP YOR021c unknown function 1 PAG1499UP YPR133c unknown function 1 PAG1500RP YOL094c RFC4 replication factor c 1 PAG1500UP 4 PAG1501RP MITO- align DNA PAG1501UP MITO- align DNA PAG1502RP YLR056w ERG3 ERG3:C-5 sterol desaturase, an iron non- 1 syntenie; heme oxygen-required enzyme of the ergosterol biosynthesis pathway, ER retention signal PAG1502UP YPL055c SPT8 member of the TBP class of SPT proteins 1 syntenie that alter transcription start site selection, functionally relatet to SPT3p and TBP PAG1503RP YNL297c unknown 1 syntenie PAG1503UP YNL294c unknown, has 6 potential TMD 1 YPL296w: q-ORF, len 104.YPL295w: len 524, unknown PAG1504RP MITO- DNA PAG1504UP MITO- DNA PAG1505RP YOR007c sim to protein phosphatases 1 PAG1505UP YML002w unknown function 1 syntenie. Two genes covered on UP-SRS YML003w unknown protein 1 syntenie with YML002w PAG1506RP YLR454w unknown function 1 PAG1506UP 4 PAG1507RP YBR053c protein with sim to glucan-1,3-beta- 1 glucosidase PAG1507UP YDR028c SRN1 REG1:regulatory subunit for protein 1 phosphatase GLC7, required for glucose repression PAG1508RP 4 PAG1508UP YKL211c TRP3 Anthranilate synthase component II, first 1 useful as TRP-selectable marker and fourth steps in Tryptophan biosynthesis gene? pathway PAG1509RP YOR166c unknown function 1 PAG1509UP 4 PAG1510RP YGR056w unknown function, has high sim to 1

syntenie YLR357w PAG1510UP YGR057c unknown function 1 syntenie

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L19: Entry 1 of 5

File: PGPB

Oct 18, 2001

DOCUMENT-IDENTIFIER: US 20010031727 A1

TITLE: Therapies using hemoproteins

Detail Description Paragraph (114):

[0150] The NO and GSNO consumption activities were low in extracts from untreated cells, but strongly induced by SNO treatment (not shown). The chromatographic fraction containing the activities exhibited a distinctive hemoglobin spectrum following SNO exposure (FIG. 7D). *E. coli* possesses a flavohemoglobin (HMP) of unknown function that is reportedly induced by NO (Poole, R. K. Ioannidis, N & Orii, Proc. R. Soc. Lond. B. Biol. Sci., 255:251-258 (1994); Poole, R. K. et al. Microbiology 142:1141-1148 (1996), Poole, R. K. et al., Microbiology 143:1557-1565 (1997); Poole, R. K. et al., J. Bacteriol., 178:5487-5492 (1996)). Further purification of the hemoprotein by SDS gel electrophoresis, assays for ferric reductase activity (Eschenbrenner, M. et al., Biochem. Biophys. Res. Commun., 198:127-131 (1994)), and studies of an HMP deficient mutant, identified the NO/GSNO metabolizing activities with HMP. In particular, extracts from the HMP mutant were unable to catalyze NADH-dependent NO consumption (FIG. 8A), and HMP deficiency markedly increased susceptibility to SNO-induced cytostasis and severely compromised the inducible resistance to nitrosative stress (FIG. 8B).

? b 155, 5, agri
16may02 12:51:07 User242957 Session D434.3
\$0.13 0.040 DialUnits File155
\$0.13 Estimated cost File155
\$0.22 0.040 DialUnits File5
\$0.22 Estimated cost File5
OneSearch, 2 files, 0.079 DialUnits FileOS
\$0.17 TELNET
\$0.52 Estimated cost this search
\$0.53 Estimated total session cost 0.305 DialUnits

SYSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1966-2002/May W2
*File 155: This file has been reloaded. Accession numbers have changed.
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(c) 2002 Cambridge Sci Abs
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File 144:Pascal 1973-2002/May W2
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File 306:Pesticide Fact File 1998/Jun
(c) 1998 BCPC
*File 306: File has been updated & reloaded. See HELP NEWS 306. New
Bluesheet available in F415 & at URL <http://library.dialog.com/bluesheets>.
File 357:Derwent Biotech Res 1982-2002/Feb W4
(c) 2002 Thomson Derwent & ISI
*File 357: Price changes as of 1/1/02. Please see HELP RATES 357.

? ds
>>>No sets currently exist
? s no (w) polyadenyl? (w) (sequenc? or signal?)
Processing
Processed 10 of 18 files ...
Completed processing all files
6800419 NO
30113 POLYADENYL?
2533366 SEQUENC?
1804260 SIGNAL?
S1 31 NO (W) POLYADENYL? (W) (SEQUENC? OR SIGNAL?)

? s s1 and py<1998
Processing
>>>File 10 processing for PY= : PY=1998
>>> started at PY=A stopped at PY=196U
Processing
Processed 10 of 18 files ...
Processing
>>>One or more prefixes are unsupported
>>> or undefined in one or more files.
Processing
Completed processing all files
31 S1
65085893 PY<1998
S2 20 S1 AND PY<1998

? rd
>>>Duplicate detection is not supported for File 235.
>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.
...completed examining records
S3 10 RD (unique items)
? t s3/3,ab/all
>>>No matching display code(s) found in file(s): 65, 235, 306

3/3,AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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09378518 97271384 PMID: 9126335
Characterization of a cDNA encoding Arabidopsis thaliana inositol
1,3,4-trisphosphate 5/6-kinase.
Wilson M P; Majerus P W
Division of Hematology-Oncology, Washington University School of
Medicine, St. Louis, Missouri 63110, USA.
Biochemical and biophysical research communications (UNITED STATES). Mar
27 1997, 232 (3) p678-81, ISSN 0006-291X Journal Code: 0372516
Contract/Grant No.: HL 07088; HL; NHLBI; HL 16634; HL; NHLBI; HL 55672;
HL; NHLBI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

* We have sequenced and recombinantly expressed as a fusion protein an
expressed sequence tag clone (GB Z25963) from Arabidopsis thaliana that
represents the plant homologue of human inositol 1,3,4 trisphosphate
5/6-kinase. The 1365 base pair clone has an open reading frame of 960 base
pairs that predicts a protein product of 36.2 kDa, with a pI of 6.1. There
is no polyadenylation signal or poly (A) tail, suggesting
that additional 3' sequence remains to be identified. The amino acid
sequence is 30% identical to the human protein. There are several short
regions with particularly high degrees of identity between the human and
Arabidopsis protein sequences, and these may be useful in identifying the

08300839 95059933 PMID: 7969906

Expression of polyadenylated and non-polyadenylated trkC transcripts in the rodent central nervous system.

Jaber M; Merlio J P; Bloch B

U.R.A. C.N.R.S. 1200-Laboratoire d'Histologie-Embryologie (U.F.R. II) Universite de Bordeaux II, France.

Neuroscience (ENGLAND) Jul 1994, 61 (2) p245-56, ISSN

0306-4522 Journal Code: 7605074

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We have previously isolated a full-length cDNA clone encoding rat TrkC, a member of the Trk family of tyrosine kinase receptors, that specifically mediates biological responses to neurotrophin-3. Here, we report the identification of five major trkC transcripts in the adult and developing rat and mouse brain suggesting the presence of several TrkC receptors. Northern blot hybridizations revealed that three of these trkC transcripts (of 14, 3.9 and 4.8 kb) were poly(A)+ messenger RNAs, while the two others, of shorter size (1.1 and 0.7 kb), were poly(A)- messenger RNAs. All transcripts were expressed in 11 brain regions but poly(A)- messenger RNAs were found at much higher levels than poly(A)+ messenger RNAs in the cerebellum. Hybridization with five oligonucleotide and two complementary DNA probes, corresponding to different parts of the full-length trkC complementary DNA, revealed that the two poly(A)- transcripts may encode for receptors truncated in their extracellular and kinase intracellular domains. During ontogeny, poly(A)- trkC messenger RNAs were found at low amounts at prenatal and early postnatal ages with a drastic increase in the cerebellum at postnatal day 30. No poly(A)- transcript was identified for the trk B gene. In situ hybridization revealed that trkC messenger RNAs are expressed both in granular and Purkinje cells in the cerebellum. Northern blot on RNA extracted from mice mutant strains with degeneration of either granular or both granular and Purkinje cells suggested that poly(A)- and poly(A)+ trkC messenger RNAs are expressed within the same cells. We have demonstrated the existence of several trkC transcripts that differ both by their size and polyadenylation. This phenomenon could be of physiological relevance in regulating TrkC functions. To the best of our knowledge, this is an original feature for a mammalian gene expression. Studies focused on poly(A)- messenger RNAs could give rise to the identification of other genes expressed in a similar fashion.

3/3,AB/4 (Item 4 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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08059537 94191102 PMID: 7511419

Poly(A)+ ribonucleic acids are enriched in spermatocyte nuclei but not in chromatoid bodies in the rat testis.

Morales C R; Hecht N B

Department of Anatomy and Cell Biology, McGill University, Montreal, Quebec, Canada.

Biology of reproduction (UNITED STATES) Feb 1994, 50 (2)

p309-19, ISSN 0006-3363 Journal Code: 0207224

Contract/Grant No.: HD28832; HD; NICHD

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

To determine whether male germ cells contain specific storage sites for poly(A)+ RNAs, in situ hybridizations were performed with sections of rat testis and a [3H]polyuridylic acid probe. The highest levels of poly(A)+ RNA were found in spermatocytes and round spermatids, while lower levels of

Georgatsou E; Mavrogiannis LA; Fragiadakis GS; Alexandraki D
Foundation for Research and Technology-Hellas, Institute of Molecular
Biology and Biotechnology, Greece.

Journal of biological chemistry (UNITED STATES) May 23 1997, 272

(21) p13786-92, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

9/3/4 / (Item 4 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

09083129 96425877 PMID: 8828219

Isolation of the mRNA-capping enzyme and **ferric-reductase**
-related genes from *Candida albicans*.

Yamada-Okabe T; Shimmi O; Doi R; Mizumoto K; Arisawa M; Yamada-Okabe H

Department of Hygiene, School of Medicine, Yokohama City University,
Japan.

Microbiology (ENGLAND) Sep 1996, 142 (Pt 9) p2515-23, ISSN

1350-0872 Journal Code: BXW

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

9/3/5 (Item 5 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

09030351 97022063 PMID: 8868423

Candida albicans has a cell-associated **ferric-reductase**
activity which is regulated in response to levels of iron and copper.

Morrissey JA; Williams PH; Cashmore AM

Department of Genetics, University of Leicester, UK.

Microbiology (ENGLAND) Mar 1996, 142 (Pt 3) p485-92, ISSN

1350-0872 Journal Code: BXW

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

9/3/6 (Item 6 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

08974373 96278882 PMID: 8662973

The **FRE1 ferric reductase** of *Saccharomyces*
cerevisiae is a cytochrome b similar to that of NADPH oxidase.

Shatwell KP; Dancis A; Cross AR; Klausner RD; Segal AW

Department of Medicine, University College London, 5 University Street,
London WC1E 6JJ, United Kingdom.

Journal of biological chemistry (UNITED STATES) Jun 14 1996, 271

(24) p14240-4, ISSN 0021-9258 Journal Code: HIV

Contract/Grant No.: AI24838, AI, NIAID

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

9/3/7 (Item 7 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

08696738 96132030 PMID: 8553699

DNA sequence analysis of a 13 kbp fragment of the left arm of **yeast**
chromosome XV containing seven new open reading frames.

Casamayor A; Aldea M; Casas C; Herrero E; Gamo FJ; Lafuente MJ; Gancedo C
; Arino J
Dept Bioquímica i Biologia Molecular, Fac. Veterinaria, Universitat
Autònoma de Barcelona, Spain.

Yeast (ENGLAND) Oct 1995, 11 (13) p1281-8, ISSN 0749-503X

Journal Code: YEA

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

9/3/8 (Item 8 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08495931 95237204 PMID: 7720713

AFT1: a mediator of iron regulated transcriptional control in
Saccharomyces cerevisiae.

Yamaguchi-Iwai Y; Dancis A; Klausner RD
Cell Biology and Metabolism Branch, National Institute of Child Health
and Human Development, National Institutes of Health, Bethesda, MD, USA.

EMBO journal (ENGLAND) Mar 15 1995, 14 (6) p1231-9, ISSN
0261-4189 Journal Code: EMB

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

9/3/9 (Item 9 from file: 155).
DIALOG(R) File 155:MEDLINE(R)

08383261 95070025 PMID: 7526783

Potentiation of bleomycin cytotoxicity in **Saccharomyces
cerevisiae**.

Moore CW
Department of Microbiology, City University of New York Medical
School/Sophie Davis School of Biomedical Education, New York 10031.

Antimicrobial agents and chemotherapy (UNITED STATES) Jul 1994,
38 (7) p1615-9, ISSN 0066-4804 Journal Code: 6HK

Contract/Grant No.: CA25609, CA, NCI

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

9/3/10 (Item 10 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08241456 94378726 PMID: 8091865

Sequencing of a 13.2 kb segment next to the left telomere of **yeast**
chromosome XI revealed five open reading frames and recent recombination
events with the right arms of chromosomes III and V.

Alexandraki D; Tzermia M
Foundation for Research and Technology-HELLAS, Institute of Molecular
Biology and Biotechnology, Crete, Greece.

Yeast (ENGLAND) Apr 1994, 10 Suppl A pS81-91, ISSN 0749-503X
Journal Code: YEA

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

9/3/11 (Item 11 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08138846 94217704 PMID: 8164662

Two distinctly regulated genes are required for ferric reduction, the first step of iron uptake in *Saccharomyces cerevisiae*.

Georgatsou E; Alexandraki D

Foundation for Research and Technology-HELLAS, Institute of Molecular Biology and Biotechnology, Crete, Greece.

Molecular and cellular biology (UNITED STATES) May 1994, 14 (5)

p3065-73, ISSN 0270-7306 Journal Code: NGY

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

9/3/12 (Item 12 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

07258051 90220614 PMID: 2183029

Genetic evidence that **ferric reductase** is required for iron uptake in *Saccharomyces cerevisiae*.

Dancis A; Klausner RD; Hinnebusch AG; Barriocanal JG

Cell Biology and Metabolism Branch, National Institute of Child Health and Human Development, Bethesda, Maryland 20892.

Molecular and cellular biology (UNITED STATES) May 1990, 10 (5)

p2294-301, ISSN 0270-7306 Journal Code: NGY

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

9/3/13 (Item 13 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

07051042 93309468 PMID: 8321236

The fission yeast **ferric reductase** gene *frp1+* is required for ferric iron uptake and encodes a protein that is homologous to the gp91-phox subunit of the human NADPH phagocyte oxidoreductase.

Roman DG; Dancis A; Anderson GJ; Klausner RD

Cell Biology and Metabolism Branch, National Institute of Child Health and Human Development, Bethesda, Maryland 20892.

Molecular and cellular biology (UNITED STATES) Jul 1993, 13 (7)

p4342-50, ISSN 0270-7306 Journal Code: NGY

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

9/3/14 (Item 14 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

06891008 93057491 PMID: 1431884

Ferric iron reduction and iron assimilation in *Saccharomyces cerevisiae*.

Anderson GJ; Lesuisse E; Dancis A; Roman DG; Labbe P; Klausner RD

Cell Biology and Metabolism Branch, National Institute of Child Health and Human Development, Bethesda, Maryland 20892.

Journal of inorganic biochemistry (UNITED STATES) Aug 15-Sep 1992

, 47 (3-4) p249-55, ISSN 0162-0134 Journal Code: JAR

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

9/3/15 (Item 1 from file: 5)

DIALOG(R) File 5:Biosis Previews(R)

(c) 2002 BIOSIS. All rts. reserv.

11557976 BIOSIS NO.: 199800339308

Introduction of artificially synthesized gene, *refrel*, which encodes **yeast ferric reductase** into tobacco plants.

AUTHOR: Ohki Hiroyuki; Yamaguchi Hirotaka; Nakanishi Hiromi; Mori Satoshi

AUTHOR ADDRESS: Dep. Appl. Biol. Chem., Univ. Tokyo, Tokyo**Japan

JOURNAL: Plant and Cell Physiology 39 (SUPPL.):pS135 1998

CONFERENCE/MEETING: 1998 Annual Meeting of the Japanese Society of Plant Pathologists Tokyo, Japan May 3-5, 1998

SPONSOR: Japanese Society of Plant Pathologists

ISSN: 0032-0781

RECORD TYPE: Citation

LANGUAGE: English

9/3/16 (Item 2 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2002 BIOSIS. All rts. reserv.

11239791 BIOSIS NO.: 199800021123

Ascorbate stabilization at the plasma membrane of **Saccharomyces cerevisiae**.

AUTHOR: Navas P(a); Cordoba F; Villalba J M; Crane F L; Clarke C F; Santos-Ocana C

AUTHOR ADDRESS: (a)Dep. Biol. Celular, Univ. Cordoba, 14004 Cordoba**Spain

JOURNAL: Molecular Biology of the Cell 8 (SUPPL.):p293A Nov., 1997

CONFERENCE/MEETING: 37th Annual Meeting of the American Society for Cell Biology Washington, D.C., USA December 13-17, 1997

SPONSOR: American Society for Cell Biology

ISSN: 1059-1524

RECORD TYPE: Citation

LANGUAGE: English

9/3/17 (Item 3 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2002 BIOSIS. All rts. reserv.

09839271 BIOSIS NO.: 199598294189

AFT1: Activator of ferrous transport regulates iron uptake transcriptionally in **S. cerevisiae**.

AUTHOR: Yamaguchi-Iwai Yuko; Yuan Daniel S; Dancis Andrew; Klausner Richard D

AUTHOR ADDRESS: Cell Biol., Metabolism Branch, NICHD, NIH, Bethesda, MD 20892**USA

JOURNAL: Journal of Cellular Biochemistry Supplement 0 (21A):p251 1995

CONFERENCE/MEETING: Keystone Symposium on Metal and Oxygen Regulation of Gene Expression Park City, Utah, USA March 18-24, 1995

ISSN: 0733-1959

RECORD TYPE: Citation

LANGUAGE: English

9/3/18 (Item 4 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2002 BIOSIS. All rts. reserv.

09839257 BIOSIS NO.: 199598294175

The FRE1 and FRE2 **Saccharomyces cerevisiae** genes essential for iron uptake participate also in copper metabolism.

AUTHOR: Georgatsou E(a); Mavrogiannis L; Alexandraki D(a)

AUTHOR ADDRESS: (a)Foundation Res. Technol.-HELLAS, Inst. Mol. Biol.



Biotechnol., PO Box 1527, Heraklion 711 10 Cre**Greece
JOURNAL: Journal of Cellular Biochemistry Supplement 0 (21A):p248
1995
CONFERENCE/MEETING: Keystone Symposium on Metal and Oxygen Regulation of
Gene Expression Park City, Utah, USA March 18-24, 1995
ISSN: 0733-1959
RECORD TYPE: Citation
LANGUAGE: English

9/3/19 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

09839256 BIOSIS NO.: 199598294174
The involvement of stress-related transcription factors in the
iron-dependent regulation of the FRE2 **ferric reductase** gene
of **Saccharomyces cerevisiae**.
AUTHOR: Alexandraki D(a); Klinakis A; Georgatsou E(a)
AUTHOR ADDRESS: (a)Foundation Res. Technol.-HELLAS, Inst. Mol. Biol.
Biotechnol., PO Box 1527, Heraklion 711 10 Cre**Greece
JOURNAL: Journal of Cellular Biochemistry Supplement 0 (21A):p248
1995
CONFERENCE/MEETING: Keystone Symposium on Metal and Oxygen Regulation of
Gene Expression Park City, Utah, USA March 18-24, 1995
ISSN: 0733-1959
RECORD TYPE: Citation
LANGUAGE: English

9/3/20 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

09628693 BIOSIS NO.: 199598083611
A genetic approach to elucidating eukaryotic iron metabolism.
AUTHOR: Klausner Richard D; Dancis Andrew
AUTHOR ADDRESS: Cell Biol. Metabolism Branch, NICHD, NIH, Bethesda, MD
20892**USA
JOURNAL: FEBS Letters 355 (2):p109-113 1994
ISSN: 0014-5793
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

9/3/21 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

08204884 BIOSIS NO.: 000094017157
FERRIC REDUCTASE OF SACCHAROMYCES-CEREVISIAE
MOLECULAR CHARACTERIZATION ROLE IN IRON UPTAKE AND TRANSCRIPTIONAL
CONTROL BY IRON
AUTHOR: DANCIS A; ROMAN D G; ANDERSON G J; HINNEBUSCH A G; KLAUSNER R D
AUTHOR ADDRESS: CELL BIOL. METABOLISM BRANCH, LAB. MOL. GENETICS, NATIONAL
INST. CHILD HEALTH, HUMAN DEVELOPMENT, BETHESDA, MD. 20892.
JOURNAL: PROC NATL ACAD SCI U S A 89 (9). 1992. 3869-3873. 1992
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

9/3/22 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

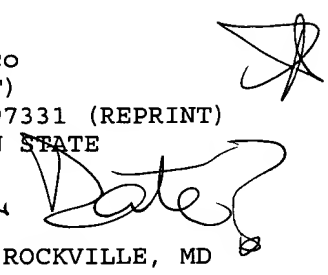
07409055 Genuine Article#: 162GE No. References: 32
Title: The induction of the 'turbo reductase' is inhibited by
cycloheximide, cordycepin and ethylene inhibitors in Fe-deficient
cucumber (*Cucumis sativus* L.) plants
Author(s): Romera FJ (REPRINT) ; Alcantara E; delaGuardia MD
Corporate Source: ESCUELA TS INGN AGRON & MONTES, DEPT AGRON, APDO
3048/E-14080 CORDOBA//SPAIN/ (REPRINT)
Journal: PROTOPLASMA, 1998, V205, N1-4, P156-162
ISSN: 0033-183X Publication date: 19980000
Publisher: SPRINGER-VERLAG WIEN, SACHSENPLATZ 4-6, PO BOX 89, A-1201
VIENNA, AUSTRIA
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/23 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

07341315 Genuine Article#: 153DJ No. References: 22
Title: Siderophore-mediated iron uptake in *Saccharomyces*
cerevisiae: the SIT1 gene encodes a ferrioxamine B permease that
belongs to the major facilitator superfamily
Author(s): Lesuisse E (REPRINT) ; SimonCasteras M; Labbe P
Corporate Source: UNIV PARIS 07, INST JACQUES MONOD, LAB BIOCHIM
PORPHYRINES, TOUR 43, 2 PL JUSSIEU/F-75251 PARIS 05//FRANCE/ (REPRINT)
Journal: MICROBIOLOGY-UK, 1998, V144, 12 (DEC), P3455-3462
ISSN: 1350-0872 Publication date: 19981200
Publisher: SOC GENERAL MICROBIOLOGY, MARLBOROUGH HOUSE, BASINGSTOKE RD,
SPENCERS WOODS, READING RG7 1AE, BERKS, ENGLAND
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)


9/3/24 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

07070603 Genuine Article#: 120KG No. References: 33
Title: Expression of the yeast FRE genes in transgenic tobacco
Author(s): Samuelsen AI; Martin RC; Mok DWS; Mok MC (REPRINT)
Corporate Source: OREGON STATE UNIV, DEPT HORT/CORVALLIS//OR/97331 (REPRINT)
; OREGON STATE UNIV, DEPT HORT/CORVALLIS//OR/97331; OREGON STATE
UNIV, CTR GENE RES & BIOTECHNOL/CORVALLIS//OR/97331
Journal: PLANT PHYSIOLOGY, 1998, V118, N1 (SEP), P51-58
ISSN: 0032-0889 Publication date: 19980900
Publisher: AMER SOC PLANT PHYSIOLOGISTS, 15501 MONONA DRIVE, ROCKVILLE, MD
20855
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)



9/3/25 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

07056793 Genuine Article#: 119JT No. References: 32
Title: Metalloregulation of FRE1 and FRE2 homologs in *Saccharomyces*
cerevisiae
Author(s): Martins LJ; Jensen LT; Simons JR; Keller GL; Winge DR (REPRINT)
Corporate Source: UNIV UTAH, HLTH SCI CTR/SALT LAKE CITY//UT/84132 (REPRINT)



; UNIV UTAH, HLTH SCI CTR/SALT LAKE CITY//UT/84132
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1998, V273, N37 (SEP 11), P
23716-23721
ISSN: 0021-9258 Publication date: 19980911
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE
PIKE, BETHESDA, MD 20814
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/26 (Item 5 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

07013335 Genuine Article#: 114NY No. References: 13
Title: Site-directed mutagenesis of the **yeast** multicopper oxidase
Fet3p
Author(s): Askwith CC; Kaplan J (REPRINT)
Corporate Source: UNIV UTAH, SCH MED, DEPT PATHOL, DIV CELL BIOL & IMMUNOL,
50 N MED DR/SALT LAKE CITY//UT/84132 (REPRINT); UNIV UTAH, SCH MED, DEPT
PATHOL, DIV CELL BIOL & IMMUNOL/SALT LAKE CITY//UT/84132
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1998, V273, N35 (AUG 28), P
22415-22419
ISSN: 0021-9258 Publication date: 19980828
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE
PIKE, BETHESDA, MD 20814
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/27 (Item 6 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06987037 Genuine Article#: 106YR No. References: 136
Title: The molecular biology of metal ion transport in **Saccharomyces**
cerevisiae
Author(s): Eide DJ (REPRINT)
Corporate Source: UNIV MISSOURI, NUTR SCI PROGRAM/COLUMBIA//MO/65203
(REPRINT)
Journal: ANNUAL REVIEW OF NUTRITION, 1998, V18, P441-469
ISSN: 0199-9885 Publication date: 19980000
Publisher: ANNUAL REVIEWS INC, 4139 EL CAMINO WAY, PO BOX 10139, PALO ALTO,
CA 94303-0139
Language: English Document Type: REVIEW (ABSTRACT AVAILABLE)

Handwritten: Date?

9/3/28 (Item 7 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06628565 Genuine Article#: ZG113 No. References: 27
Title: Genetic analysis of iron uptake in the **yeast**
Saccharomyces cerevisiae
Author(s): Dancis A (REPRINT)
Corporate Source: UNIV PENN, DEPT MED, DIV HEMATOL ONCOL, 1009 STELLAR CHASE
LABS, 422 CURIE BLVD/PHILADELPHIA//PA/19104 (REPRINT); NICHHD, CELL BIOL
& METAB BRANCH, NIH/BETHESDA//MD/20892
Journal: JOURNAL OF PEDIATRICS, 1998, V132, N3, 2, S (MAR), PS24-S29
ISSN: 0022-3476 Publication date: 19980300
Publisher: MOSBY-YEAR BOOK INC, 11830 WESTLINE INDUSTRIAL DR, ST LOUIS, MO
63146-3318
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

Handwritten: Date?

9/3/29 (Item 8 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06620438 Genuine Article#: ZF226 No. References: 42

Title: Coenzyme Q(6) and iron reduction are responsible for the
extracellular ascorbate stabilization at the plasma membrane of
Saccharomyces cerevisiae

Author(s): SantosOcana C; Cordoba F; Crane FL; Clarke CF; Navas P
(REPRINT)

Corporate Source: UNIV CORDOBA, FAC CIENCIAS, DEPT BIOL CELULAR, AVE SAN
ALBERTO MAGNO S-N/E-14004 CORDOBA//SPAIN/ (REPRINT); UNIV CORDOBA, FAC
CIENCIAS, DEPT BIOL CELULAR/E-14004 CORDOBA//SPAIN/; UNIV HUELVA, DEPT
CIENCIAS AGROFORESTALES/HUELVA 21819//SPAIN/; PURDUE UNIV, DEPT BIOL
SCI/W LAFAYETTE//IN/47907; UNIV CALIF LOS ANGELES, INST MOL BIOL, DEPT
CHEM & BIOCHEM/LOS ANGELES//CA/90095

Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1998, V273, N14 (APR 3), P
8099-8105

ISSN: 0021-9258 Publication date: 19980403

Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE
PIKE, BETHESDA, MD 20814

Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/30 (Item 9 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06609349 Genuine Article#: ZE277 No. References: 43

Title: Influence of copper depletion on iron uptake mediated by SFT, a
stimulator of Fe transport

Author(s): Yu JM (REPRINT) ; WesslingResnick M

Corporate Source: HARVARD UNIV, SCH PUBL HLTH, DEPT NUTR, 666 HUNTINGTON
AVE/BOSTON//MA/02115 (REPRINT)

Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1998, V273, N12 (MAR 20), P
6909-6915

ISSN: 0021-9258 Publication date: 19980320

Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE
PIKE, BETHESDA, MD 20814

Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/31 (Item 10 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06607537 Genuine Article#: ZE202 No. References: 36

Title: The surface of rat hepatocytes can transfer iron from stable
chelates to external acceptors

Author(s): Scheiber B; Goldenberg H (REPRINT)

Corporate Source: UNIV VIENNA, INST MED CHEM, WAEHRINGERSTR 10/A-1090
VIENNA//AUSTRIA/ (REPRINT); UNIV VIENNA, INST MED CHEM/A-1090
VIENNA//AUSTRIA/

Journal: HEPATOLOGY, 1998, V27, N4 (APR), P1075-1080

ISSN: 0270-9139 Publication date: 19980400

Publisher: W B SAUNDERS CO, INDEPENDENCE SQUARE WEST CURTIS CENTER, STE
300, PHILADELPHIA, PA 19106-3399

Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/32 (Item 11 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06603908 Genuine Article#: ZD917 No. References: 37

Title: Regulation of high affinity iron uptake in the yeast
Saccharomyces cerevisiae - Role of dioxygen and Fe(II)
Author(s): Hassett RF; Romeo AM; Kosman DJ (REPRINT)
Corporate Source: SUNY BUFFALO, SCH MED & BIOMED SCI, DEPT BIOCHEM, 140
FARBER HALL, 3435 MAIN ST/BUFFALO//NY/14214 (REPRINT); SUNY BUFFALO, SCH
MED & BIOMED SCI, DEPT BIOCHEM/BUFFALO//NY/14214
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1998, V273, N13 (MAR 27), P
7628-7636
ISSN: 0021-9258 Publication date: 19980327
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE
PIKE, BETHESDA, MD 20814
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/33 (Item 12 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06579193 Genuine Article#: ZC522 No. References: 42
Title: Helicobacter pylori ribBA-mediated riboflavin production is involved
in tron acquisition
Author(s): Worst DJ; Gerrits MM; VandenbrouckeGrauls CMJE; Kusters JG
(REPRINT)
Corporate Source: FREE UNIV AMSTERDAM, FAC MED, DEPT MED MICROBIOL, VAN DER
BOECHORSTSTR 7/NL-1081 BT AMSTERDAM//NETHERLANDS/ (REPRINT); FREE UNIV
AMSTERDAM, FAC MED, DEPT MED MICROBIOL/NL-1081 BT
AMSTERDAM//NETHERLANDS/
Journal: JOURNAL OF BACTERIOLOGY, 1998, V180, N6 (MAR), P1473-1479
ISSN: 0021-9193 Publication date: 19980300
Publisher: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW,
WASHINGTON, DC 20005-4171
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/34 (Item 13 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06542680 Genuine Article#: ZA144 No. References: 11
Title: Cytochrome P-450 reductase is responsible for the ferrireductase
activity associated with isolated plasma membranes of
Saccharomyces cerevisiae
Author(s): Lesuisse E (REPRINT) ; CasterasSimon M; Labbe P
Corporate Source: UNIV PARIS 07, INST JACQUES MONOD, LAB BIOCHIM
PORPHYRINES, TOUR 43, 2 PL JUSSIEU/F-75251 PARIS 05//FRANCE/ (REPRINT)
Journal: FEMS MICROBIOLOGY LETTERS, 1997, V156, N1 (NOV 1), P147-152
ISSN: 0378-1097 Publication date: 19971101
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/35 (Item 14 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06453998 Genuine Article#: BK30A No. References: 124
Title: Molecular biology of iron transport in fungi
Author(s): Leong SA (REPRINT) ; Winkelmann G
Corporate Source: UNIV WISCONSIN, USDA ARS/MADISON//WI/53706 (REPRINT); UNIV
WISCONSIN, DEPT PLANT PATHOL/MADISON//WI/53706; UNIV TUBINGEN, /D-72076
TUBINGEN//GERMANY/
, 1998, V35, P147-186
ISSN: 0161-5149 Publication date: 19980000
Publisher: MARCEL DEKKER, 270 MADISON AVE, NEW YORK, NY 10016METAL IONS IN

BIOLOGICAL SYSTEMS

Series: METAL IONS IN BIOLOGICAL SYSTEMS
Language: English Document Type: REVIEW

9/3/36 (Item 15 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06334656 Genuine Article#: YK389 No. References: 37
Title: **Saccharomyces cerevisiae** mutants altered in vacuole
function are defective in copper detoxification and iron-responsive
gene transcription
Author(s): Szczypka MS; Zhu ZW; Silar P; Thiele DJ (REPRINT)
Corporate Source: UNIV MICHIGAN,SCH MED, DEPT BIOL CHEM/ANN ARBOR//MI/48109
(REPRINT); UNIV MICHIGAN,SCH MED, DEPT BIOL CHEM/ANN ARBOR//MI/48109
Journal: YEAST, 1997, V13, N15 (DEC), P1423-1435
ISSN: 0749-503X Publication date: 19971200
Publisher: JOHN WILEY & SONS LTD, BAFFINS LANE CHICHESTER, W SUSSEX,
ENGLAND PO19 1UD
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/37 (Item 16 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05993995 Genuine Article#: XM844 No. References: 28
Title: Molecular biology of iron and zinc uptake in eukaryotes
Author(s): Eide D (REPRINT)
Corporate Source: UNIV MISSOURI,NUTR SCI PROGRAM, 217 GWYNN
HALL/COLUMBIA//MO/65211 (REPRINT)
Journal: CURRENT OPINION IN CELL BIOLOGY, 1997, V9, N4 (AUG), P
573-577
ISSN: 0955-0674 Publication date: 19970800
Publisher: CURRENT BIOLOGY LTD, 34-42 CLEVELAND STREET, LONDON, ENGLAND W1P
6LB
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/38 (Item 17 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05958160 Genuine Article#: XK165 No. References: 41
Title: Homeostatic regulation of copper uptake in **yeast** via direct
binding of MAC1 protein to upstream regulatory sequences of FRE1 and
CTR1
Author(s): YamaguchiIwai Y; Serpe M; Haile D; Yang WM; Kosman DJ; Klausner
RD; Dancis A (REPRINT)
Corporate Source: UNIV PENN,STELLAR CHANCE LABS 1009, DEPT MED, DIV HEMATOL
ONCOL, 422 CURIE BLVD/PHILADELPHIA//PA/19104 (REPRINT); NICHHD,CELL
BIOL & METAB BRANCH, NIH/BETHESDA//MD/20892; SUNY ALBANY,SCH MED &
BIOMED SCI, DEPT BIOCHEM/BUFFALO//NY/14214; NCI,BIOCHEM LAB,
NIH/BETHESDA//MD/20892
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1997, V272, N28 (JUL 11), P
17711-17718
ISSN: 0021-9258 Publication date: 19970711
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE
PIKE, BETHESDA, MD 20814
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/39 (Item 18 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05887040 Genuine Article#: XE435 No. References: 62
Title: The AFT1 transcriptional factor is differentially required for
expression of high-affinity iron uptake genes in **Saccharomyces
cerevisiae**
Author(s): Casas C; Aldea M; Espinet C; Gallego C; Gil R; Herrero E
(REPRINT)
Corporate Source: UNIV LLEIDA, FAC MED, DEPT CIENCIAS MED BASIQUES, ROVIRA
ROURE 44/LLEIDA 25198//SPAIN/ (REPRINT); UNIV LLEIDA, FAC MED, DEPT
CIENCIAS MED BASIQUES/LLEIDA 25198//SPAIN/
Journal: YEAST, 1997, V13, N7 (JUN 15), P621-637
ISSN: 0749-503X Publication date: 19970615
Publisher: JOHN WILEY & SONS LTD, BAFFINS LANE CHICHESTER, W SUSSEX,
ENGLAND PO19 1UD
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/40 (Item 19 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05790026 Genuine Article#: WX569 No. References: 54
Title: Characterization of the FET4 protein of **yeast** - Evidence for a
direct role in the transport of iron
Author(s): Dix D; Bridgham J; Broderius M; Eide D (REPRINT)
Corporate Source: UNIV MISSOURI, DEPT FOOD SCI & HUMAN
NUTR/COLUMBIA//MO/65211 (REPRINT); UNIV MINNESOTA, DEPT BIOCHEM & MOL
BIOL/DULUTH//MN/55812
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1997, V272, N18 (MAY 2), P
11770-11777
ISSN: 0021-9258 Publication date: 19970502
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE
PIKE, BETHESDA, MD 20814
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

9/3/41 (Item 20 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05463514 Genuine Article#: WA564 No. References: 15
Title: AN OXIDASE-PERMEASE-BASED IRON TRANSPORT-SYSTEM IN
SCHIZOSACCHAROMYCES-POMBE AND ITS EXPRESSION IN **SACCHAROMYCES-
CEREVISIAE**
Author(s): ASKWITH C; KAPLAN J
Corporate Source: UNIV UTAH, SCH MED, DEPT PATHOL, DIV CELL BIOL & IMMUNOL, 50
N MED DR/SALT LAKE CITY//UT/84132; UNIV UTAH, SCH MED, DEPT PATHOL, DIV
CELL BIOL & IMMUNOL/SALT LAKE CITY//UT/84132
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1997, V272, N1 (JAN 3), P
401-405
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/42 (Item 21 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05407223 Genuine Article#: VW686 No. References: 27
Title: INTRAMEMBRANE BIS-HEME MOTIF FOR TRANSMEMBRANE ELECTRON-TRANSPORT
CONSERVED IN A **YEAST** IRON REDUCTASE AND THE HUMAN NADPH OXIDASE
Author(s): FINEGOLD AA; SHATWELL KP; SEGAL AW; KLAUSNER RD; DANCIS A

Corporate Source: UNIV PENN,DEPT MED,DIV HEMATOL ONCOL,1009 STELLAR CHANCE
LABS,422 CURIE BLVD/PHILADELPHIA//PA/19104; NICHHD,CELL BIOL & METAB
BRANCH,NIH/BETHESDA//MD/20892; UNIV LONDON UNIV COLL,SCH MED,DEPT
MED/LONDON WC1E 6JJ//ENGLAND/
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1996, V271, N49 (DEC 6), P
31021-31024
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/43 (Item 22 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05206227 Genuine Article#: VH089 No. References: 39
Title: RBOHA A RICE HOMOLOG OF THE MAMMALIAN GP91PHOX RESPIRATORY BURST
OXIDASE GENE
Author(s): GROOM QJ; TORRES MA; FORDHAMSKELTON AP; HAMMONDKOSACK KE;
ROBINSON NJ; JONES JDG
Corporate Source: UNIV NEWCASTLE,DEPT BIOCHEM & GENET/NEWCASTLE TYNE NE2
4HH/TYNE & WEAR/ENGLAND//; JOHN INNES CTR PLANT SCI RES,SAINSBURY
LAB/NORWICH NR4 7UH/NORFOLK/ENGLAND/
Journal: PLANT JOURNAL, 1996, V10, N3 (SEP), P515-522
ISSN: 0960-7412
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/44 (Item 23 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05040312 Genuine Article#: TL436 No. References: 29
Title: EXTRACELLULAR ASCORBATE STABILIZATION AS A RESULT OF TRANSPLASMA
ELECTRON-TRANSFER IN **SACCHAROMYCES-CEREVISIAE**
Author(s): SANTOSOCANA C; NAVAS P; CRANE FL; CORDOBA F
Corporate Source: UNIV CORDOBA,DEPT BIOL CELULAR/E-14004 CORDOBA//SPAIN//;
PURDUE UNIV,DEPT BIOL SCI/W LAFAYETTE//IN/47907; UNIV HUELVA,DEPT
CIENCIAS AGROFORESTALES/E-21819 HUELVA//SPAIN/
Journal: JOURNAL OF BIOENERGETICS AND BIOMEMBRANES, 1995, V27, N6 (DEC), P597-603
ISSN: 0145-479X
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/45 (Item 24 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04875082 Genuine Article#: UP385 No. References: 31
Title: EVIDENCE FOR THE **SACCHAROMYCES-CEREVISIAE** FERRIREDUCTASE
SYSTEM BEING A MULTICOMPONENT ELECTRON-TRANSPORT CHAIN
Author(s): LESUISSE E; CASTERASSIMON M; LABBE P
Corporate Source: UNIV PARIS 07,INST JACQUES MONOD,LAB BIOCHIM
PORPHYRINES,TOUR 43,2 PL JUSSIEU/F-75251 PARIS 05//FRANCE/
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1996, V271, N23 (JUN 7), P
13578-13583
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/46 (Item 25 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04773243 Genuine Article#: UG238 No. References: 54
Title: MOLECULAR-BIOLOGY OF IRON ACQUISITION IN **SACCHAROMYCES-
CEREVISIAE**

Author(s): ASKWITH CC; DESILVA D; KAPLAN J
Corporate Source: UNIV UTAH,MED CTR,DEPT PATHOL,DIV CELL BIOL &
IMMUNOL/SALT LAKE CITY//UT/84132; UNIV UTAH,MED CTR,DEPT PATHOL,DIV
CELL BIOL & IMMUNOL/SALT LAKE CITY//UT/84132
Journal: MOLECULAR MICROBIOLOGY, 1996, V20, N1 (APR), P27-34
ISSN: 0950-382X
Language: ENGLISH Document Type: REVIEW (Abstract Available)

9/3/47 (Item 26 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04755243 Genuine Article#: UF024 No. References: 21
Title: PARTIAL CHARACTERIZATION AND IDENTIFICATION OF A TRANSFERRIN-LIKE
MOLECULE OF PATHOGENIC **YEAST** CRYPTOCOCCUS-NEOFORMANS
Author(s): TESFASELA F; HAY RJ
Corporate Source: UNIV BATH,DEPT BIOCHEM/BATH BA2 7AY/AVON/ENGLAND//; GUYS
HOSP,ST JOHNS INST DERMATOL/LONDON SE1 9RT//ENGLAND/
Journal: JOURNAL OF GENERAL AND APPLIED MICROBIOLOGY, 1996, V42, N1 (FEB), P61-70
ISSN: 0022-1260
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/48 (Item 27 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04644962 Genuine Article#: TZ983 No. References: 57
Title: A PERMEASE-OXIDASE COMPLEX INVOLVED IN HIGH-AFFINITY IRON UPTAKE IN
YEAST
Author(s): STEARMAN R; YUAN DS; YAMAGUCHIIWAI Y; KLAUSNER RD; DANCIS A
Corporate Source: NICHHD,CELL BIOL & METAB BRANCH,NIH/BETHESDA//MD/20892;
NICHHD,CELL BIOL & METAB BRANCH,NIH/BETHESDA//MD/20892
Journal: SCIENCE, 1996, V271, N5255 (MAR 15), P1552-1557
ISSN: 0036-8075
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/49 (Item 28 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04488026 Genuine Article#: TF713 No. References: 26
Title: TOPOGRAPHY OF THE 27-AND 31-KDA ELECTRON-TRANSPORT PROTEINS IN THE
ONION ROOT PLASMA-MEMBRANE
Author(s): CORDOBA MC; SERRANO A; CORDOBA F; GONZALEZREYES JA; NAVAS P;
VILLALBA JM
Corporate Source: UNIV CORDOBA,FAC CIENCIAS,DEPT BIOL CELULAR,AVDA SAN
ALBERTO MAGNO S-N/E-14004 CORDOBA//SPAIN//; UNIV CORDOBA,FAC
CIENCIAS,DEPT BIOL CELULAR/E-14004 CORDOBA//SPAIN/
Journal: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, 1995, V
216, N3 (NOV 22), P1054-1059
ISSN: 0006-291X
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/50 (Item 29 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04469768 Genuine Article#: TG210 No. References: 51
Title: MOLECULAR CHARACTERIZATION OF A PUTATIVE ARABIDOPSIS-THALIANA COPPER
TRANSPORTER AND ITS **YEAST** HOMOLOG
Author(s): KAMPFENKEL K; KUSHNIR S; BABIYCHUK E; INZE D; VANMONTAGU M
Corporate Source: STATE UNIV GHENT, GENET LAB, KL LEDEGANCKSTRAAT 35/B-9000
GHENT//BELGIUM/; STATE UNIV GHENT, INRA LAB/B-9000 GHENT//BELGIUM/
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1995, V270, N47 (NOV 24), P
28479-28486
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/51 (Item 30 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04469221 Genuine Article#: TF217 No. References: 22
Title: EFFECTS OF CADMIUM AND OF YAP1 AND CAD1/YAP2 GENES ON
IRON-METABOLISM IN THE **YEAST SACCHAROMYCES-CEREVISIAE**
Author(s): LESUISSE E; LABBE P
Corporate Source: UNIV PARIS 07, INST JACQUES MONOD, BIOCHIM PORPHYRINES
LAB, TOUR 43, 2 PL JUSSIEU/F-75251 PARIS 05//FRANCE/
Journal: MICROBIOLOGY-UK, 1995, V141, NOV (NOV), P2937-2943
ISSN: 1350-0872
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/52 (Item 31 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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04391108 Genuine Article#: RZ986 No. References: 24
Title: CELLULAR MECHANISMS UNDERLYING THE INCREASED DUODENAL
IRON-ABSORPTION IN RATS IN RESPONSE TO PHENYLHYDRAZINE-INDUCED
HEMOLYTIC-ANEMIA
Author(s): ORIORDAN DK; SHARP P; SYKES RM; SRAI SK; EPSTEIN O; DEBNAM ES
Corporate Source: ROYAL FREE HOSP, SCH MED, DEPT PHYSIOL, ROWLAND HILL
ST/LONDON NW3 2PF//ENGLAND/; ROYAL FREE HOSP, SCH MED, DEPT
PHYSIOL/LONDON NW32PF//ENGLAND/; ROYAL FREE HOSP, SCH MED, DEPT
MED/LONDON NW3 2PF//ENGLAND/; ROYAL FREE HOSP, SCH MED, DEPT BIOCHEM &
MOLEC BIOL/LONDON NW3 2PF//ENGLAND/
Journal: EUROPEAN JOURNAL OF CLINICAL INVESTIGATION, 1995, V25, N10 (OCT), P722-727
ISSN: 0014-2972
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/53 (Item 32 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04184046 Genuine Article#: RL538 No. References: 26
Title: CHARACTERIZATION AND PARTIAL-PURIFICATION OF A FERRIREDUCTASE FROM
HUMAN DUODENAL MICROVILLUS MEMBRANES
Author(s): RIEDEL HD; REMUS AJ; FITSCHER BA; STREMMEL W
Corporate Source: UNIV HEIDELBERG HOSP, DEPT MED, BERGHEIMER STR 58/D-69115
HEIDELBERG//GERMANY/; UNIV HEIDELBERG HOSP, DEPT MED/D-69115
HEIDELBERG//GERMANY/
Journal: BIOCHEMICAL JOURNAL, 1995, V309, AUG (AUG 1), P745-748
ISSN: 0264-6021
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/54 (Item 33 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03916283 Genuine Article#: QR536 No. References: 13
Title: FERRIREDUCTASE ACTIVITY IN **SACCHAROMYCES-CEREVISIAE** AND
OTHER FUNGI - COLORIMETRIC ASSAYS ON AGAR PLATES
Author(s): LESUISSE E; CASTERASSIMON M; LABBE P
Corporate Source: UNIV PARIS 07, INST JACQUES MONOD, BIOCHIM PORPHYRINES
LAB, TOUR 43, 2 PL JUSSIEU/F-75251 PARIS 05//FRANCE/
Journal: ANALYTICAL BIOCHEMISTRY, 1995, V226, N2 (APR 10), P375-377
ISSN: 0003-2697
Language: ENGLISH Document Type: NOTE

9/3/55 (Item 34 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03901674 Genuine Article#: QR037 No. References: 41
Title: AFT1 - A MEDIATOR OF IRON-REGULATED TRANSCRIPTIONAL CONTROL IN
SACCHAROMYCES-CEREVISIAE
Author(s): YAMAGUCHIIWAI Y; DANCIS A; KLAUSNER RD
Corporate Source: NICHHD, CELL BIOL & METAB BRANCH/BETHESDA//MD/20892;
NICHHD, CELL BIOL & METAB BRANCH/BETHESDA//MD/20892
Journal: EMBO JOURNAL, 1995, V14, N6 (MAR 15), P1231-1239
ISSN: 0261-4189
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/56 (Item 35 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03885689 Genuine Article#: QP889 No. References: 40
Title: THE MENKES-WILSON-DISEASE GENE HOMOLOG IN **YEAST** PROVIDES
COPPER TO A CERULOPLASMIN-LIKE OXIDASE REQUIRED FOR IRON UPTAKE
Author(s): YUAN DS; STEARMAN R; DANCIS A; DUNN T; BEELER T; KLAUSNER RD
Corporate Source: NICHHD, CELL BIOL & METAB BRANCH/BETHESDA//MD/20892;
NICHHD, CELL BIOL & METAB BRANCH/BETHESDA//MD/20892; UNIFORMED SERV UNIV
HLTH SCI, DEPT BIOCHEM/BETHESDA//MD/20814
Journal: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED
STATES OF AMERICA, 1995, V92, N7 (MAR 28), P2632-2636
ISSN: 0027-8424
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/57 (Item 36 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03740872 Genuine Article#: QB967 No. References: 53
Title: POTENTIAL MOLECULAR TARGETS OF METABOLIC PATHWAYS
Author(s): BOYLE SM; SZANISZLO PJ; NOZAWA Y; JACOBSON ES; COLE GT
Corporate Source: UNIV TEXAS, DEPT BOT/AUSTIN//TX/78713; UNIV TEXAS, DEPT
BOT/AUSTIN//TX/78713; VIRGINIA MARYLAND REG COLL VET
MED/BLACKSBURG//VA/24061; GIFU UNIV, SCH MED/GIFU 500//JAPAN//; MCGUIRE
DEPT VET AFFAIRS MED CTR/RICHMOND//VA/23298
Journal: JOURNAL OF MEDICAL AND VETERINARY MYCOLOGY, 1994, V32, S1, P
79-89
ISSN: 0268-1218
Language: ENGLISH Document Type: ARTICLE

9/3/58 (Item 37 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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03709253 Genuine Article#: QA287 No. References: 38
Title: EVIDENCE FOR CU(II) REDUCTION AS A COMPONENT OF COPPER UPTAKE BY
SACCHAROMYCES-CEREVISIAE
Author(s): HASSETT R; KOSMAN DJ
Corporate Source: SUNY BUFFALO,SCH MED & BIOMED SCI,DEPT
BIOCHEM/BUFFALO//NY/14214; SUNY BUFFALO,SCH MED & BIOMED SCI,DEPT
BIOCHEM/BUFFALO//NY/14214
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1995, V270, N1 (JAN 6), P
128-134
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/59 (Item 38 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03608102 Genuine Article#: PQ930 No. References: 41
Title: THE FET4 GENE ENCODES THE LOW-AFFINITY FE(II) TRANSPORT PROTEIN OF
SACCHAROMYCES-CEREVISIAE
Author(s): DIX DR; BRIDGHAM JT; BRODERIUS MA; BYERSDORFER CA; EIDE DJ
Corporate Source: UNIV MINNESOTA,DEPT BIOCHEM & MOLEC BIOL/DULUTH//MN/55812
; UNIV MINNESOTA,DEPT BIOCHEM & MOLEC BIOL/DULUTH//MN/55812
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1994, V269, N42 (OCT 21), P
26092-26099
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/60 (Item 39 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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03601129 Genuine Article#: PQ491 No. References: 44
Title: THE **SACCHAROMYCES-CEREVISIAE** COPPER TRANSPORT PROTEIN
(CTR1P) - BIOCHEMICAL, CHARACTERIZATION, REGULATION BY COPPER, AND
PHYSIOLOGICAL-ROLE IN COPPER UPTAKE
Author(s): DANCIS A; HAILE D; YUAN DS; KLAUSNER RD
Corporate Source: NICHHD,CELL BIOL & METAB BRANCH/BETHESDA//MD/20892;
NICHHD,CELL BIOL & METAB BRANCH/BETHESDA//MD/20892
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1994, V269, N41 (OCT 14), P
25660-25667
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/61 (Item 40 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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03215083 Genuine Article#: NM944 No. References: 20
Title: SEQUENCING OF A 13.2-KB SEGMENT NEXT TO THE LEFT TELOMERE OF
YEAST CHROMOSOME-XI REVEALED 5 OPEN READING FRAMES AND RECENT
RECOMBINATION EVENTS WITH THE RIGHT ARMS OF CHROMOSOME-III AND
CHROMOSOME-V
Author(s): ALEXANDRAKI D; TZERMIA M
Corporate Source: INST MOLEC BIOL & BIOTECHNOL,FDN RES & TECHNOL HELLAS,POB
1527/GR-71110 IRAKLION//GREECE//; UNIV CRETE,DEPT BIOL/GR-71110
IRAKLION//GREECE/
Journal: YEAST, 1994, V10, SA (APR), PS81-S91

ISSN: 0749-503X
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/62 (Item 41 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03077925 Genuine Article#: NA966 No. References: 31
Title: IRON - NUTRITIOUS, NOXIOUS, AND NOT READILY AVAILABLE
Author(s): GUERINOT ML; YI Y
Corporate Source: DARTMOUTH COLL,DEPT BIOL SCI/HANOVER//NH/03755
Journal: PLANT PHYSIOLOGY, 1994, V104, N3 (MAR), P815-820
ISSN: 0032-0889
Language: ENGLISH Document Type: EDITORIAL

9/3/63 (Item 42 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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02943453 Genuine Article#: MU678 No. References: 40
Title: THE FET3 GENE OF **SACCHAROMYCES-CEREVISIAE** ENCODES A
MULTICOPPER OXIDASE REQUIRED FOR FERROUS IRON UPTAKE
Author(s): ASKWITH C; EIDE D; VANHO A; BERNARD PS; LI LT; DAVISKAPLAN S;
SIPE DM; KAPLAN J
Corporate Source: UNIV UTAH,DEPT PATHOL,DIV CELL BIOL & IMMUNOL/SALT LAKE
CITY//UT/84132; UNIV MINNESOTA,SCH MED,DEPT BIOCHEM & MOLEC
BIOL/DULUTH//MN/55812
Journal: CELL, 1994, V76, N2 (JAN 28), P403-410
ISSN: 0092-8674
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/64 (Item 43 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

02943452 Genuine Article#: MU678 No. References: 43
Title: MOLECULAR CHARACTERIZATION OF A COPPER TRANSPORT PROTEIN IN
SACCHAROMYCES-CEREVISIAE - AN UNEXPECTED ROLE FOR COPPER IN
IRON TRANSPORT
Author(s): DANCIS A; YUAN DS; HAILE D; ASKWITH C; EIDE D; MOEHLE C; KAPLAN
J; KLAUSNER RD
Corporate Source: NICHHD,CELL BIOL & METAB BRANCH/BETHESDA//MD/20892; UNIV
UTAH,COLL MED,DEPT PATHOL,DIV CELL BIOL & IMMUNOL/SALT LAKE
CITY//UT/84132; UNIV MINNESOTA,SCH MED,DEPT BIOCHEM & MOLEC
BIOL/DULUTH//MN/55812; NICHHD,MOLEC GENET LAB/BETHESDA//MD/20892
Journal: CELL, 1994, V76, N2 (JAN 28), P393-402
ISSN: 0092-8674
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/65 (Item 44 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

02875407 Genuine Article#: MM120 No. References: 29
Title: MAC1, A NUCLEAR REGULATORY PROTEIN RELATED TO CU-DEPENDENT
TRANSCRIPTION FACTORS IS INVOLVED IN CU/FE UTILIZATION AND STRESS
RESISTANCE IN **YEAST**
Author(s): JUNGSMANN J; REINS HA; LEE JW; ROMEO A; HASSETT R; KOSMAN D;
JENTSCH S
Corporate Source: MAX PLANCK GESELL,FRIEDRICH MIESCHER LAB,SPEMANNSTR

37-39/D-72076 TUBINGEN//GERMANY//; MAX PLANCK GESELL, FRIEDRICH MIESCHER
LAB, SPEMANNSTR 37-39/D-72076 TUBINGEN//GERMANY/
Journal: EMBO JOURNAL, 1993, V12, N13 (DEC 15), P5051-5056
ISSN: 0261-4189
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/66 (Item 45 from file: 34)
DIALOG(R) File 34: SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

02872505 Genuine Article#: ML714 No. References: 45
Title: THE GEF1 GENE OF *SACCHAROMYCES-CEREVISIAE* ENCODES AN
INTEGRAL MEMBRANE-PROTEIN - MUTATIONS IN WHICH HAVE EFFECTS ON
RESPIRATION AND IRON-LIMITED GROWTH
Author(s): GREENE JR; BROWN NH; DIDOMENICO BJ; KAPLAN J; EIDE DJ
Corporate Source: SCHERING PLOUGH CORP, RES INST, 2015 GALLOPING HILL
RD/KENILWORTH//NJ/07033; UNIV UTAH, MED CTR, DEPT PATHOL/SALT LAKE
CITY//UT/84132; UNIV MINNESOTA, DEPT BIOCHEM & MOLEC
BIOL/DULUTH//MN/55812
Journal: MOLECULAR & GENERAL GENETICS, 1993, V241, N5-6 (DEC), P
542-553
ISSN: 0026-8925
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

9/3/67 (Item 1 from file: 44)
DIALOG(R) File 44: Aquatic Sci&Fish Abs
(c) 2002 FAO (for ASFA Adv Brd). All rts. reserv.

00623483 ASFA Accession Number: 4309826
Cloning and characterization of high-CO sub(2)-specific cDNAs from a marine
microalga, *Chlorococccum littorale*, and effect of CO sub(2) concentration
and iron deficiency on the gene expression
Sasaki, T; Kurano, N; Miyachi, S
Mar. Biotechnol. Inst., Kamaishi Labs., 3-75-1 Heita, Kamaishi City,
Iwate, 026-0001, Japan
Plant & Cell Physiology "PLANT CELL PHYSIOL.", vol. 39, no. 2, p.
131-138, Feb 1998

9/3/68 (Item 1 from file: 76)
DIALOG(R) File 76: Life Sciences Collection
(c) 2002 Cambridge Sci Abs. All rts. reserv.

02306107 4414478
Coenzyme Q sub(6) and iron reduction are responsible for the extracellular
ascorbate stabilization at the plasma membrane of *Saccharomyces*
cerevisiae
Santos Ocana, C.; Cordoba, F.; Crane, F.L.; Clarke, C.F.; Navas, P.
Depto. de Biologia Celular, Fac. de Cienc., Univ. de Cordoba, Avenida San
Alberto Magno, s/n, 14004 Cordoba, Spain
J. BIOL. CHEM. vol. 273, no. 14, pp. 8099-8105 (1998)
ISSN: 0021-9258
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Microbiology Abstracts C: Algology, Mycology & Protozoology

9/3/69 (Item 2 from file: 76)
DIALOG(R) File 76: Life Sciences Collection
(c) 2002 Cambridge Sci Abs. All rts. reserv.

02047561 3926485
Effect of heme and vacuole deficiency on FRE1 gene expression and

ferrireductase activity in **Saccharomyces cerevisiae**
Amillet, J. M.; Galiano, F.; Labbe Bois, R.
Lab. Biochimie des Porphyrines, Inst. Jacques Monod, Univ. Paris 7, 2 Place
Jussieu, 75251 Paris Cedex 05, France
FEMS MICROBIOL. LETT. vol. 137, no. 1, pp. 25-29 (1996)
ISSN: 0378-1097
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Microbiology Abstracts C: Algology, Mycology & Protozoology;
Biochemistry Abstracts 2: Nucleic Acids

9/3/70 (Item 3 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
(c) 2002 Cambridge Sci Abs. All rts. reserv.

01911822 3725990
AFT1: A mediator of iron regulated transcriptional control in
Saccharomyces cerevisiae
Yamaguchi Iwai, Y.; Dancis, A.; Klausner, R.D.
Cell Biol. and Metab. Branch, NICH and Hum. Dev., NIH, Bethesda, MD, USA
EMBO J. vol. 14, no. 6, pp. 1231-1239 (1995)
ISSN: 0261-4189
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Biochemistry Abstracts 2: Nucleic Acids; Genetics Abstracts;
Microbiology Abstracts C: Algology, Mycology & Protozoology

9/3/71 (Item 4 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
(c) 2002 Cambridge Sci Abs. All rts. reserv.

01715998 2996674
The fission yeast **ferric reductase** gene *frp1* super(+) is
required for ferric iron uptake and encodes a protein that is homologous
to the gp91-phox subunit of the human NADPH phagocyte oxidoreductase.
Roman, D.G.; Dancis, A.; Anderson, G.J.; Klausner, R.D.
Cell Biol. and Metab. Branch, Natl. Inst. Child Health and Hum. Dev.,
Bethesda, MD 20892, USA
MOL. CELL. BIOL. vol. 13, no. 7, pp. 4342-4350 (1993.)
ISSN: 0270-7306
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Microbiology Abstracts Section C: Algology, Mycology and
Protozoology; Biochemistry Abstracts Part 2: Nucleic Acids; Genetics
Abstracts

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? s fre(w)1 or ferric (w) reductas? or ferric (w) chelate (w) reductas?
Processing
Processed 10 of 22 files ...
Completed processing all files
      1066 FRE
    14496581 1
      14 FRE(W)1
    46666 FERRIC
    261816 REDUCTAS?
      529 FERRIC(W) REDUCTAS?
    46666 FERRIC
    33174 CHELATE
    261816 REDUCTAS?
      196 FERRIC(W) CHELATE(W) REDUCTAS?
S1      711 FRE(W)1 OR FERRIC (W) REDUCTAS? OR FERRIC (W) CHELATE (W)
      REDUCTAS?

? s s1 and py<1998
Processing
>>>File 10 processing for PY= : PY=1998
>>> started at PY=A stopped at PY=1961
Processing
Processed 10 of 22 files ...
Processing
>>>One or more prefixes are unsupported
>>> or undefined in one or more files.
Processed 20 of 22 files ...
Processing
Completed processing all files
      711 S1
    68008976 PY<1998
S2      317 S1 AND PY<1998
? s s1 and py>1998 and py<1999
>>>One or more prefixes are unsupported
>>> or undefined in one or more files.
      711 S1
    639 PY>1998 AND PY<1999
S3      0 S1 AND PY>1998 AND PY<1999
? s s1 and py<1999 and not s2
>>>Operator "NOT" in invalid position
? s s1 and py<1999 not s2
>>>File 10 processing for PY= : PY=1999
>>> started at PY=A stopped at PY=1961
Processing
Processed 10 of 22 files ...
Processing
>>>One or more prefixes are unsupported
>>> or undefined in one or more files.
Processed 20 of 22 files ...
Completed processing all files
      711 S1
    71981655 PY<1999
      317 S2
S4      77 S1 AND PY<1999 NOT S2

? rd
>>>Duplicate detection is not supported for File 235.
>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.
...examined 50 records (50)
...completed examining records
S5      38 RD (unique items)
? t s5/3,ab/all
>>>No matching display code(s) found in file(s): 65, 235, 306

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5/3,AB/1 (Item 1 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

10327088 99078442 PMID: 9861449

The plasma membrane Fe(3+)-reductase activity of Caco-2 cells is modulated during differentiation.

Ekmekcioglu C; Strauss-Blasche G; Marktl W

Department of Medical Physiology, University of Vienna, Medical School, Austria. cem.ekmekcioglu@univie.ac.at

Biochemistry and molecular biology international (AUSTRALIA) Dec 1998, 46 (5) p951-61, ISSN 1039-9712 Journal Code: BOD

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

The aim of the present study was to investigate whether the brush border membrane **ferric reductase** activity of Caco-2 cells is modulated during cell differentiation. The **ferric reductase** activity was determined in whole cells and isolated microvillous membranes at different stages of cell differentiation by measuring the amount of Fe³⁺ reduced during the incubation time. Our results indicated that the **ferric reductase** activity decreased in fastly growing cells and reactivated in postconfluent cells in contrast to the alkaline phosphatase and sucrase activities which were progressively expressed during differentiation as conventional indicators of cell maturity. The lowest **ferric reductase** activity was found in cells at the log phase of proliferation, while freshly seeded or highly differentiated cells had significantly higher enzyme activities. Cells grown under serum-free conditions had similar ferric iron reduction rates as cells propagated under standard conditions. Reagents or hormones affecting cell metabolism through different pathways had no significant effect on this transplasma membrane redox system.

5/3,AB/2 (Item 2 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

10031245 99059681 PMID: 9841863

Monocyte-macrophage **ferric reductase** activity is inhibited by iron and stimulated by cellular differentiation.

Partridge J; Wallace DF; Raja KB; Dooley JS; Walker AP

Department of Medicine, Royal Free and University College Medical School, Royal Free Campus, Rowland Hill Street, London NW3 2PF, U.K.

Biochemical journal (ENGLAND) Dec 15 1998, 336 (Pt 3) p541-3, ISSN 0264-6021 Journal Code: 9YO

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

The enzyme **ferric reductase** catalyses the reduction of Fe(III) as a prerequisite to its transportation across the cell membrane. Duodenal mucosal biopsies from iron overloaded patients with genetic haemochromatosis (GH) have increased **ferric reductase** activity and iron absorption compared with controls, yet the GH mucosa is iron deficient. A similar GH-related iron deficiency is also seen in macrophages. The aim of this study was to investigate whether macrophage **ferric reductase** activity is altered in GH, and to determine **ferric reductase** activity in monocytes and differentiated macrophages. The erythroleukaemic K562 cell line was studied as a clonal reference cell line. The basal K562 **ferric reductase** activity is characteristic of a membrane bound enzyme, being both temperature and protease sensitive. **Ferric reductase** activity was also demonstrated in human leucocyte, monocyte and macrophage preparations. Assays of K562 and macrophage cell supernatants confirmed that the **ferric reductase** activity was not due to a secreted factor.

Assay of **ferric reductase** in normalized-iron and iron-enriched (100 microM ferric citrate) conditions showed no significant difference between Cys282Tyr (Cys282-->Tyr) homozygous GH macrophages and Cys282-Tyr negative control activities ($P>0.05$). However, a 900% increase in **ferric reductase** activity was observed during monocyte to macrophage differentiation ($P<0.05$), possibly reflecting the co-ordinate up-regulation of iron metabolism in these cells. The demonstration of approx. 25% activity after macrophage differentiation at high free-iron concentrations compared with 'normalized' iron is consistent with repression of human **ferric reductase** activity by iron. The identification of the human **ferric reductase** gene and its protein will ultimately provide insight into its regulation and role in mammalian iron metabolism.

5/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09971927 99008319 PMID: 9794217

The effect of differentiation on the brush border membrane **ferric reductase** activity in Caco-2 cells.

Ekmekcioglu C; Marktl W

In vitro cellular & developmental biology (UNITED STATES) Oct 1998, 34 (9) p674-6, ISSN 1071-2690 Journal Code: BZE

Languages: ENGLISH

Document type: Letter

Record type: Completed

5/3,AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09878324 98380361 PMID: 9712764

Ferrous iron uptake in *Cryptococcus neoformans*.

Jacobson ES; Goodner AP; Nyhus KJ

Research Service, McGuire Veterans Affairs Medical Center, Richmond, Virginia 23249, and Department of Internal Medicine, Virginia Commonwealth University, Richmond, Virginia 23298-0049, USA. jacobson.eric.s@richmond.va.gov

Infection and immunity (UNITED STATES) Sep 1998, 66 (9) p4169-75, ISSN 0019-9567 Journal Code: GO7

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Previous studies have implicated ferric reduction in the iron uptake pathway of the opportunistic pathogen *Cryptococcus neoformans*. Here we studied iron uptake directly, using ^{55}Fe in the presence of reductants. Uptake was linear with respect to time and number of yeast cells. The plot of uptake versus concentration exhibited a steep rise up to about 1 microM, a plateau between 1 and 25 microM, and a second steep rise above 25 microM, consistent with high- and low-affinity uptake systems. A K_m for high-affinity uptake was estimated to be 0.6 microM Fe(II); 1 microM was used for standardized uptake assays. At this concentration, the uptake rate was 110 ± 3 pmol/10(6) cells/h. Iron repletion (15 microM) and copper starvation drastically decreased high-affinity iron uptake. Incubation at 0 degreesC or in the presence of 2 mM KCN abolished high-affinity iron uptake, suggesting that uptake requires metabolic energy. When exogenous reducing agents were not supplied and the culture was washed free of secreted reductants, uptake was reduced by 46%; the remaining uptake activity presumably was dependent upon the cell membrane **ferric reductase**. Further decreases in free Fe(II) levels achieved by trapping with bathophenanthroline disulfonate or reoxidizing with potassium nitrosodisulfonate reduced iron uptake very drastically, suggesting that it is the Fe(II) species which is transported by the high-affinity

transporter. The uptake of Fe was stimulated two- to threefold by deferoxamine, but this increment could be abolished by copper starvation or inhibition of the **ferric reductase** by Pt, indicating that Fe solubilized by this molecule also entered the reductive iron uptake pathway.

5/3,AB/5 (Item 5 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09725388 98220314 PMID: 9559558

Cloning and characterization of high-CO₂-specific cDNAs from a marine microalga, *Chlorococcum littorale*, and effect of CO₂ concentration and iron deficiency on the gene expression.

Sasaki T; Kurano N; Miyachi S

Marine Biotechnology Institute, Kamaishi Laboratories, Iwate, Japan.

Plant & cell physiology (JAPAN) Feb 1998, 39 (2) p131-8,

ISSN 0032-0781 Journal Code: B1G

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Two cDNA clones exclusively induced under an extremely high-CO₂ concentration (20%) were isolated from *Chlorococcum littorale* by differential screening and named HCR (high-CO₂ response) 1 and 2, respectively. The amino acid sequence of the protein encoded by HCR2 exhibited homology to the gp91-phox protein, a critical component of a human phagocyte oxidoreductase, and to the yeast **ferric reductases**, *Saccharomyces cerevisiae* FRE1 and FRE2 and *Schizosaccharomyces pombe* Frp1. The induction of both HCR mRNAs required extremely high-CO₂ conditions and iron deficiency, being suppressed under air conditions and by iron sufficiency, suggesting that the expression of these two HCR genes required extremely high-CO₂ conditions and iron deficiency in combination. The HCR2 protein was detected in the membrane fractions of cells grown under conditions which would favor the induction of HCR2-mRNA and the protein level was lowered when the cells were transferred from iron deficient to 10 microm FeSO₄ conditions (with 20% CO₂).

5/3,AB/6 (Item 6 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09720317 98192599 PMID: 9525912

Coenzyme Q6 and iron reduction are responsible for the extracellular ascorbate stabilization at the plasma membrane of *Saccharomyces cerevisiae*.

Santos-Ocana C; Cordoba F; Crane FL; Clarke CF; Navas P

Departamento de Biologia Celular, Facultad de Ciencias, Universidad de Cordoba, Avenida San Alberto Magno, s/n, 14004 Cordoba, Spain.

Journal of biological chemistry (UNITED STATES) Apr 3 1998, 273

(14) p8099-105, ISSN 0021-9258 Journal Code: HIV

Contract/Grant No.: GM-45952, GM, NIGMS

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Yeast plasma membrane contains an electron transport system that maintains ascorbate in its reduced form in the apoplast. Reduction of ascorbate free radical by this system is comprised of two activities, one of them dependent on coenzyme Q6 (CoQ6). Strains with defects in CoQ6 synthesis exhibit decreased capacity for ascorbate stabilization compared with wild type or with atp2 or cor1 respiratory-deficient mutant strains. Both CoQ6 content in plasma membranes and ascorbate stabilization were increased during log phase growth. The addition of exogenous CoQ6 to whole cells resulted in its incorporation in the plasma membrane, produced levels of CoQ6 in the coq3 mutant strain that were 2-fold higher than in the wild

type, and increased ascorbate stabilization activity in both strains, although it was higher in the *coq3* mutant than in wild type. Other antioxidants, such as benzoquinone or alpha-tocopherol, did not change ascorbate stabilization. The CoQ6-independent reduction of ascorbate free radical was not due to copper uptake, pH changes or to the presence of CoQ6 biosynthetic intermediates, but decreased to undetectable levels when *coq3* mutant strains were cultured in media supplemented with ferric iron. Plasma membrane CoQ6 levels were unchanged by either the presence or absence of iron in wild type, *atp2*, or *cor1* strains. Ascorbate stabilization appears to be a function of the yeast plasma membrane, which is partially based on an electron transfer chain in which CoQ6 is the central electron carrier, whereas the remainder is independent of CoQ6 and other antioxidants but is dependent on the iron-regulated **ferric reductase** complex.

5/3,AB/7 (Item 7 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09669412 98096784 PMID: 9435058

Anaerobic killing of oral streptococci by reduced, transition metal cations.

Dunning JC; Ma Y; Marquis RE
Department of Microbiology and Immunology, University of Rochester, New York 14642-8672, USA.

Applied and environmental microbiology (UNITED STATES) Jan 1998,

64 (1) p27-33, ISSN 0099-2240 Journal Code: 6K6

Contract/Grant No.: P01DE11549, DE, NIDCR; R01DE06127, DE, NIDCR

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Reduced, transition metal cations commonly enhance oxidative damage to cells caused by hydroperoxides formed as a result of oxygen metabolism or added externally. As expected, the cations Fe²⁺ and Cu⁺ enhanced killing of *Streptococcus mutans* GS-5 by hydroperoxides. However, unexpectedly, they also induced lethal damage under fully anaerobic conditions in a glove box with no exposure to O₂ or hydroperoxides from initial treatment with the cations. Sensitivities to anaerobic killing by Fe²⁺ varied among the organisms tested. The oral streptococci *Streptococcus gordonii* ATCC 10558, *Streptococcus rattus* FA-1, and *Streptococcus sanguis* NCTC 10904 were approximately as sensitive as *S. mutans* GS-5. *Enterococcus hirae* ATCC 9790, *Actinomyces viscosus* OMZ105E, and *Actinomyces naeslundii* WVU45 had intermediate sensitivity, while *Lactobacillus casei* ATCC 4646 and *Escherichia coli* B were insensitive. Killing of *S. mutans* GS-5 in response to millimolar levels of added Fe²⁺ occurred over a wide range of temperatures and pH. The organism was able to take up ferrous iron, but **ferric reductase** activity could not be detected. Chelators, uric acid, and thiocyanate were not effective inhibitors of the lethal damage. Sulfhydryl compounds, ferricyanide, and ferrocyanide were protective if added prior to Fe²⁺ exposure. Fe²⁺, but not Fe³⁺, acted to reduce the acid tolerance of glycolysis by intact cells of *S. mutans*. The reduction in acid tolerance appeared to be related directly to Fe²⁺ inhibition of F-ATPase, which could be assayed with permeabilized cells, isolated membranes, or F1 enzyme separated from membranes. Cu⁺ and Cu²⁺ also inhibited F-ATPase and sensitized glycolysis by intact cells to acid. All of these damaging actions occurred anaerobically and thus did not appear to involve reactive oxygen species.

5/3,AB/8 (Item 8 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09639035 98114376 PMID: 9453631

Identification and characterization of a novel extracellular **ferric reductase** from *Mycobacterium paratuberculosis*.

Homuth M; Valentin-Weigand P; Rohde M; Gerlach GF
Institut für Mikrobiologie und Tierseuchen, Tierärztliche Hochschule
Hannover, Germany.

Infection and immunity (UNITED STATES) Feb 1998, 66 (2) p710-6

, ISSN 0019-9567 Journal Code: GO7

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

A novel extracellular mycobacterial enzyme was identified in the ruminant pathogen *Mycobacterium paratuberculosis*. The enzyme was capable of mobilizing iron from different sources such as ferric ammonium citrate, ferritin, and transferrin by reduction of the metal. The purified reductase had a calculated Mr of 17,000, was sensitive to proteinase K treatment, and had an isoelectric point of pH 9. Analysis of the amino acid composition revealed glycine, serine, asparagine (or aspartic acid), and glutamine (or glutamic acid) as the most frequently occurring residues. Enzymatic activity was highest at 37 degrees C and between pH 5 and 10. The calculated Km and Vmax for ferric ammonium citrate were 0.213 mM and 0.345 mM min⁻¹ mg⁻¹, respectively. Using a specific antireductase antibody in immunoelectron microscopy, we were able to detect the enzyme associated with intracellular mycobacteria in naturally *M. paratuberculosis*-infected bovine tissue. We propose that the reductase of *M. paratuberculosis* represents an alternative strategy of mycobacteria to mobilize ferric iron and discuss its potential role in bacterial evasion of intracellular defense mechanisms.

5/3,AB/9 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11899845 BIOSIS NO.: 199900145954

Changes in sugar beet leaf plasma membrane Fe(III)-chelate reductase activities mediated by Fe-deficiency, assay buffer composition, anaerobiosis and the presence of flavins.

AUTHOR: Gonzalez-Vallejo E B; Susin S; Abadia A; Abadia J(a)

AUTHOR ADDRESS: (a)Dep. Nutr. Vegetal, Estacion Experimental Aula Dei, C.S.I.C., Apdo. 202, E-50080 Zaragoza**Spain

JOURNAL: Protoplasma 205 (1-4):p163-168 1998

ISSN: 0033-183X

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Different assay conditions induce changes in the **ferric chelate reductase** activities of leaf plasma membrane preparations from Fe-deficient and Fe-sufficient sugar beet. With an apoplast-type assay medium the **ferric chelate reductase** activities did not change significantly when Fe(III)-EDTA was the substrate. However, with ferric citrate as substrate, the effect depended on the citrate-to-Fe ratio. When the citrate-to-Fe ratio was 20:1, the effects were practically unappreciable. However, with a lower citrate-to-Fe ratio of 5:1 the activities were significantly lower with the apoplast-type medium than with the standard assay medium. Our data also indicate that anaerobiosis during the assay facilitates the reduction of ferric malate and Fe(III)-EDTA by plasma membrane preparations. Anaerobiosis increased by approximately 50% the plasma membrane **ferric chelate reductase** activities when Fe(III)-EDTA was the substrate. With ferric malate anaerobiosis increased activities by 70-90% over the values obtained in aerobic conditions. However, with ferric citrate the increase in activity by anaerobiosis was not significant. We have also tested the effect of riboflavin, flavin adenine dinucleotide, and flavin mononucleotide on the plasma membrane **ferric chelate reductase** activities. The presence of

flavins generally increased activities in plasma membrane preparations from control and Fe-deficient plants. Increases in activity were generally moderate (lower than twofold). These increases occurred with Fe(III)EDTA and Fe(III)-citrate as substrates.

1998

5/3,AB/10 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

11899332 BIOSIS NO.: 199900145441

Molecular biology of plasma membrane redox enzymes: A survey of current knowledge.

AUTHOR: Goldenberg H(a)

AUTHOR ADDRESS: (a)Inst. Med. Chemie, Univ. Wien, Waehringerstr. 10, A-1090
Wien**Austria

JOURNAL: Protoplasma 205 (1-4):p3-9 1998

ISSN: 0033-183X

DOCUMENT TYPE: Literature Review

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Despite a large body of evidence for enzymatic activities and physiological function, of plasma membrane redox function, few of these enzymes have been characterized in terms of molecular biology. Examples for these with at least some molecular data up to complete sequences, membrane topology and binding sites for substrates and coenzymes or prosthetic groups are NADH-ferricyanide reductase of Ehrlich ascites membranes, NADH-coenzyme Q reductase of liver, NADH oxidase ectoenzyme of liver and HeLa (and possibly other) cells, protein disulfide isomerase which is widespread, and relatives thereof, as well as cytochromes P-450 and b558, NADPH oxidase of fat and thyroid cells and fat cell amine oxidase. Ferricyanide reductase and coenzyme Q reductase may be identical, but NADH oxidase ectoenzyme is distinct and possibly functions also as a disulfide and a copper reductase. On the other hand, the plasma-membrane-located protein disulfide isomerase (PDI), despite its similar enzymatic activity, is completely different from the ectooxidase. The latter is shed from the membrane into the surrounding medium by proteolysis, whereas PDI is not an integral membrane protein and is secreted intact. Another disulfide reductase has been demonstrated in THP-1 cells, which again is totally different from the former two. It turns out that enzymatic activities are insufficient to describe redox enzymes. Special forms of cytochrome P-450 can be induced to expression at the cell membrane of liver, where they are transported by the cytoskeleton-associated secretory pathway. Why some isoforms are expressed at the surface and some are not is not yet clear. Cytochrome b558, the flavocytochrome of neutrophils, is described in other cells too, but there are different isoforms, which are genetically distinct. A relative has also been identified in duodenal cells, where it functions as a **ferric reductase** involved in iron absorption. NADPH oxidase of fat cells has very similar properties, but the identity is unproved, whereas thyroid oxidase is a non-heme protein which is calcium-sensitive and does not need assembly of subunits for activation. Finally, fat cell membranes also possess a quinone-containing amine-oxidase which may be involved in signaling of glucose-transport regulation, as it is also found in GLUT4-containing vesicles. However, the physiological connection has yet to be demonstrated.

1998

5/3,AB/11 (Item 3 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

11851462 BIOSIS NO.: 199900097571

The plasma membrane Fe³⁺-reductase activity of Caco-2 cells is modulated during differentiation.

AUTHOR: Ekmekcioglu Cem(a); Strauss-Blasche Gerhard; Marktl Wolfgang

AUTHOR ADDRESS: (a)Univ. Vienna, Med. Sch., Dep. Med. Physiol.,

Schwarzspanierstr. 17, A-1090 Vienna**Austria

JOURNAL: Biochemistry and Molecular Biology International 46 (5):p951-961
Dec., 1998

ISSN: 1039-9712

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The aim of the present study was to investigate whether the brush border membrane **ferric reductase** activity of Caco-2 cells is modulated during cell differentiation. The **ferric reductase** activity was determined in whole cells and isolated microvillous membranes at different stages of cell differentiation by measuring the amount of Fe³⁺ reduced during the incubation time. Our results indicated that the **ferric reductase** activity decreased in fastly growing cells and reactivated in postconfluent cells in contrast to the alkaline phosphatase and sucrase activities which were progressively expressed during differentiation as conventional indicators of cell maturity. The lowest **ferric reductase** activity was found in cells at the log phase of proliferation, while freshly seeded or highly differentiated cells had significantly higher enzyme activities. Cells grown under serum-free conditions had similar ferric iron reduction rates as cells propagated under standard conditions. Reagents or hormones affecting cell metabolism through different pathways had no significant effect on this transplasma membrane redox system.

1998

5/3,AB/12 (Item 4 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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11801254 BIOSIS NO.: 199900047363

Ferrous iron is transported across the peribacteroid membrane of soybean nodules.

AUTHOR: Moreau Sophie; Day David A; Puppo Alain(a)

AUTHOR ADDRESS: (a)Laboratoire Biologie Vegetale Microbiologie, CRNS ERS

590, Universite Nice-Sophia Antipolis, Par**France

JOURNAL: Planta (Berlin) 207 (1):p83-87 Dec., 1998

ISSN: 0032-0935

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Symbiosomes and bacteroids isolated from soybean (Glycine max Merr.) nodules are able to take up ferrous iron. This uptake activity was completely abolished in the presence of ferrous-iron chelators. The kinetics of uptake were characterized by initially high rates of iron internalization, but no saturation was observed with increasing iron concentration. This process does not appear to involve the **ferric reductase** of the peribacteroid membrane. The transport of ferrous iron was inhibited by other transition metals, particularly copper. Ferrous iron was taken up by symbiosomes more efficiently than the ferric form. This indicates that the iron transport from the plant host cell to the microsymbiont in vivo may occur mainly as the ferrous form.

1998

5/3,AB/13 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11727596 BIOSIS NO.: 199800509327

Orientation of NAHD-linked ferric chelate (turbo) reductase in plasma membranes from roots of *Plantago lanceolata*.

AUTHOR: Schmidt W(a); Bartels M

AUTHOR ADDRESS: (a)Fachbereich Biologie, Carl Von Ossietzky Universitaet Oldenburg, Postfach 2503, D-26111 Oldenbur**Germany

JOURNAL: Protoplasma 203 (3-4):p186-193 1998

ISSN: 0033-183X

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Plasma membrane vesicles isolated from roots of *Plantago lanceolata* L. revealed approximately 70% right-side-out orientation based on structure-linked latency with H⁺-ATPase as a marker. Incubation with 0.05% Brij 58 caused the formation of sealed inside-out vesicles, evidenced by assaying ATP-dependent proton pumping activity with the optical pH probe acridine orange. NADH-linked FeEDTA reductase activity was stimulated by including either Triton X-100 or Brij 58 in the assay medium. The activity of inverted (Brij-treated) vesicles was not further increased by the addition of Triton, suggesting that maximum activity was obtained in inside-out vesicles. Iron deficiency resulted in a ca. 2-fold increase in the specific activity of both ATPase and Fe(III) chelate reductase but did not cause significant alterations with respect to the effect of detergents. It is concluded that in vitro both donor and acceptor sites of NADH-FeEDTA reductase are located on the cytosolic face of the membrane and trans-oriented flow of electrons is not detectable in plasma membrane vesicles. Unlike Fe chelate reduction in vivo, the plasma membrane-bound reductase activity was insensitive towards application of the translation inhibitor cycloheximide prior to isolation of the membranes, implying the involvement of a regulatory enzyme in the electron transport in vivo.

1998

5/3,AB/14 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11660635 BIOSIS NO.: 199800442366

Human transferrin as a source of iron for *Streptococcus intermedius*.

AUTHOR: Brochu Vicky; Grenier Daniel(a); Mayrand Denis

AUTHOR ADDRESS: (a)Groupe Rech. Ecol. Buccale, Fac. Med. Dent., Univ. Laval, Quebec, PQ G1K 7P4**Canada

JOURNAL: FEMS Microbiology Letters 166 (1):p127-133 Sept. 1, 1998

ISSN: 0378-1097

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: *Streptococcus intermedius* is well known to produce severe infections in various areas of the body. In this study, we evaluated the ability of *S. intermedius* to utilise human transferrin as a source of iron and investigated the mechanism by which iron can be obtained from this plasma protein. Adding either ferrous sulfate or holotransferrin to

an iron-deficient culture medium allowed growth of *S. intermedius*. Cultivation of *S. intermedius* under an iron-poor condition was associated with the over expression of a 58 kDa cell surface protein. Neither siderophore activity nor reductase activity could be detected. Moreover, cells of *S. intermedius* did not show transferrin-binding activity or proteolytic activity toward transferrin. It was found that *S. intermedius* could rapidly decrease the pH of the medium during cell growth, resulting in a release of iron from holotransferrin. When the buffering capacity of the culture medium was significantly increased, the holotransferrin could not support growth of *S. intermedius*. It is suggested that under certain circumstances, *S. intermedius* may migrate from its normal niche (oral cavity), reach a particular site and create a localised environment where the pH can be lowered with the subsequent release of iron from transferrin. This would allow bacterial growth and initiation of the infectious process.

1998

5/3,AB/15 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

11634088 BIOSIS NO.: 199800415819
Iron uptake from lactoferrin by *Trichomonas vaginalis* requires a surface **ferric reductase**.

AUTHOR: Tarango M; Lehker M W
AUTHOR ADDRESS: Univ. Texas El Paso, El Paso, TX**USA
JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 98p96-97 1998
CONFERENCE/MEETING: 98th General Meeting of the American Society for Microbiology Atlanta, Georgia, USA May 17-21, 1998
SPONSOR: American Society for Microbiology
ISSN: 1060-2011
RECORD TYPE: Citation
LANGUAGE: English
1998

5/3,AB/16 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

11633945 BIOSIS NO.: 199800415676
The development of a rapid-screen analysis for putative virulence-related genes in *Trichomonas vaginalis*.

AUTHOR: Maier S M; Lehker M W
AUTHOR ADDRESS: Univ. Texas El Paso, El Paso, TX**USA
JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 98p72 1998
CONFERENCE/MEETING: 98th General Meeting of the American Society for Microbiology Atlanta, Georgia, USA May 17-21, 1998
SPONSOR: American Society for Microbiology
ISSN: 1060-2011
RECORD TYPE: Citation
LANGUAGE: English
1998

5/3,AB/17 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

11557976 BIOSIS NO.: 199800339308

Introduction of artificially synthesized gene, *refrel*, which encodes yeast **ferric reductase** into tobacco plants.

AUTHOR: Ohki Hiroyuki; Yamaguchi Hirotaka; Nakanishi Hiromi; Mori Satoshi

AUTHOR ADDRESS: Dep. Appl. Biol. Chem., Univ. Tokyo, Tokyo**Japan

JOURNAL: Plant and Cell Physiology 39 (SUPPL.):pS135 1998

CONFERENCE/MEETING: 1998 Annual Meeting of the Japanese Society of Plant Pathologists Tokyo, Japan May 3-5, 1998

SPONSOR: Japanese Society of Plant Pathologists

ISSN: 0032-0781

RECORD TYPE: Citation

LANGUAGE: English

1998

5/3,AB/18 (Item 10 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2002 BIOSIS. All rts. reserv.

11481502 BIOSIS NO.: 199800262834

Induction of **ferric reductase** activity and of iron uptake capacity in *Chlorococcum littorale* cells under extremely high-CO₂ and iron-deficient conditions.

AUTHOR: Sasaki Takayuki(a); Kurano Norihide(a); Miyachi Shigetoh

AUTHOR ADDRESS: (a)Marine Biotechnol. Inst., Kamaishi Lab., 3-75-1 Heita, Kamaishi City, Iwate 026-0001**Japan

JOURNAL: Plant and Cell Physiology 39 (4):p405-410 April 1998

ISSN: 0032-0781

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The marine green alga, *Chlorococcum littorale*, accumulated iron in its cells and showed high activity of plasma membrane **ferric reductase** under high-CO₂ and iron-deficient conditions. These activities disappeared upon exposure to ordinary air and by adding excess FeSO₄. The iron uptake had high affinity for the Fe(II) form (K_m of 0.13 μM). Carbonylcyanide m-chlorophenylhydrazine and N,N-dicyclohexylcarbodiimide significantly suppressed the iron uptake, suggesting that the Fe(II) uptake was driven by ATPase. These results indicate that high CO₂ and iron deficiency cooperatively induce the Fe(II) uptake and cell-surface **ferric reductase** activity.

1998

5/3,AB/19 (Item 11 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2002 BIOSIS. All rts. reserv.

11436747 BIOSIS NO.: 199800218079

Iron limitation results in induction of ferricyanide reductase and **ferric chelate reductase** activities in *Chlamydomonas reinhardtii*.

AUTHOR: Lynnes Jaret A; Derzaph Tina L M; Weger Harold G(a)

AUTHOR ADDRESS: (a)Dep. Biol., Univ. Regina, Regina, SK S4S 0A2**Canada

JOURNAL: Planta (Berlin) 204 (3):p360-365 March, 1998

ISSN: 0032-0935

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The green alga *Chlamydomonas reinhardtii* Dangeard CW-15 exhibited very low rates of plasma-membrane Fe(III) reductase activity when grown under Fe-sufficient conditions. After switching the medium to an Fe-free

formulation, both ferricyanide reductase and **ferric chelate reductase** activities rapidly increased, reaching a maximum after 3 d under iron-free conditions. Both of the Fe(III) reductase activities increased in parallel over time, they exhibited similar K_m values (approximately 10 μ M) with respect to Fe(III), displayed the same pH profile of activity, and both exhibited the same degree of light stimulation which could be inhibited by 3-(3',4'-dichlorophenyl)-1,1-dimethylurea (DCMU). Furthermore, ferricyanide competitively inhibited ferric chelate reduction by iron-limited cells. These results indicate that both Fe(III) reductase activities were mediated by the same iron-limitation-induced plasma-membrane reductase. No evidence was found for the presence of Fe(III)-reducing substances in the culture medium, or for the involvement of active oxygen species in the process of Fe(III) reduction. *Chlamydomonas reinhardtii* appears to respond to iron limitation in a manner similar to Strategy I higher plants.

1998

5/3,AB/20 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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07409055 Genuine Article#: 162GE Number of References: 32
Title: The induction of the 'turbo reductase' is inhibited by cycloheximide, cordycepin and ethylene inhibitors in Fe-deficient cucumber (*Cucumis sativus* L.) plants (ABSTRACT AVAILABLE)
Author(s): Romera FJ (REPRINT) ; Alcantara E; delaGuardia MD
Corporate Source: ESCUELA TS INGN AGRON & MONTES,DEPT AGRON, APDO 3048/E-14080 CORDOBA//SPAIN/ (REPRINT)
Journal: PROTOPLASMA, 1998, V205, N1-4, P156-162
ISSN: 0033-183X Publication date: 19980000
Publisher: SPRINGER-VERLAG WIEN, SACHSENPLATZ 4-6, PO BOX 89, A-1201 VIENNA, AUSTRIA
Language: English Document Type: ARTICLE
Abstract: Dicotyledonous plants respond to Fe deficiency by enhancing the capacity of their roots to reduce Fe(III) to Fe(II). It has been suggested that there are two different ferric redox systems in the roots: the standard reductase, active with ferricyanide and not inducible by Fe deficiency, and the turbo reductase, active with both ferricyanide and ferric chelates and inducible by Fe deficiency. We have used different experimental approaches to test whether or not the Fe(III)-reducing capacity of cucumber (*Cucumis sativus* L. cv. Ashley) roots can be explained by considering the standard and the turbo reductase as the same enzyme. For this, we used both Fe-sufficient and Fe-deficient plants, which were treated with ethylene inhibitors (cobalt or silver thiosulfate; found to inhibit the turbo reductase in a previous work), a protein synthesis inhibitor (cycloheximide), or an mRNA polyadenylation inhibitor (cordycepin). At different times after application of these inhibitors, reduction of both ferricyanide and Fe(III)-EDTA were determined. In addition, we studied the effects of pH and temperature on the reduction of ferricyanide and Fe(III)-EDTA by both Fe-sufficient and Fe-deficient plants. Results suggest that there are, at least, two different ferric redox systems in the roots. Enhancement of Fe(III)-reducing capacity (turbo reductase) by Fe-deficient plants probably requires the de novo synthesis of a (or several) protein(s), which has a high turnover rate and whose expression is presumably regulated by ethylene.

5/3,AB/21 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

07341315 Genuine Article#: 153DJ Number of References: 22
Title: Siderophore-mediated iron uptake in *Saccharomyces cerevisiae*: the SIT1 gene encodes a ferrioxamine B permease that belongs to the major facilitator superfamily (ABSTRACT AVAILABLE)
Author(s): Lesuisse E (REPRINT) ; SimonCasteras M; Labbe P
Corporate Source: UNIV PARIS 07, INST JACQUES MONOD, LAB BIOCHIM PORPHYRINES, TOUR 43, 2 PL JUSSIEU/F-75251 PARIS 05//FRANCE/ (REPRINT)
Journal: MICROBIOLOGY-UK, 1998, V144, 12 (DEC), P3455-3462
ISSN: 1350-0872 Publication date: 19981200
Publisher: SOC GENERAL MICROBIOLOGY, MARLBOROUGH HOUSE, BASINGSTOKE RD, SPENCERS WOODS, READING RG7 1AE, BERKS, ENGLAND
Language: English Document Type: ARTICLE
Abstract: Uptake of iron from various siderophores by a Delta fet3 Delta fet4 strain of *Saccharomyces cerevisiae* was investigated. The catecholate enterobactin and the hydroxamate coprogen were taken up by the cells by passive diffusion, whereas the hydroxamates ferrioxamine B (FOB) and ferricrocin (FC) were taken up via a high-affinity energy-dependent mechanism. The kinetics of FOE and FC uptake showed reciprocal competitive inhibition. The transport was regulated by iron availability, but was independent of the Aft1p and Mac1p transcriptional activators. Mutants affected in the transport of FOE were isolated. The transport of FC was not impaired in these mutants. Functional complementation of one mutant allowed the identification of the SIT1 gene (Siderophore Iron Transport) encoding a putative permease belonging to the major facilitator superfamily. The Sit1 protein is probably a permease specific for the transport of ferrioxamine-type siderophores. The evidence suggests that the uptake of ferrichrome-type siderophores like FC involves other specific permease(s), although there seems to be a common handling of FOE and FC following their internalization by the cell.

5/3,AB/22 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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07070603 Genuine Article#: 120KG Number of References: 33
Title: Expression of the yeast FRE genes in transgenic tobacco (ABSTRACT AVAILABLE)
Author(s): Samuelsen AI; Martin RC; Mok DWS; Mok MC (REPRINT)
Corporate Source: OREGON STATE UNIV, DEPT HORT/CORVALLIS//OR/97331 (REPRINT) ; OREGON STATE UNIV, DEPT HORT/CORVALLIS//OR/97331; OREGON STATE UNIV, CTR GENE RES & BIOTECHNOL/CORVALLIS//OR/97331
Journal: PLANT PHYSIOLOGY, 1998, V118, N1 (SEP), P51-58
ISSN: 0032-0889 Publication date: 19980900
Publisher: AMER SOC PLANT PHYSIOLOGISTS, 15501 MONONA DRIVE, ROCKVILLE, MD 20855
Language: English Document Type: ARTICLE
Abstract: Two yeast genes, FRE1 and FRE2 (encoding Fe(III) reductases) were placed under the control of the cauliflower mosaic virus 35S promoter and introduced into tobacco (*Nicotiana tabacum* L.) via *Agrobacterium tumefaciens*-mediated transformation. Homozygous lines containing FRE1, FRE2, or FRE1 plus FRE2 were generated. Northern-blot analyses revealed mRNA of two different sizes in FRE1 lines, whereas all FRE2 lines had mRNA only of the expected length. Fe(III) reduction, chlorophyll contents, and re levels were determined in transgenic and control plants under Fe-sufficient and Fe-deficient conditions. In a normal growth environment, the highest root Fe(III) reduction, 4-fold higher than in controls, occurred in the double transformant (FRE1 + FRE2). Elevated Fe(III) reduction was also observed in all FRE2 and some FRE1 lines. The increased Fe(III) reduction occurred along the entire length of the roots and on shoot sections. FRE2 and double transformants were more tolerant to re deficiency in hydroponic culture, as shown by



higher chlorophyll and re concentrations in younger leaves, whereas FRE1 transformants did not differ from the controls. Overall, the beneficial effects of FRE2 were consistent, suggesting that FRE2 may be used to improve Fe efficiency in crop plants.

5/3,AB/23 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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07056793 Genuine Article#: 119JT Number of References: 32
Title: Metalloregulation of FRE1 and FRE2 homologs in *Saccharomyces cerevisiae* (ABSTRACT AVAILABLE)
Author(s): Martins LJ; Jensen LT; Simons JR; Keller GL; Winge DR (REPRINT)

Corporate Source: UNIV UTAH,HLTH SCI CTR/SALT LAKE CITY//UT/84132 (REPRINT)
; UNIV UTAH,HLTH SCI CTR/SALT LAKE CITY//UT/84132
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1998, V273, N37 (SEP 11), P 23716-23721

ISSN: 0021-9258 Publication date: 19980911
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814

Language: English Document Type: ARTICLE

Abstract: The high affinity uptake systems for iron and copper ions in *Saccharomyces cerevisiae* involve metal-specific permeases and two known cell surface Cu(II) and Fe(III) metalloredutases, Fre1 and Fre2. Five novel genes found in the *S. cerevisiae* genome exhibit marked sequence similarity to Fre1 and Fre2, suggesting that the homologs are part of a family of proteins related to Fre1 and Fre2. The homologs are expressed genes in *S. cerevisiae*, and their expression is metalloregulated as is true with FRE1 and FRE2. Four of the homologs (FRE3-FRE6) are specifically hen-regulated through the Aft1 transcription factor. These genes are expressed either in cells limited for iron ion uptake by treatment with a chelator or in cells lacking the high affinity iron uptake system. Expression of FRE3-FRE6 is elevated in AFT1-1(up) cells and attenuated in aft1 null cells, showing that iron modulation occurs through the Aft1 transcriptional activator. The fifth homolog FRE7 is specifically copper-metalloregulated, FRE7 is expressed in cells limited in copper ion uptake by a Cu(I)-specific chelator or in cells lacking the high affinity Cu(I) permeases. The constitutive expression of FRE7 in MAC1(up1) cells and the lack of expression in mac1-1 cells are consistent with Mad being the critical transcriptional activator of FRE7 expression. The 5' promoter sequence of FRE7 contains three copper-responsive promoter elements. Two elements are critical for Mad-dependent FRE7 expression. Combinations of either the distal and central elements or the central and proximal elements result in copper-regulated FRE7 expression. Spacing between Mac1-responsive sites is important as shown by the attenuated expression of FRE7 and CTR1 when two elements are separated by over 100 base pairs. From the three Mac1-responsive elements in FRE7, a new consensus sequence for Mad binding can be established as TTTGC(T/G)C(A/G).

5/3,AB/24 (Item 5 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

07013335 Genuine Article#: 114NY Number of References: 13
Title: Site-directed mutagenesis of the yeast multicopper oxidase Fet3p (ABSTRACT AVAILABLE)
Author(s): Askwith CC; Kaplan J (REPRINT)
Corporate Source: UNIV UTAH,SCH MED, DEPT PATHOL, DIV CELL BIOL & IMMUNOL, 50 N MED DR/SALT LAKE CITY//UT/84132 (REPRINT); UNIV UTAH,SCH MED, DEPT PATHOL, DIV CELL BIOL & IMMUNOL/SALT LAKE CITY//UT/84132

Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1998, V273, N35 (AUG 28), P 22415-22419

ISSN: 0021-9258 Publication date: 19980828

Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814

Language: English Document Type: ARTICLE

Abstract: High affinity iron transport in yeast is mediated by two proteins, Fet3p and Ftr1p. The multicopper oxidase Fet3p is thought to convert extracellular ferrous iron to ferric iron, which then crosses the plasma membrane through the permease Ftr1p, Fet3p is capable of oxidizing other substrates, such as p-phenylenediamine, and there is still a question of whether it is the ferroxidase activity that is essential for iron transport. Fet3p is also required for Ftr1p localization to the cell surface, making it difficult to prove a direct role for Fet3p oxidase in high affinity iron transport. In an attempt to generate Fet3p specifically lacking ferroxidase activity, we used site-directed mutagenesis to alter residues within Fet3p that had been suggested to impart iron oxidase activity. These substitutions resulted in either a loss or retention of both p-phenylenediamine and ferroxidase activities, indicating that the ability of Fet3p to act as a ferroxidase involves other amino acids. Inactive Fet3p, however, did mediate Ftr1p localization to the cell surface but did not mediate high affinity iron transport. These observations indicate that the ferroxidase activity of Fet3p is intrinsically required for high affinity iron transport.

5/3,AB/25 (Item 6 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06997355 Genuine Article#: 112VT Number of References: 28

Title: Effect of siderophores, catecholamines, and catechol compounds on *Listeria* spp. Growth in iron-complexed medium (ABSTRACT AVAILABLE)

Author(s): Coulanges V; Andre P; Vidon DJM (REPRINT)

Corporate Source: UNIV LOUIS PASTEUR STRASBOURG 1,DEPT SCI ALIMENT, UFR SCI PHARMACEUT/F-67401 ILLKIRCH GRAFFENSTADEN//FRANCE/ (REPRINT); UNIV LOUIS PASTEUR STRASBOURG 1,DEPT SCI ALIMENT, UFR SCI PHARMACEUT, LAB BACTERIOL & CRYPTOGRAMIE/F-67401 ILLKIRCH GRAFFENSTADEN//FRANCE/

Journal: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, 1998, V 249, N2 (AUG 19), P526-530

ISSN: 0006-291X Publication date: 19980819

Publisher: ACADEMIC PRESS INC JNL-COMP SUBSCRIPTIONS, 525 B ST, STE 1900, SAN DIEGO, CA 92101-4495

Language: English Document Type: ARTICLE

Abstract: Almost all bacteria require iron for growth and virulence expression. However, *Listeria* spp. do not produce any siderophore for iron acquisition. Representative strains of each of the six species of *Listeria* were examined for their ability to use various compounds as iron suppliers in iron-restricted medium. Here we show that *L. monocytogenes*, *L. innocua*, *L. ivanovii*, *L. welshimeri*, *L. seeligeri*, and *L. grayi* were able to use exogenous siderophores and various catechol ligands, including catecholamines, to overcome growth inhibition induced by tropolone, an iron chelating agent. In contrast, no growth promoting effect was observed with normetanephrine or 4-hydroxy-3-methoxyphenylglycol-piperazine salt, which indicates that the o-diphenol function of the ligand must be free to allow iron acquisition. Furthermore, we demonstrate that catecholamines do not act through specific bacterial receptors, because no difference in growth stimulation was observed between [+]- and [-]-norepinephrine. These results show that utilization of a variety of catechol compounds to acquire iron is a general phenomenon in the genus *Listeria*. (C) 1998 Academic Press.

5/3,AB/26 (Item 7 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06987037 Genuine Article#: 106YR Number of References: 136
Title: The molecular biology of metal ion transport in *Saccharomyces cerevisiae* (ABSTRACT AVAILABLE)
Author(s): Eide DJ (REPRINT)
Corporate Source: UNIV MISSOURI,NUTR SCI PROGRAM/COLUMBIA//MO/65203 (REPRINT)
Journal: ANNUAL REVIEW OF NUTRITION, 1998, V18, P441-469
ISSN: 0199-9885 Publication date: 19980000
Publisher: ANNUAL REVIEWS INC, 4139 EL CAMINO WAY, PO BOX 10139, PALO ALTO, CA 94303-0139
Language: English Document Type: REVIEW
Abstract: Transition metals such as iron, copper, manganese, and zinc are essential nutrients. The yeast *Saccharomyces cerevisiae* is an ideal organism for deciphering the mechanism and regulation of metal ion transport. Recent studies of yeast have shown that accumulation of any single metal ion is mediated by two or more substrate-specific transport systems. High-affinity systems are active in metal-limited cells, whereas low-affinity systems play the predominant roles when the substrate is more abundant. Metal ion uptake systems of cells are tightly controlled, and both transcriptional and posttranscriptional regulatory mechanisms have been identified. Most importantly, studies of *S. cerevisiae* have identified a large number of genes that function in metal ion transport and have illuminated the existence and importance of gene families that play related roles in these processes in mammals.

5/3,AB/27 (Item 8 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06929306 Genuine Article#: 104DZ Number of References: 51
Title: Isolation and identification of sulphite- and iron reducing, hydrogenase positive facultative anaerobes from cooling water systems (ABSTRACT AVAILABLE)
Author(s): McLeod ES; Dawood Z; MacDonald R; Oosthuizen MC; Graf J; Steyn PL; Brozel VS (REPRINT)
Corporate Source: UNIV PRETORIA,DEPT MICROBIOL & PLANT PATHOL/ZA-0002 PRETORIA//SOUTH AFRICA/ (REPRINT); UNIV PRETORIA,DEPT MICROBIOL & PLANT PATHOL/ZA-0002 PRETORIA//SOUTH AFRICA/; UNIV WESTERN CAPE,DEPT MICROBIOL/ZA-7535 BELLVILLE//SOUTH AFRICA/; UNIV BERN,INST MED MICROBIOL/BERN//SWITZERLAND/
Journal: SYSTEMATIC AND APPLIED MICROBIOLOGY, 1998, V21, N2 (JUN), P 297-305
ISSN: 0723-2020 Publication date: 19980600
Publisher: GUSTAV FISCHER VERLAG, VILLEGANG 2, D-07745 JENA, GERMANY
Language: English Document Type: ARTICLE
Abstract: The significance of sulphidogenic facultative anaerobes in microbially influenced corrosion (MIC) has been overshadowed by extensive research on sulphate-reducing bacteria (SRB). An enrichment procedure with Modified Iron Sulphite (MIS) medium was employed to select for sulphidogenic facultative anaerobes from industrial cooling water systems. All isolates reduced sulphite and ferric iron, oxidised cathodic hydrogen on mild steel, and some oxidised cathodic hydrogen on stainless steel (3CR12). Facultative anaerobes generating sulphide from sulphite were identified by making use of biochemical tests, API 20 NE, BIOLOG, SDS-PAGE of the total soluble cell proteins, partial sequences of the 16S rRNA gene (rDNA) and RFLP-PCR. Our results show that *Aeromonas* isolated from cooling water systems, ie *A. veronii* biotype

sobria, *A. hydrophila* and *A. media* can reduce both ferric to ferrous iron and sulphite to hydrogen sulphide in IS medium. The results further showed that these sulphidogenic bacteria are all capable of reducing cathodic hydrogen and therefore play a role in MIC.

5/3,AB/28 (Item 9 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06628565 Genuine Article#: ZG113 Number of References: 27
Title: Genetic analysis of iron uptake in the yeast *Saccharomyces cerevisiae* (ABSTRACT AVAILABLE)
Author(s): Dancis A (REPRINT)
Corporate Source: UNIV PENN, DEPT MED, DIV HEMATOL ONCOL, 1009 STELLAR CHASE LABS, 422 CURIE BLVD/PHILADELPHIA//PA/19104 (REPRINT); NICHHD, CELL BIOL & METAB BRANCH, NIH/BETHESDA//MD/20892
Journal: JOURNAL OF PEDIATRICS, 1998, V132, N3, 2, S (MAR), PS24-S29
ISSN: 0022-3476 Publication date: 19980300
Publisher: MOSBY-YEAR BOOK INC, 11830 WESTLINE INDUSTRIAL DR, ST LOUIS, MO 63146-3318
Language: English Document Type: ARTICLE
Abstract: Objective: We used the methods of yeast genetics to identify genes involved in acquisition of iron by eukaryotic cells.

Methods: Mutants were identified with defects in cellular iron uptake. These were organized into an upstream group and a downstream group. The upstream group was involved in the delivery of copper to the multicopper oxidase FET3. Mutants of this group were characterized by defective iron uptake that could be corrected by exposure of the cells to large amounts of copper. The downstream group was more directly involved in iron uptake. Mutant phenotypes from these genes could not be corrected by copper exposure.

Results: Genes in the upstream group encoded the regulator of copper transport, MAC1, and two copper transporters, CTR1 and CCC2. Genes in the downstream group encoded the multicopper oxidase FET3 and its partner the iron permease FTR1. In addition, the downstream genes encoded the surface reductases FRE1 and FRE2 and the iron regulatory protein AFT1.

Conclusions: The iron and copper uptake processes in yeast intersect because the FET5 gene encodes a multicopper oxidase that is required for iron transport. In human beings, an analogous function may be served by ceruloplasmin, a multicopper oxidase with a role in iron homeostasis.

5/3,AB/29 (Item 10 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06620438 Genuine Article#: ZF226 Number of References: 42
Title: Coenzyme Q(6) and iron reduction are responsible for the extracellular ascorbate stabilization at the plasma membrane of *Saccharomyces cerevisiae* (ABSTRACT AVAILABLE)
Author(s): SantosOcana C; Cordoba F; Crane FL; Clarke CF; Navas P (REPRINT)
Corporate Source: UNIV CORDOBA, FAC CIENCIAS, DEPT BIOL CELULAR, AVE SAN ALBERTO MAGNO S-N/E-14004 CORDOBA//SPAIN/ (REPRINT); UNIV CORDOBA, FAC CIENCIAS, DEPT BIOL CELULAR/E-14004 CORDOBA//SPAIN/; UNIV HUELVA, DEPT CIENCIAS AGROFORESTALES/HUELVA 21819//SPAIN/; PURDUE UNIV, DEPT BIOL SCI/W LAFAYETTE//IN/47907; UNIV CALIF LOS ANGELES, INST MOL BIOL, DEPT CHEM & BIOCHEM/LOS ANGELES//CA/90095

Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1998, V273, N14 (APR 3), P
8099-8105

ISSN: 0021-9258 Publication date: 19980403

Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE
PIKE, BETHESDA, MD 20814

Language: English Document Type: ARTICLE

Abstract: Yeast plasma membrane contains an electron transport system that maintains ascorbate in its reduced form in the apoplast, Reduction of ascorbate free radical by this system is comprised of two activities, one of them dependent on coenzyme Q(6) (CoQ(6)), Strains with defects in CoQ(6) synthesis exhibit decreased capacity for ascorbate stabilization compared with wild type or with atp2 or cor1 respiratory-deficient mutant strains, Both CoQ(6) content in plasma membranes and ascorbate stabilization were increased during log phase growth, The addition of exogenous CoQ(6) to whole cells resulted in its incorporation in the plasma membrane, produced levels of CoQ(6) in the coq3 mutant strain that were 2-fold higher than in the wild type, and increased ascorbate stabilization activity in both strains, although it was higher in the coq3 mutant than in wild type, Other antioxidants, such as benzoquinone or alpha-tocopherol, did not change ascorbate stabilization.

The CoQ(6)-independent reduction of ascorbate free radical was not due to copper uptake, pH changes or to the presence of CoQ(6) biosynthetic intermediates, but decreased to undetectable levels when coq3 mutant strains were cultured in media supplemented with ferric iron, Plasma membrane CoQ(6) levels were unchanged by either the presence or absence of iron in wild type, atp2, or cor1 strains, Ascorbate stabilization appears to be a function of the yeast plasma membrane, which is partially based on an electron transfer chain in which CoQ(6) is the central electron carrier, whereas the remainder is independent of CoQ(6) and other antioxidants but is dependent on the iron-regulated **ferric reductase** complex.

5/3,AB/30 (Item 11 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06609349 Genuine Article#: ZE277 Number of References: 43
Title: Influence of copper depletion on iron uptake mediated by SFT, a stimulator of Fe transport (ABSTRACT AVAILABLE)
Author(s): Yu JM (REPRINT) ; WesslingResnick M
Corporate Source: HARVARD UNIV,SCH PUBL HLTH, DEPT NUTR, 666 HUNTINGTON AVE/BOSTON//MA/02115 (REPRINT)
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1998, V273, N12 (MAR 20), P 6909-6915

ISSN: 0021-9258 Publication date: 19980320

Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE
PIKE, BETHESDA, MD 20814

Language: English Document Type: ARTICLE

Abstract: We recently identified a novel factor involved in cellular iron assimilation called SFT or Stimulator of Fe Transport (Gutierrez, J. A., Yu, J., Rivera, S., and Wessling-Resnick, M. (1997) J. Cell Biol. 149, 895-905). When stably expressed in HeLa cells, SFT was found to stimulate the uptake of both transferrin- and nontransferrin-bound Fe (iron), Assimilation of nontransferrin-bound Fe by HeLa cells stably expressing SFT was time- and temperature-dependent; both the rate and extent of uptake was enhanced relative to the activity of control nontransfected cells, Although the apparent K-m for Fe uptake was unaffected by expression of SFT (5.6 versus 5.1 mu M measured for control), the V-max of transport was increased from 7.0 to 14.7 pmol/min/mg protein, Transport mediated by SFT was inhibitable by diethylenetriaminepentaacetic acid and ferrozine, Fe3+- and

Fe²⁺-specific chelators, Because cellular copper status is known to influence Fe assimilation, we investigated the effects of Cu (copper) depletion on SFT function, After 4 days of culture in Cu-deficient media, HeLa cell Cu,Zn superoxide dismutase activity was reduced by more than 60%, Both control cells and cells stably expressing SFT displayed reduced Fe uptake as well; levels of transferrin-mediated import fell by similar to 80%, whereas levels of nontransferrin-bound Fe uptake were similar to 50% that of Cu-replete cells, The failure of SFT expression to stimulate Fe uptake above basal levels in Cu-depleted cells suggests a critical role for Cu in SFT function, A current model for both transferrin-and nontransferrin-bound Fe uptake involves the function of a ferrireductase that acts to reduce Fe³⁺ to Fe²⁺, with subsequent transport of the divalent cation across the membrane bilayer, SFT expression did not enhance levels of HeLa cell surface reductase activity; however, Cu depletion was found to reduce endogenous activity by 60%, suggesting impaired ferrireductase function may account for the influence of Cu depletion on SFT-mediated Fe uptake, To test this hypothesis, the ability of SFT to directly mediate Fe²⁺ import was examined, Although expression of SFT enhanced Fe²⁺ uptake by HeLa cells, Cu depletion did not significantly reduce this activity, Thus, we conclude that a ferrireductase activity is required for SFT function in Fe³⁺ transport and that Cu depletion reduces cellular iron assimilation by affecting this activity.

5/3,AB/31 (Item 12 from file: 34)
 DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
 (c) 2002 Inst for Sci Info. All rts. reserv.

06607537 Genuine Article#: ZE202 Number of References: 36
 Title: The surface of rat hepatocytes can transfer iron from stable
 chelates to external acceptors (ABSTRACT AVAILABLE)
 Author(s): Scheiber B; Goldenberg H (REPRINT)
 Corporate Source: UNIV VIENNA, INST MED CHEM, WAEHRINGERSTR 10/A-1090
 VIENNA//AUSTRIA/ (REPRINT); UNIV VIENNA, INST MED CHEM/A-1090
 VIENNA//AUSTRIA/
 Journal: HEPATOLOGY, 1998, V27, N4 (APR), P1075-1080
 ISSN: 0270-9139 Publication date: 19980400
 Publisher: W B SAUNDERS CO, INDEPENDENCE SQUARE WEST CURTIS CENTER, STE
 300, PHILADELPHIA, PA 19106-3399

Language: English Document Type: ARTICLE

Abstract: The chelator diethylenetriaminepentaacetate (DTPA) forms a stable complex with iron that does not donate iron to transferrin under physiological conditions, i.e., pH above 7 and isotonic milieu, It does, however, deliver iron to hepatocytes, This uptake is initiated by a mobilization of the metal from the complex by the cell surface. When an external chelator is added simultaneously, it can bind the iron and inhibit its accumulation by the cells. This is shown here with the impermeant siderophore conjugate hydroxyethyl-starch coupled desferrioxamine, as well as with apotransferrin, We also demonstrate exchange of iron between DTPA and holo-transferrin, or at least movement from the chelator to the protein, which may have lost its iron to the cell in advance, providing new binding sites for mobilized iron. The efficient hepatocyte iron donor lactoferrin greatly stimulates iron uptake from DTPA, apparently by binding iron and transferring it into the cells by endocytosis. Ferritin is unable to do this; therefore, the mobilization of iron is not caused by a reducing activity at the cell surface, because iron is readily transferred from DTPA to ferritin by the reductant ascorbic acid, The transfer process is dependent on the temperature, the time, and the amount of cells present, and is partly inhibited by sulfhydryl reagents, We conclude that this activity represents a hitherto unidentified first step in the movement of iron through the cell membrane and may be relevant for transferrin-bound, as well as for non-transferrin-bound, iron uptake by hepatocytes.

5/3,AB/32 (Item 13 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

06603908 Genuine Article#: ZD917 Number of References: 37
Title: Regulation of high affinity iron uptake in the yeast *Saccharomyces cerevisiae* - Role of dioxygen and Fe(II) (ABSTRACT AVAILABLE)
Author(s): Hassett RF; Romeo AM; Kosman DJ (REPRINT)
Corporate Source: SUNY BUFFALO, SCH MED & BIOMED SCI, DEPT BIOCHEM, 140 FARBER HALL, 3435 MAIN ST/BUFFALO//NY/14214 (REPRINT); SUNY BUFFALO, SCH MED & BIOMED SCI, DEPT BIOCHEM/BUFFALO//NY/14214
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1998, V273, N13 (MAR 27), P 7628-7636
ISSN: 0021-9258 Publication date: 19980327
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814

Language: English Document Type: ARTICLE

Abstract: High affinity iron uptake in *Saccharomyces cerevisiae* requires a metal reductase, a multicopper ferroxidase, and an iron permease. Fet3, the apparent ferroxidase, is proposed to facilitate iron uptake by catalyzing the oxidation of reductase-generated Fe(II) to Fe(III) by O₂; in this model, Fe(III) is the substrate for the iron permease, encoded by FTR1 (Kaplan, J., and O'Halloran, T. V. (1996) Science 271, 1510-1512). We show here that dioxygen also plays an essential role in the expression of these iron uptake activities. Cells grown anaerobically exhibited no Fe(III) reductase or high affinity iron uptake activity, even if assayed for these activities under air. Northern blot analysis showed that the amount of those mRNAs encoding proteins associated with this uptake was repressed in anaerobic cultures but was rapidly induced by exposure of the culture to dioxygen. The anaerobic repression was reduced in cells expressing an iron-independent form of the trans activator, Aft1, a protein that regulates the expression of these proteins. Thus, the effect of oxygenation on this expression appeared due at least in part to the state or distribution of iron in the cells. In support of this hypothesis, the membrane-permeant Fe(II) chelator, 2,2'-bipyridyl, in contrast to the impermeant chelator bathophenanthroline disulfonate, caused a strong and rapid induction of these transcripts under anaerobic conditions. An increase in the steady-state levels of iron-regulated transcripts upon oxygenation or 2,2'-bipyridyl addition occurred within 5 min, indicating that a relatively small, labile intracellular pool of Fe(II) regulates the expression of these activities. The strength of the anaerobic repression was dependent on the low affinity, Fe(II)-specific iron transporter, encoded by FET4, suggesting that this Fe(II) pool was linked in part to iron brought into the cell via Fet4 protein. The data suggest a model in which dioxygen directly or indirectly modulates the Fe(III)/Fe(II) ratio in an iron pool linked to Aft1 protein while bipyridyl increases this ratio by chelating Fe(II). These results indicate that dioxygen both modulates the sensitivity to iron-dependent transcriptional regulation and acts as substrate for Fet3 in the ferroxidase reaction catalyzed by this ceruloplasmin homologue.

5/3,AB/33 (Item 14 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06579193 Genuine Article#: ZC522 Number of References: 42
Title: *Helicobacter pylori* ribBA-mediated riboflavin production is involved in iron acquisition (ABSTRACT AVAILABLE)
Author(s): Worst DJ; Gerrits MM; VandenbrouckeGrauls CMJE; Kusters JG

(REPRINT)

Corporate Source: FREE UNIV AMSTERDAM, FAC MED, DEPT MED MICROBIOL, VAN DER BOECHORSTSTR 7/NL-1081 BT AMSTERDAM//NETHERLANDS/ (REPRINT); FREE UNIV AMSTERDAM, FAC MED, DEPT MED MICROBIOL/NL-1081 BT AMSTERDAM//NETHERLANDS/

Journal: JOURNAL OF BACTERIOLOGY, 1998, V180, N6 (MAR), P1473-1479

ISSN: 0021-9193 Publication date: 19980300

Publisher: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW, WASHINGTON, DC 20005-4171

Language: English Document Type: ARTICLE

Abstract: In this study, we cloned and sequenced a DNA fragment from an ordered cosmid library of Helicobacter pylori NCTC 11638 which confers to a siderophore synthesis mutant of Escherichia coli (EB53 aroB hemA) the ability to grow on iron-restrictive media and to reduce ferric iron. Sequence analysis of the DNA fragment revealed the presence of an open reading frame with high homology to the ribA gene of Bacillus subtilis. This gene encodes a bifunctional enzyme with the activities of both 3,4-dihydroxy-2-butanone 4-phosphate (DHBP) synthase and GTP cyclohydrolase II, which catalyze two essential steps in riboflavin biosynthesis. Expression of the gene (designated ribBA) resulted in the formation of one translational product, which was able to complement both the ribA and the ribB mutation in E. coli. Expression of ribBA was iron regulated, as was suggested by the presence of a putative FUR box in its promoter region and as shown by RNA dot blot analysis. Furthermore, we showed that production of riboflavin in H. pylori cells is iron regulated. E. coli EB53 containing the plasmid with H. pylori ribBA excreted riboflavin in the culture medium, and this riboflavin excretion also appeared to be iron regulated. We postulate that the iron-regulated production of riboflavin and ferric-iron-reduction activity by E. coli EB53 transformed with the H. pylori ribBA gene is responsible for the survival of EB53 on iron-restrictive medium. Because disruption of ribBA in H. pylori eliminates its ferric-iron-reduction activity, we conclude that ribBA has an important role in ferric-iron reduction and iron acquisition by H. pylori.

5/3,AB/34 (Item 15 from file: 34)

DIALOG(R) File 34:SciSearch(R) Cited Ref Sci

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06453998 Genuine Article#: BK30A Number of References: 124

Title: Molecular biology of iron transport in fungi

Author(s): Leong SA (REPRINT) ; Winkelmann G

Corporate Source: UNIV WISCONSIN, USDA ARS/MADISON//WI/53706 (REPRINT); UNIV WISCONSIN, DEPT PLANT PATHOL/MADISON//WI/53706; UNIV TUBINGEN, D-72076 TUBINGEN//GERMANY/

, 1998, V35, P147-186

ISSN: 0161-5149 Publication date: 19980000

Publisher: MARCEL DEKKER, 270 MADISON AVE, NEW YORK, NY 10016 METAL IONS IN BIOLOGICAL SYSTEMS

Series: METAL IONS IN BIOLOGICAL SYSTEMS

Language: English Document Type: REVIEW

5/3,AB/35 (Item 1 from file: 44)

DIALOG(R) File 44:Aquatic Sci&Fish Abs

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00623483 ASFA Accession Number: 4309826

Cloning and characterization of high-CO sub(2)-specific cDNAs from a marine microalga, Chlorococcum littorale, and effect of CO sub(2) concentration and iron deficiency on the gene expression

Sasaki, T; Kurano, N; Miyachi, S

Mar. Biotechnol. Inst., Kamaishi Labs., 3-75-1 Heita, Kamaishi City,

Iwate, 026-0001, Japan

Plant & Cell Physiology "PLANT CELL PHYSIOL.", vol. 39, no. 2, p. 131-138, Feb 1998

Two cDNA clones exclusively induced under an extremely high-CO sub(2) concentration (20%) were isolated from *Chlorococcum littorale* by differential screening and named HCR (high-CO sub(2) response) 1 and 2, respectively. The amino acid sequence of the protein encoded by HCR2 exhibited homology to the gp91-phox protein, a critical component of a human phagocyte oxidoreductase, and to the yeast **ferric reductases**, *Saccharomyces cerevisiae* FRE1 and FRE2 and *Schizosaccharomyces pombe* Frp1. The induction of both HCR mRNAs required extremely high-CO sub(2) conditions and iron deficiency, being suppressed under air conditions and by iron sufficiency, suggesting that the expression of these two HCR genes required extremely high-CO sub(2) conditions and iron deficiency in combination. The HCR2 protein was detected in the membrane fractions of cells grown under conditions which would favor the induction of HCR2-mRNA and the protein level was lowered when the cells were transferred from iron deficient to 10 μ M FeSO sub(4) conditions (with 20% CO sub(2)).

5/3,AB/36 (Item 1 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
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02306107 4414478

Coenzyme Q sub(6) and iron reduction are responsible for the extracellular ascorbate stabilization at the plasma membrane of *Saccharomyces cerevisiae*

Santos Ocana, C.; Cordoba, F.; Crane, F.L.; Clarke, C.F.; Navas, P.
Depto. de Biologia Celular, Fac. de Cienc., Univ. de Cordoba, Avenida San Alberto Magno, s/n, 14004 Cordoba, Spain
J. BIOL. CHEM. vol. 273, no. 14, pp. 8099-8105 (1998)
ISSN: 0021-9258

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH

SUBFILE: Microbiology Abstracts C: Algology, Mycology & Protozoology

Yeast plasma membrane contains an electron transport system that maintains ascorbate in its reduced form in the apoplast. Reduction of ascorbate free radical by this system is comprised of two activities, one of them dependent on coenzyme Q sub(6) (CoQ sub(6)). Strains with defects in CoQ sub(6) synthesis exhibit decreased capacity for ascorbate stabilization compared with wild type or with atp2 or cor1 respiratory-deficient mutant strains. Both CoQ sub(6) content in plasma membranes and ascorbate stabilization were increased during log phase growth. The addition of exogenous CoQ sub(6) to whole cells resulted in its incorporation in the plasma membrane, produced levels of CoQ sub(6) in the coq3 mutant strain that were 2-fold higher than in the wild type, and increased ascorbate stabilization activity in both strains, although it was higher in the coq3 mutant than in wild type. Other antioxidants, such as benzoquinone or α -tocopherol, did not change ascorbate stabilization. The CoQ sub(6)-independent reduction of ascorbate free radical was not due to copper uptake, pH changes or to the presence of CoQ sub(6) biosynthetic intermediates, but decreased to undetectable levels when coq3 mutant strains were cultured in media supplemented with ferric iron. Plasma membrane CoQ sub(6) levels were unchanged by either the presence or absence of iron in wild type, atp2, or cor1 strains. Ascorbate stabilization appears to be a function of the yeast plasma membrane, which is partially based on an electron transfer chain in which CoQ sub(6) is the central electron carrier, whereas the remainder is independent of CoQ sub(6) and other antioxidants but is dependent on the iron-regulated **ferric reductase** complex.

5/3,AB/37 (Item 1 from file: 144)
DIALOG(R) File 144:Pascal
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13811834 PASCAL No.: 98-0527344
Induction of **ferric reductase** activity and of iron uptake capacity in *Chlorococcum littorale* cells under extremely high-CO SUB 2 and iron-deficient conditions
SASAKI T; KURANO N; MIYACHI S
Marine Biotechnology Institute, Kamaishi Laboratories, 3-75-1 Heita, Kamaishi City, Iwate, 026-0001, Japan; Marine Biotechnology Institute, Head Office, 1-28-10 Hongo, Bunkyo-ku, Tokyo, 113-0033, Japan
Journal: Plant and cell physiology, 1998, 39 (4) 405-410
Language: English

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5/3,AB/38 (Item 2 from file: 144)
DIALOG(R) File 144:Pascal
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13717056 PASCAL No.: 98-0408339
Iron assimilation in *Chlamydomonas reinhardtii* involves ferric reduction and is similar to Strategy I higher plants
ECKHARDT U; BUCKHOUT T J
Angewandte Botanik, Humboldt Universitaet zu Berlin, Invalidenstrasse 42, 10115 Berlin, Germany
Journal: Journal of Experimental Botany, 1998, 49 (324) 1219-1226
Language: English

The mechanism of adaptation to Fe-deficiency stress was investigated in the unicellular green alga, *Chlamydomonas reinhardtii*. Upon removal of nutritional Fe, the activity of a cell surface Fe(III)-chelate reductase was increased by at least 15-fold within 24 h. This increase was negatively correlated with the Fe concentration in the growth media. Incubation of cells in the presence of the Fe SUP 2 SUP + -specific chelator, bathophenanthrolinedisulphonic acid, led to an increased Fe SUP 3 SUP + reductase activity, even when sufficient Fe was present. Growth of cells in Cu-free media for 48 h led to no statistically significant increase in Fe SUP 3 SUP + reductase activity. The Fe(III)-chelate reductase activity in Fe-starved cells was saturable with an apparent K SUB m of 31 mu M and was inhibited by uncouplers of the transmembrane proton gradient but not by SH-specific reagents. Fe uptake was only observed in Fe-deficient cells. Uptake was specific for Fe in that a 100-fold excess of a number of metal ions in the transport assay did not inhibit uptake activity. However, a 100-fold excess of Cu resulted in a 87% inhibition of Fe uptake. The V SUB m SUB a SUB x for Fe SUP 3 SUP + reduction activity was 250-fold greater than for Fe uptake; although the K SUB m values for both processes differed by only 10-fold. Thus, the rate limiting step in Fe assimilation was transport and not reduction. These results indicate that Fe assimilation in *C. reinhardtii* involves a reductive step and thus resembles the mechanism of Fe uptake in Strategy I higher plants.

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ds

Set	Items	Description
S1	711	FRE(W)1 OR FERRIC (W) REDUCTAS? OR FERRIC (W) CHELATE (W) - REDUCTAS?
S2	317	S1 AND PY<1998
S3	0	S1 AND PY>1998 AND PY<1999
S4	77	S1 AND PY<1999 NOT S2
S5	38	RD (unique items)

? rd s2

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>>>Duplicate detection is not supported for File 306.

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...examined 50 records (150)

...examined 50 records (200)

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S6 152 RD S2 (unique items)

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6/3,AB/1 (Item 1 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

09570367 97431481 PMID: 9286986

Redox buffering by melanin and Fe(II) in *Cryptococcus neoformans*.

Jacobson ES; Hong JD

Hunter Holmes McGuire Veterans Affairs Medical Center, Richmond, Virginia 23249, USA. jacobson.eric s@richmond.va.gov

Journal of bacteriology (UNITED STATES) Sep 1997, 179 (17)

p5340-6, ISSN 0021-9193 Journal Code: HH3

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Melanin is a fungal extracellular redox buffer which, in principle, can neutralize antimicrobial oxidants generated by immunologic effector cells, but its source of reducing equivalents is not known. We wondered whether Fe(II) generated by the external **ferric reductase** of fungi might have the physiologic function of reducing fungal melanin and thereby promoting pathogenesis. We observed that exposure of a melanin film electrode to reductants decreased the open-circuit potential (OCP) and reduced the area of a cyclic voltammetric reduction wave whereas exposure to oxidants produced the opposite effects. Exposure to 10, 100, 1,000 or 10,000 microM Fe(II) decreased the OCP of melanin by 0.015, 0.038, 0.100, and 0.120 V, respectively, relative to a silver-silver chloride standard, and decreased the area of the cyclic voltammetric reduction wave by 27, 35, 50, and 83%, respectively. Moreover, exposure to Fe(II) increased the buffering capacity by 44%, while exposure to millimolar dithionite did not increase the buffering capacity. The ratio of the amount of bound iron to the amount of the incremental increase in the following oxidation wave was approximately 1.0, suggesting that bound iron participates in buffering. Light absorption by melanin suspensions was decreased 14% by treatment with Fe(II), consistent with reduction of melanin. Light absorption by suspensions of melanized *Cryptococcus neoformans* was decreased 1.3% by treatment with Fe(II) ($P < 0.05$). Cultures of *C. neoformans* generated between 2 and 160 microM Fe(II) in culture supernatant, depending upon the strain and the conditions [the higher values were achieved by a constitutive **ferric reductase** mutant in high concentrations of Fe(III)]. We infer that Fe(II) can reduce melanin under physiologic conditions; moreover, it binds to melanin and cooperatively increases redox

buffering. The data support a model for physiologic redox cycling of fungal melanin, whereby electrons exported by the yeast to form extracellular Fe(II) maintain the reducing capacity of the extracellular redox buffer.

6/3,AB/2 (Item 2 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09403151 97342753 PMID: 9199450

Utilization of iron-catecholamine complexes involving **ferric reductase** activity in *Listeria monocytogenes*.

Coulanges V; Andre P; Ziegler O; Buchheit L; Vidon DJ

Departement des Sciences de l'Aliment, Universite Louis Pasteur, U.F.R. des Sciences Pharmaceutiques, Illkirch, France.

Infection and immunity (UNITED STATES) Jul 1997, 65 (7)
p2778-85, ISSN 0019-9567 Journal Code: GO7

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Listeria monocytogenes is a ubiquitous potentially pathogenic organism requiring iron for growth and virulence. Although it does not produce siderophores, *L. monocytogenes* is able to obtain iron by using either exogenous siderophores produced by various microorganisms or natural catechol compounds widespread in the environment. In the presence of tropolone, an iron-chelating agent, growth of *L. monocytogenes* is completely inhibited. However, the growth inhibition can be relieved by the addition of dopamine or norepinephrine under their different isomeric forms, while the catecholamine derivatives 4-hydroxy-3-methoxyphenylglycol and normetanephrine did not relieve the inhibitory effect of tropolone. Preincubation of *L. monocytogenes* with chlorpromazine and yohimbine did not antagonize the growth-promoting effect of catecholamines in iron-complexed medium. In addition, norepinephrine stimulated the growth-promoting effect induced by human transferrin in iron-limited medium. Furthermore, dopamine and norepinephrine allowed ⁵⁵Fe uptake by iron-deprived bacterial cells. The uptake of iron was energy dependent, as indicated by inhibition of ⁵⁵Fe uptake at 0 degrees C as well as by preincubating the bacteria with KCN. Inhibition of ⁵⁵Fe uptake by *L. monocytogenes* was also observed in the presence of Pt(II). Moreover, when assessed by a whole-cell **ferric reductase** assay, reductase activity of *L. monocytogenes* was inhibited by Pt(II). These data demonstrate that dopamine and norepinephrine can function as siderophore-like compounds in *L. monocytogenes* owing to their ortho-diphenol function and that catecholamine-mediated iron acquisition does not involve specific catecholamine receptors but acts through a cell-bound ferrireductase activity.

6/3,AB/3 (Item 3 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09338752 97298086 PMID: 9153234

The yeast Fre1p/Fre2p cupric reductases facilitate copper uptake and are regulated by the copper-modulated Mac1p activator.

Georgatsou E; Mavrogiannis LA; Fragiadakis GS; Alexandraki D

Foundation for Research and Technology-Hellas, Institute of Molecular Biology and Biotechnology, Greece.

Journal of biological chemistry (UNITED STATES) May 23 1997, 272

(21) p13786-92, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Fre1p and Fre2p are **ferric reductases** which account for the total plasma membrane associated activity, a prerequisite for iron uptake, in *Saccharomyces cerevisiae*. The two genes are transcriptionally induced by iron depletion. In this communication, we provide evidence that Fre2p has

also cupric reductase activity, as has been previously shown for Frelp (Hassett, R., and Kosman, D.J. (1995) J. Biol. Chem. 270, 128-134). Both Frelp and Fre2p enzymes are functionally significant for copper uptake, as monitored by the accumulation of the copper-regulated CUP1 and CTR1 mRNAs in fre1Delta, fre2Delta, and fre1Deltafre2Delta mutant strains. However, only Frelp activity is induced by copper depletion, even in the presence of iron. This differential copper-dependent regulation of Frelp and Fre2p is exerted at the transcriptional level of the two genes. We have shown that Mac1p, known to affect the basal levels of FRE1 gene expression (Jungmann, J., Reins, H.-A., Lee, J., Romeo, A., Hassett, R., Kosman, D., and Jentsch, S. (1993) EMBO J. 12, 5051-5056), accounts for both the copper-dependent induction of FRE1 and down-regulation of FRE2 gene. Finally, Mac1p transcriptional activation function is itself modulated by the availability of copper.

6/3,AB/4 (Item 4 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09083129 96425877 PMID: 8828219

Isolation of the mRNA-capping enzyme and **ferric-reductase**-related genes from *Candida albicans*.

Yamada-Okabe T; Shimmi O; Doi R; Mizumoto K; Arisawa M; Yamada-Okabe H
Department of Hygiene, School of Medicine, Yokohama City University, Japan.

Microbiology (ENGLAND) Sep 1996, 142 (Pt 9) p2515-23, ISSN 1350-0872 Journal Code: BXW

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

The mRNA-capping enzyme (mRNA 5'-guanylyltransferase) gene was cloned from a *Candida albicans* genomic DNA library by functional complementation of a *Saccharomyces cerevisiae* ceg1 delta null mutation. This gene, referred to as CGT1 (*C. albicans* guanylyltransferase 1), can encode a 52 kDa protein that is highly homologous to *S. cerevisiae* Ceg1p. CGT1 in a single-copy plasmid complemented the lethality of the *S. cerevisiae* ceg1 delta null mutation and, like *S. cerevisiae* Ceg1p, bacterially expressed Cgt1p was able to form a stable complex with the GMP moiety of GTP and to synthesize the cap structure in vitro, demonstrating that CGT1 is the *C. albicans* mRNA 5'-guanylyltransferase gene. CGT1 seemed to exist as a single copy in the *C. albicans* genome and was actively transcribed into mRNA. Another ORF was found in an opposite strand very close to the CGT1 locus. This gene shared significant sequence homology with *S. cerevisiae* FRE1, the gene encoding **ferric reductase**, and therefore was designated CFL1 (*C. albicans* **ferric-reductase**-like gene 1). Despite its sequence homology with *S. cerevisiae* FRE1, CFL1 mRNA was not induced by iron deprivation, and CFL1 did not complement the slow growth of a *S. cerevisiae* fre1 delta null mutant in the absence of iron, suggesting that CFL1 is functionally distinct from *S. cerevisiae* FRE1.

6/3,AB/5 (Item 5 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09030351 97022063 PMID: 8868423

Candida albicans has a cell-associated **ferric-reductase** activity which is regulated in response to levels of iron and copper.

Morrissey JA; Williams PH; Cashmore AM

Department of Genetics, University of Leicester, UK.

Microbiology (ENGLAND) Mar 1996, 142 (Pt 3) p485-92, ISSN 1350-0872 Journal Code: BXW

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

For survival, pathogenic organisms such as *Candida albicans* must possess an efficient mechanism for acquiring iron in the iron-restricted environment of the human body. *C. albicans* can use iron from a variety of sources found within the host. However, it is not clear how biologically active ferrous iron is obtained from these sources. One strategy adopted by some organisms is to reduce iron extracellularly and then specifically transport the ferrous iron into the cell. We have shown that clinical isolates of *C. albicans* do have a cell-associated **ferric-reductase** activity. The determination of **ferric-reductase** activity of cells growing exponentially in either low- or high-iron media over a period of time indicated that *C. albicans* reductase activity is induced when in low-iron conditions. Moreover, we have demonstrated that *C. albicans* reductase activity is also regulated in response to the growth phase of the culture, with induction occurring upon exit from stationary phase and maximal levels being reached in early exponential stage irrespective of the iron content of the medium. These results suggest that *C. albicans* reductase activity is regulated in a very similar manner to the *Saccharomyces cerevisiae* **ferric-reductase**. Iron reduction and uptake in *S. cerevisiae* are closely connected to copper reduction, and possibly copper uptake. In this report we show that iron and copper reduction also appear to be linked in *C. albicans*. The **ferric-reductase** activity is negatively regulated by copper. Moreover, quantitative cupric-reductase assays indicated that *C. albicans* is capable of reducing copper and that this cupric-reductase activity is negatively regulated by both iron and copper. This is the first report that *C. albicans* has an iron- and copper-mediated ferri-reductase activity.

6/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09010119 96409227 PMID: 8814209

A **ferric reductase** activity is found in brush border membrane vesicles isolated from Caco-2 cells.

Ekmekcioglu C; Feyertag J; Marktl W

University of Vienna, Medical School, Department of Medical Physiology, Austria.

Journal of nutrition (UNITED STATES) Sep 1996, 126 (9)
p2209-17, ISSN 0022-3166 Journal Code: JEV

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Brush border membrane vesicles isolated from Caco-2 cells were used to examine whether there is an apical membrane-associated **ferric reductase** activity in small intestinal enterocytes. A **ferric reductase** activity which was dependent on NADH or NADPH as reductants was shown. Reduction of Fe(III) was quantified by the formation of a stable Fe(II)/ferrozine complex. The **ferric reductase** revealed saturation kinetics with a $K(m)$ of 4.12 ± 0.65 micromol/L and a V_{max} of 3.11 ± 0.043 nmol/(min.mg protein) for NADH. About 25% of the electrons for the NADH-dependent ferric iron reduction were transferred indirectly from the superoxide anion as verified by the superoxide dismutase inhibitable ferric iron reduction rate. However, the main part of Fe(III) reduction occurs directly by catalyzed electron transfer from NADH to ferric iron through (an) enzyme(s) located in the brush border membrane. The **ferric reductase** activity was inhibited by Pt(II) and especially p-chloromercuribenzoate. Ferricyanide, which is also reduced by the enzyme, is a competitive inhibitor of the Fe(III)/nitrilotriacetate (NTA) complex with a K_i of 43 micromol/L. These results suggest that brush border membranes of enterocytes possess a **ferric reductase** that reduces ferric to ferrous iron before the iron is transported through the microvillous membrane.

6/3,AB/7 (Item 7 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08992546 96291724 PMID: 8754685

A metal-accumulator mutant of *Arabidopsis thaliana*.
Delhaize E

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Research Organisation, Canberra, Australia. manny@pican.pi.csiro.au

Plant physiology (UNITED STATES) Jul 1996, 111 (3) p849-55,
ISSN 0032-0889 Journal Code: P98

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

A mutation designated man1 (for manganese accumulator) was found to cause *Arabidopsis thaliana* seedlings to accumulate a range of metals. The man1 mutation segregated as a single recessive locus located on chromosome 3. When grown on soil, mutant seedlings accumulated Mn (7.5 times greater than wild type), Cu (4.6 times greater than wild type), Zn (2.8 times greater than wild type), and Mg (1.8 times greater than wild type) in leaves. In addition to these metals, the man1 mutant accumulated 2.7-fold more S in leaves, primarily in the oxidized form, than wild-type seedlings. Analysis of seedlings grown by hydroponic culture showed a similar accumulation of metals in leaves of man1 mutants. Roots of man1 mutants also accumulated metals, but unlike leaves they accumulated 10-fold more total Fe (symplasmic and apoplasmic combined) than wild-type roots. Roots of man1 mutants possessed greater (from 1.8- to 20-fold) **ferric-chelate reductase** activity than wild-type seedlings, and this activity was not responsive to changes of Mn nutrition in either genotype. Taken together, these results suggest that the man1 mutation disrupts the regulation of metal-ion uptake or homeostasis in *Arabidopsis*.

6/3,AB/8 (Item 8 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08974373 96278882 PMID: 8662973

The FRE1 **ferric reductase** of *Saccharomyces cerevisiae* is a cytochrome b similar to that of NADPH oxidase.

Shatwell KP; Dancis A; Cross AR; Klausner RD; Segal AW

Department of Medicine, University College London, 5 University Street,
London WC1E 6JJ, United Kingdom.

Journal of biological chemistry (UNITED STATES) Jun 14 1996, 271

(24) p14240-4, ISSN 0021-9258 Journal Code: HIV


Contract/Grant No.: AI24838, AI, NIAID

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Plasma membrane preparations from strains of the yeast *Saccharomyces cerevisiae* gave a reduced minus oxidized spectrum characteristic of a b-type cytochrome and very similar to the spectrum of flavocytochrome b558 of human neutrophils. The magnitude of the signal correlated with the level of **ferric reductase** activity and the copy number of the FRE1 gene, indicating that the FRE1 protein is a cytochrome b. Sequence similarities with the flavin binding site of flavocytochrome b558 and other members of the ferredoxin-NADP reductase family, together with increased levels of noncovalently bound FAD and iodonitrotetrazolium violet reductase activity in membranes from a yeast strain overexpressing **ferric reductase**, suggested that the FRE1 protein may also carry a flavin group. Potentiometric titrations indicated that FRE1, like neutrophil NADPH oxidase, has an unusually low redox potential, in the region of -250 mV, and binds CO.



6/3,AB/9 (Item 9 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

08798155 96032023 PMID: 7551061

Reduction of exogenous ferric iron by a surface-associated **ferric reductase** of *Listeria* spp.

Deneer HG; Healey V; Boychuk I
Department of Microbiology, University of Saskatchewan, Saskatoon, Canada.

Microbiology (ENGLAND) Aug 1995, 141 (Pt 8) p1985-92, ISSN 1350-0872 Journal Code: BXW

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

The reduction of exogenous ferric iron by *Listeria monocytogenes*, a Gram-positive food-borne pathogen, was investigated. Using an assay incorporating the ferrous iron chelator ferrozine, we showed that intact cells of *L. monocytogenes*, when exposed to ferric iron, were able to rapidly reduce and solubilize the iron to the ferrous form. Reduction occurred only after direct contact between the bacteria and the iron source. A number of different ferric iron chelates, including transferrin and lactoferrin-bound iron, haemoglobin, ferritin, and iron complexed to siderophores, could be reduced. The **ferric reductase** activity was expressed by both reference strains and clinical isolates of *L. monocytogenes* and by all other species of *Listeria*, although significant quantitative differences were observed. In *L. monocytogenes*, the expression of **ferric reductase** was not affected by the growth phase of the bacteria nor by the presence or absence of iron in the growth medium. However, expression was greatly reduced in bacteria grown anaerobically and when cultured in media of reduced pH. In addition, bacteria grown at a cold temperature displayed greater **ferric reductase** activity than cells grown at higher temperatures. A surface-associated **ferric reductase** system may be one component of a general iron scavenging mechanism which can be used by *Listeria* growing in a variety of environments.

6/3,AB/10 (Item 10 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08696738 96132030 PMID: 8553699

DNA sequence analysis of a 13 kbp fragment of the left arm of yeast chromosome XV containing seven new open reading frames.

Casamayor A; Aldea M; Casas C; Herrero E; Gamo FJ; Lafuente MJ; Gancedo C; Arino J

Dept Bioquímica i Biologia Molecular, Fac. Veterinaria, Universitat Autònoma de Barcelona, Spain.

Yeast (ENGLAND) Oct 1995, 11 (13) p1281-8, ISSN 0749-503X
Journal Code: YEA

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

The sequence of a 13 kbp fragment located in the vicinity of the left telomere of chromosome XV (cosmid pEOA179) has been determined. Seven new open reading frames (ORFs) encoding polypeptides longer than 100 residues have been found (AOB629, AOA342, AOC231, AOE555, AOE236, AOA236 and AOE1045). Three of them show no identity with proteins deposited in the data banks. ORF AOB629 (629 amino acids) has some similarity with previously described **ferric reductases** from *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe*. ORF AOA342 encodes a polypeptide reminiscent of dihydroflavonol-4-reductases from a number of plant species. AOE236 displays a high level of identity when compared with peroxisomal membrane proteins previously cloned from the methylotrophic yeast *Candida boidinii*. Finally, AOE1045 encodes a large protein (1045 residues) with some identity with a hypothetical 147 kDa protein identified during the

sequencing of *Caenorhabditis elegans* chromosome 3.

6/3,AB/11 (Item 11 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08522841 95218608 PMID: 7766049

Responses to iron deficiency in *Arabidopsis thaliana*: the Turbo iron reductase does not depend on the formation of root hairs and transfer cells.

Moog PR; van der Kooij TA; Bruggemann W; Schiefelbein JW; Kuiper PJ
Department of Plant Physiology, University of Groningen, The Netherlands.
Planta (GERMANY) 1995, 195 (4) p505-13, ISSN 0032-0935

Journal Code: BNG

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Arabidopsis thaliana (L.) Heynh. Columbia wild type and a root hair-less mutant RM57 were grown on iron-containing and iron-deficient nutrient solutions. In both genotypes, **ferric chelate reductase** (FCR) of intact roots was induced upon iron deficiency and followed a Michaelis-Menten kinetic with a K_m of 45 and 54 μM Fe^{III} -EDTA and a V_{max} of 42 and 33 $\text{nmol Fe}^{2+} \cdot (\text{g FW})^{-1} \cdot \text{min}^{-1}$ for the wild type and the mutant, respectively. The pH optimum for the reaction was around pH 5.5. The approximately four fold stimulation of FCR activity was independent of formation of root hairs and/or transfer cells induced by iron deficiency. Iron-deficiency-induced chlorosis and the development of a rigid root habit disappeared when ferric chelate was applied to the leaves, while FCR activity remained unchanged. The time course of the responses to iron deficiency showed that morphological and physiological responses were controlled separately.

6/3,AB/12 (Item 12 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08495931 95237204 PMID: 7720713

AFT1: a mediator of iron regulated transcriptional control in *Saccharomyces cerevisiae*.

Yamaguchi-Iwai Y; Dancis A; Klausner RD
Cell Biology and Metabolism Branch, National Institute of Child Health and Human Development, National Institutes of Health, Bethesda, MD, USA.

EMBO journal (ENGLAND) Mar 15 1995, 14 (6) p1231-9, ISSN 0261-4189
Journal Code: EMB

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Using a scheme for selecting mutants of *Saccharomyces cerevisiae* with abnormalities of iron metabolism, we have identified a gene, AFT1, that mediates the control of iron uptake. AFT1 encodes a 78 kDa protein with a highly basic amino terminal domain and a glutamine-rich C-terminal domain, reminiscent of transcriptional activators. The protein also contains an amino terminal and a C-terminal region with 10% His residues. A dominant mutant allele of this gene, termed AFT1-lup, results in high levels of **ferric reductase** and ferrous iron uptake that are not repressed by exogenous iron. The increased iron uptake is associated with enhanced susceptibility to iron toxicity. These effects may be explained by the failure of iron to repress transcription of FRE1, FRE2 and FET3. FRE1 and FRE2 encode plasma membrane **ferric reductases**, obligatory for ferric iron assimilation, and FET3 encodes a copper-dependent membrane-associated oxidase required for ferrous iron uptake. Conversely, a strain with interruption of the AFT1 gene manifests low **ferric reductase** and ferrous iron uptake and is susceptible to iron deprivation, because of deficient expression of FRE1 and negligible

expression of FRE2 and FET3. Thus, AFT1 functions to activate transcription of target genes in response to iron deprivation and thereby plays a central role in iron homeostasis.

6/3,AB/13 (Item 13 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08383261 95070025 PMID: 7526783

Potential of bleomycin cytotoxicity in *Saccharomyces cerevisiae*.

Moore CW

Department of Microbiology, City University of New York Medical School/Sophie Davis School of Biomedical Education, New York 10031.

Antimicrobial agents and chemotherapy (UNITED STATES) Jul 1994,

38 (7) p1615-9, ISSN 0066-4804 Journal Code: 6HK

Contract/Grant No.: CA25609, CA, NCI

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Lesions introduced into cellular DNAs prelabeled with [2-14C]thymidine or [6-3H]thymidine, as well as cell killing, were inhibited by the presence of EDTA during 20-min reactions of *Saccharomyces cerevisiae* cells with the low-molecular-weight bleomycin family of anticancer antibiotics. In contrast, the level of killing by low concentrations of bleomycin was higher among cells which had grown for three generations in defined synthetic complete medium supplemented with ferrous sulfate than among cells grown without iron supplementation. In *S. cerevisiae*, the uptake of iron is facilitated by a plasma membrane **ferric reductase** activity and a high-affinity ($K_m = 5 \times 10^{-6}$ M) ferrous uptake system. Lethal effects of 1.3×10^{-6} M bleomycin increased approximately 50% with 10^{-5} M Fe(II), nearly twofold with 10^{-4} M Fe(II), and 2.8 times with 10^{-3} M Fe(II). Thus, iron preloading is a new experimental approach to increasing and studying the effects of the glycopeptides on cellular DNAs and other cellular targets. This approach could also be used for studying and better understanding DNA repair genes and could serve as a model for studies of redox active chemicals in biological systems.

6/3,AB/14 (Item 14 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08325167 95121577 PMID: 7821543

Duodenal **ferric reductase**: purification and characterisation.

Pountney DJ; Simpson RJ; Wrigglesworth JM

Department of Clinical Biochemistry, King's College School of Medicine and Dentistry, London.

Biochemical Society transactions (ENGLAND) Aug 1994, 22 (3)

p284S, ISSN 0300-5127 Journal Code: E48

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

6/3,AB/15 (Item 15 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08256391 95017141 PMID: 7931710

Enhanced Fe(3+)-reducing capacity does not seem to play a major role in increasing iron absorption in iron-deficient rats.

Wien EM; Van Campen DR

U.S. Department of Agriculture-Agriculture Research Service, Plant, Soil and Nutrition Laboratory, Ithaca, NY 14853.

Journal of nutrition (UNITED STATES) Oct 1994, 124 (10)

p2006-15, ISSN 0022-3166 Journal Code: JEV

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Some eucaryotic organisms, including many plants, yeast and mice, have a higher iron uptake during iron deficiency because the capacity to reduce Fe^{3+} from the environment to Fe^{2+} is greatly enhanced. To determine whether this occurs in rats, a common experimental model for iron absorption in humans, we compared the in vivo capacity to reduce intraluminal Fe^{3+} in iron-deficient and normal rats. We also measured potential Fe^{3+} -reducing components within the intestinal lumen and on the mucosal surface. Iron-reducing capacity was higher in iron-deficient rats, by a significant ($P = 0.026$) but modest 20%, in parallel with higher mucosal weight ($R^2 = 0.501$, $P = 0.003$). In vitro iron reduction by lumen contents was correlated with mucosal weight, even though mucosal tissue was not present in the assays. This capacity was not related to ascorbic acid, glutathione or other nonprotein sulfhydryls. Mucosal **ferric reductase** activity was higher in iron-deficient rats in parallel with higher tissue weight, but the specific activity did not differ and the higher total activity was not associated with the brush border fraction. The role of endogenous Fe^{3+} reduction in regulating iron absorption should be investigated in humans and in other experimental models.

6/3,AB/16 (Item 16 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08241456 94378726 PMID: 8091865

Sequencing of a 13.2 kb segment next to the left telomere of yeast chromosome XI revealed five open reading frames and recent recombination events with the right arms of chromosomes III and V.

Alexandraki D; Tzermia M

Foundation for Research and Technology-HELLAS, Institute of Molecular Biology and Biotechnology, Crete, Greece.

Yeast (ENGLAND) Apr 1994, 10 Suppl A pS81-91, ISSN 0749-503X

Journal Code: YEA

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

We report the entire sequence of a 13.2 kb segment next to the left telomere of chromosome XI of *Saccharomyces cerevisiae*. A 1.2 kb fragment near one end is 91% homologous to the right arm of chromosome III and 0.7 kb of that are 77% homologous to the right arm of chromosome V. Five open reading frames are included in the sequenced segment. Two of them are almost identical to the known YCR104W and YCR103C hypothetical proteins of chromosome III. A third one contains a region homologous to the Zn (2)-Cys (6) binuclear cluster pattern of fungal transcriptional activators. The fourth one, part of which is similar to the mammalian putative transporter of mevalonate, has the structure of membrane transporters. The fifth one is similar to yeast **ferric reductase**.

6/3,AB/17 (Item 17 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08138846 94217704 PMID: 8164662

Two distinctly regulated genes are required for ferric reduction, the first step of iron uptake in *Saccharomyces cerevisiae*.

Georgatsou E; Alexandraki D

Foundation for Research and Technology-HELLAS, Institute of Molecular Biology and Biotechnology, Crete, Greece.

Molecular and cellular biology (UNITED STATES) May 1994, 14 (5)

p3065-73, ISSN 0270-7306 Journal Code: NGY

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Iron uptake in *Saccharomyces cerevisiae* involves at least two steps: reduction of ferric to ferrous ions extracellularly and transport of the reduced ions through the plasma membrane. We have cloned and molecularly characterized FRE2, a gene which is shown to account, together with FRE1, for the total membrane-associated **ferric reductase** activity of the cell. Although not similar at the nucleotide level, the two genes encode proteins with significantly similar primary structures and very similar hydrophobicity profiles. The FRE1 and FRE2 proteins are functionally related, having comparable properties as **ferric reductases**. FRE2 expression, like FRE1 expression, is induced by iron deprivation, and at least part of this control takes place at the transcriptional level, since 156 nucleotides upstream of the initiator AUG conferred iron-dependent regulation when fused to a heterologous gene. However, the two gene products have distinct temporal regulation of their activities during cell growth.

6/3,AB/18 (Item 18 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08118543 94162850 PMID: 8118169

Ferric reductases or flavin reductases?

Fontecave M; Coves J; Pierre JL

Laboratoire d'Etudes Dynamiques et Structurales de la Selectivite, Unite de Recherche Associee au CNRS 332, Universite Joseph Fourier, Grenoble, France.

Biomaterials (ENGLAND) Jan 1994, 7 (1) p3-8, ISSN 0966-0844

Journal Code: BID

Languages: ENGLISH

Document type: Journal Article; Review; Review, Tutorial

Record type: Completed

Assimilation of iron by microorganisms requires the presence of **ferric reductases** which participate in the mobilization of iron from ferrisiderophores. The common structural and catalytic properties of these enzymes are described and shown to be identical to those of flavin reductases. This strongly suggests that, in general, the reduction of iron depends on reduced flavins provided by flavin reductases.

6/3,AB/19 (Item 19 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08108416 94121620 PMID: 8292013

Ferric reductases in *Escherichia coli*: the contribution of the haemoglobin-like protein.

Eschenbrenner M; Coves J; Fontecave M

Laboratoire d'Etudes Dynamiques et Structurales de la Selectivite, Universite Joseph Fourier, Grenoble, France.

Biochemical and biophysical research communications (UNITED STATES) Jan 14 1994, 198 (1) p127-31, ISSN 0006-291X Journal Code: 9Y8

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

The haemoglobin-like protein (HMP) of *E. coli* previously isolated as a dihydropteridine reductase was shown to be also a ferric citrate reductase. We demonstrate that, in fact, HMP is a flavin reductase and that its **ferric reductase** activity is a result of its ability to reduce free flavins. However, when compared to the two main ferric/flavin reductases of *E. coli*, i.e., the NAD(P)H: flavin oxidoreductase and the sulfite reductase, one can conclude that the contribution of HMP to iron reduction is negligible.

6/3,AB/20 (Item 20 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07923233 93364157 PMID: 8358204

Ferric reductases of *Legionella pneumophila*.

Poch MT; Johnson W

Department of Microbiology, University of Iowa, Iowa City 52242.

Biomaterials (ENGLAND) Summer 1993, 6 (2) p107-14, ISSN

0966-0844 Journal Code: BID

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Ferric reductase enzymes requiring a reductant for maximal activity were purified from the cytoplasmic and periplasmic fractions of avirulent and virulent *Legionella pneumophila*. The cytoplasmic and periplasmic enzymes are inhibited by zinc sulfate, constitutive and active under aerobic or anaerobic conditions. However, the periplasmic and cytoplasmic reductases are two distinct enzymes as shown by their molecular weights, specific activities, reductant specificities and other characteristics. The molecular weights of the cytoplasmic and periplasmic **ferric reductases** are approximately 38 and 25 kDa, respectively. The periplasmic reductase ($K_m = 7.0$ μ M) has a greater specific activity and twice the affinity for ferric citrate as the cytoplasmic enzyme ($K_m = 15.3$ μ M). Glutathione serves as the optimum reductant for the periplasmic reductase, but is inactive for the cytoplasmic enzyme. In contrast, NADPH is the optimum reductant for the cytoplasmic enzyme. **Ferric reductases** of avirulent cells show a 2-fold increase in their activities when NADPH is used as a reductant in comparison with NADH. In contrast, **ferric reductases** from virulent cells demonstrated an equivalent activity with NADH or NADPH as reductants. With the exception of their response to NADPH, the **ferric reductase** at each respective location appears to be similar for avirulent and virulent cells.

6/3,AB/21 (Item 21 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07437294 91346008 PMID: 1908693

Characterization of a soluble **ferric reductase** from *Neisseria gonorrhoeae*.

Le Faou AE; Morse SA

Division of Sexually Transmitted Diseases Laboratory Research, Centers for Disease Control, Atlanta, Georgia 30333.

Biology of metals (GERMANY) 1991, 4 (2) p126-31, ISSN

0933-5854 Journal Code: AU2

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

An NADH-dependent **ferric reductase** was identified in extracts of *Neisseria gonorrhoeae*. Enzyme activity was measured in an assay using ferrozine as the ferrous iron acceptor. **Ferric reductase** activity was enhanced by Mg^{2+} and flavine nucleotides. The enzyme reduced both citrate- and diphosphate-bound ferric iron as well as ferric hydroxide (Imferon). However, no activity was observed with either 30%-iron-saturated transferrin or with the gonococcal iron-binding protein, Fbp. The **ferric reductase** was found primarily within the cytoplasmic cell fraction. The soluble **ferric reductase** was purified 110-fold by ammonium sulfate precipitation, gel and anion-exchange chromatography. Results obtained following gel chromatography and SDS/polyacrylamide gel electrophoresis suggested that the enzyme had a molecular mass of about 25 kDa.

6/3,AB/22 (Item 22 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07258051 90220614 PMID: 2183029

Genetic evidence that **ferric reductase** is required for iron uptake in *Saccharomyces cerevisiae*.

Dancis A; Klausner RD; Hinnebusch AG; Barriocanal JG
Cell Biology and Metabolism Branch, National Institute of Child Health and Human Development, Bethesda, Maryland 20892.

Molecular and cellular biology (UNITED STATES) May 1990, 10 (5)
p2294-301, ISSN 0270-7306 Journal Code: NGY

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

The requirement for a reduction step in cellular iron uptake has been postulated, and the existence of plasma membrane **ferric reductase** activity has been described in both procaryotic and eucaryotic cells. In the yeast *Saccharomyces cerevisiae*, there is an externally directed reductase activity that is regulated by the concentration of iron in the growth medium; maximal activity is induced by iron starvation. We report here the isolation of a mutant of *S. cerevisiae* lacking the reductase activity. This mutant is deficient in the uptake of ferric iron and is extremely sensitive to iron deprivation. Genetic analysis of the mutant demonstrates that the reductase and ferric uptake deficiencies are due to a single mutation that we designate *frel-1*. Both phenotypes cosegregate in meiosis, corevert with a frequency of 10⁻⁷, and are complemented by a 3.5-kilobase fragment of genomic DNA from wild-type *S. cerevisiae*. This fragment contains *FRE1*, the wild-type allele of the mutant gene. The level of the gene transcript is regulated by iron in the same way as the reductase activity. The ferrous ion product of the reductase must traverse the plasma membrane. A high-affinity (K_m = 5 microm) ferrous uptake system is present in both wild-type and mutant cells. Thus, iron uptake in *S. cerevisiae* is mediated by two plasma membrane components, a reductase and a ferrous transport system.

6/3,AB/23 (Item 23 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07079703 93384270 PMID: 8396885

NAD(P)H:ferric iron reductase in endosomal membranes from rat liver.

Scheiber B; Goldenberg H

Department of Medical Chemistry, University of Vienna Medical School, Austria.

Archives of biochemistry and biophysics (UNITED STATES) Sep 1993,
305 (2) p225-30, ISSN 0003-9861 Journal Code: 6SK

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Endosomes isolated from rat liver, characterized by high enrichment of endocytosed ligand after liver perfusion, displayed **ferric reductase** activity with higher affinity for NADH (1.7 microm) than for NADPH (7.1 microm). The ferric-NTA complex was reduced by NADH with a molar stoichiometry of 2:1 for the iron complex to pyridine nucleotide ratio under near anaerobic conditions. Superoxide radicals were not apparently involved in the reduction of ferric iron under these conditions, despite measurable generation of superoxide under aerobic atmosphere. The reaction was inhibited by sulfhydryl reagents, was heat labile, and may account for reduction of ferric to ferrous iron during hepatic iron uptake from transferrin or from other iron sources.

6/3,AB/24 (Item 24 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07058307 93321164 PMID: 8330259

Reduction of ferric iron by *Listeria monocytogenes* and other species of *Listeria*.

Deneer HG; Boychuk I

Department of Microbiology, University of Saskatchewan, Saskatoon, Canada.

Canadian journal of microbiology (CANADA) May 1993, 39 (5)

p480-5, ISSN 0008-4166 Journal Code: CJ3

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

One mechanism by which *Listeria monocytogenes* is thought to obtain iron required for growth is through the extracellular reduction of a ferric iron source to the ferrous form. To better characterize this reductase activity we have developed a simple plate assay that allows detection of colonies of *Listeria* species able to reduce ferric iron. Cells are plated on an agar base medium containing a ferric iron source and ethylenediamine dihydroxyphenylacetic acid. Colonies are then overlain with soft agarose containing NADH, flavin mononucleotide, and Ferrozine, a chelator of ferrous iron. Colonies able to reduce the ferric iron source form a red-purple color as the ferrous iron is complexed with ferrozine. Using this qualitative assay we have shown that all species of *Listeria* are able to reduce ferric iron when presented as ferric ammonium citrate whereas most other species of Gram-positive and Gram-negative bacteria are not. Only *Clostridium perfringens* was able to reduce ferric iron to the same extent as *Listeria*. *Listeria monocytogenes* was further shown to be capable of reducing various ferric iron salts as well as iron bound to ferritin, transferrin, and 2,3-dihydroxybenzoic acid in the agar plate assay. The utility of this assay was demonstrated by using it to screen a bank of Tn916-derived mutants of *L. monocytogenes* for clones unable to reduce ferric iron. Four such mutants were identified and all were shown to have greatly decreased **ferric reductase** activity.

6/3,AB/25 (Item 25 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07051042 93309468 PMID: 8321236

The fission yeast **ferric reductase** gene *frp1+* is required for ferric iron uptake and encodes a protein that is homologous to the gp91-phox subunit of the human NADPH phagocyte oxidoreductase.

Roman DG; Dancis A; Anderson GJ; Klausner RD

Cell Biology and Metabolism Branch, National Institute of Child Health and Human Development, Bethesda, Maryland 20892.

Molecular and cellular biology (UNITED STATES) Jul 1993, 13 (7)

p4342-50, ISSN 0270-7306 Journal Code: NGY

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

We have identified a cell surface **ferric reductase** activity in the fission yeast *Schizosaccharomyces pombe*. A mutant strain deficient in this activity was also deficient in ferric iron uptake, while ferrous iron uptake was not impaired. Therefore, reduction is a required step in cellular ferric iron acquisition. We have cloned *frp1+*, the wild-type allele of the mutant gene. *frp1+* mRNA levels were repressed by iron addition to the growth medium. Fusion of 138 nucleotides of *frp1+* promoter sequences to a reporter gene, the bacterial chloramphenicol acetyltransferase gene, conferred iron-dependent regulation upon the latter when introduced into *S. pombe*. The predicted amino acid sequence of the *frp1+* gene exhibits hydrophobic regions compatible with transmembrane domains. It shows similarity to the *Saccharomyces cerevisiae* FRE1 gene product and the gp91-phox protein, a component of the human NADPH phagocyte oxidoreductase that is deficient in X-linked chronic granulomatous disease.

6/3,AB/26 (Item 26 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06891008 93057491 PMID: 1431884

Ferric iron reduction and iron assimilation in *Saccharomyces cerevisiae*.
Anderson GJ; Lesuisse E; Dancis A; Roman DG; Labbe P; Klausner RD
Cell Biology and Metabolism Branch, National Institute of Child Health
and Human Development, Bethesda, Maryland 20892.

Journal of inorganic biochemistry (UNITED STATES) Aug 15-Sep 1992
, 47 (3-4) p249-55, ISSN 0162-0134 Journal Code: JAR

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

We have used the yeast *Saccharomyces cerevisiae* as a model organism to study the role of ferric iron reduction in eucaryotic iron uptake. *S. cerevisiae* is able to utilize ferric chelates as an iron source by reducing the ferric iron to the ferrous form, which is subsequently internalized by the cells. A gene (FRE1) was identified which encodes a protein required for both ferric iron reduction and efficient ferric iron assimilation, thus linking these two activities. The predicted FRE1 protein appears to be a membrane protein and shows homology to the beta-subunit of the human respiratory burst oxidase. These data suggest that FRE1 is a structural component of the **ferric reductase**. Subcellular fractionation studies showed that the **ferric reductase** activity of isolated plasma membranes did not reflect the activity of the intact cells, implying that cellular integrity was necessary for function of the major *S. cerevisiae* **ferric reductase**. An NADPH-dependent plasma membrane **ferric reductase** was partially purified from plasma membranes. Preliminary evidence suggests that the cell surface **ferric reductase** may, in addition to mediating cellular iron uptake, help modulate the intracellular redox potential of the yeast cell.

6/3,AB/27 (Item 27 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05938623 89291757 PMID: 2525550

Ferric reductase activity in *Azotobacter vinelandii* and its inhibition by Zn²⁺.

Huyer M; Page WJ

Department of Microbiology, University of Alberta, Edmonton, Canada.

Journal of bacteriology (UNITED STATES) Jul 1989, 171 (7)
p4031-7, ISSN 0021-9193 Journal Code: HH3

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Ferric reductase activity was examined in *Azotobacter vinelandii* and was found to be located in the cytoplasm. The specific activities of soluble cell extracts were not affected by the iron concentration of the growth medium; however, activity was inhibited by the presence of Zn²⁺ during cell growth and also by the addition of Zn²⁺ to the enzyme assays. Intracellular Fe²⁺ levels were lower and siderophore production was increased in Zn²⁺-grown cells. The **ferric reductase** was active under aerobic conditions, had an optimal pH of approximately 7.5, and required flavin mononucleotide and Mg²⁺ for maximum activity. The enzyme utilized NADH to reduce iron supplied as a variety of iron chelates, including the ferrisiderophores of *A. vinelandii*. The enzyme was purified by conventional protein purification techniques, and the final preparation consisted of two major proteins with molecular weights of 44,600 and 69,000. The apparent Km values of the **ferric reductase** for Fe³⁺ (supplied as ferric citrate) and NADH were 10 and 15.8 microM, respectively, and the data for the enzyme reaction were

consistent with Ping Pong Bi Bi kinetics. The approximate K_i values resulting from inhibition of the enzyme by Zn^{2+} , which was a hyperbolic (partial) mixed-type inhibitor, were 25 μM with respect to iron and 1.7 μM with respect to NADH. These results suggested that **ferric reductase** activity may have a regulatory role in the processes of iron assimilation in *A. vinelandii*.

6/3,AB/28 (Item 28 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05751975 87036908 PMID: 3021982

Isolation of a lentivirus from a macaque with lymphoma: comparison with HTLV-III/LAV and other lentiviruses.

Benveniste RE; Arthur LO; Tsai CC; Sowder R; Copeland TD; Henderson LE; Oroszlan S

Journal of virology (UNITED STATES) Nov 1986, 60 (2) p483-90,
ISSN 0022-538X Journal Code: KCV

Contract/Grant No.: N01-CO-23909, CO, NCI; N01-CO-23910, CO, NCI;
RR-00166, RR, NCRR

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

A retrovirus has been isolated on the human T-cell line HuT 78 after cocultivation of a lymph node from a pig-tailed macaque (*Macaca nemestrina*) that had died with malignant lymphoma in 1982 at the University of Washington primate center. This isolate, designated MnIV (WPRC-1) (*M. nemestrina* immunodeficiency virus, Washington Primate Research Center) shows the characteristic morphology of a lentivirus and replicates to high titers in various lymphocyte lines of human and primate origin. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis of purified MnIV revealed multiple bands of structural proteins, including a major viral gag protein of 28 kilodaltons, that did not comigrate with the viral proteins of a human immunodeficiency virus (HIV [FRE-1]) that was also isolated on HuT 78 cells. The relatedness of MnIV to other lentiviruses (HTLV-III/LAV, EIAV, and visna) was examined in radioimmunoassays, by immunoblot techniques, and by N-terminal amino acid sequence analysis of the viral p28 gag protein. The immunoassays revealed cross-reactivity only between MnIV p28 and HTLV-III/LAV p24, and sequence analysis showed that 14 of the 24 N-terminal residues of MnIV p28 and HTLV-III/LAV p24 are identical. These results indicate that MnIV belongs to the same lentivirus family as HTLV-III/LAV but is only partially related to these human acquired immune deficiency syndrome retroviruses.

6/3,AB/29 (Item 29 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

04123961 83048930 PMID: 6814479

Nitrogen-15 nuclear magnetic resonance investigation of nitrite reductase-substrate interaction.

Timkovich R; Cork MS

Biochemistry (UNITED STATES) Aug 3 1982, 21 (16) p3794-7,
ISSN 0006-2960 Journal Code: A0G

Contract/Grant No.: GM-23869, GM, NIGMS; GM-26071-0251, GM, NIGMS

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Nitrogen-15 nuclear magnetic resonance (^{15}N NMR) spectroscopy at 30.4 MHz was employed to determine the interaction of the substrate nitrite (97.2% enriched) with bacterial nitrite reductase, denoted cytochrome cd1, from *Pseudomonas aeruginosa*. The addition of ferric enzyme to nitrite did not alter the chemical shift of the bulk nitrite resonance, nor was it possible to observe a new resonance from a hypothetical bound form. However, the

spin-lattice relaxation time (T1) was lowered from 13.2 to 2.7 s, and the spin-spin relaxation time (T2) was halved. Values of T1 were measured by progressive saturation and values of T2 by line widths. Control experiments involving ferric cytochrome c and metmyoglobin demonstrated that the perturbations did not arise from the bulk paramagnetic properties of the protein solutions. Variable enzyme/substrate ratios were measured to assess the strength of interaction. The most reasonable model consistent with the data proposes a weak association between nitrite and **ferric reductase** with a value of 1.3 M⁻¹ for the association constant.

6/3,AB/30 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11399254 BIOSIS NO.: 199800180586
Accumulation of metallothionein transcripts in response to iron, copper and zinc: Metallothionein and metal-chelate reductase.
AUTHOR: Fordham-Skelton Anthony P(a); Wilson Jonathan R; Groom Quentin; Robinson Nigel J
AUTHOR ADDRESS: (a)Dep. Biological Sciences, Univ. Durham, Durham DH1 3LE**
UK
JOURNAL: Acta Physiologiae Plantarum 19 (4):p451-457 1997
ISSN: 0137-5881
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: It has been proposed that plant metallothionein (MT) sequesters excess copper, and possibly zinc, thereby preventing adverse metal-protein interactions. These metals can accumulate either gratuitously in response to other nutritional deficiencies or in plants grown in either copper- or zinc-enriched medium. Data are presented which confirm that in pea roots grown in low available iron there is increased (i) copper accumulation, (ii) MT transcript abundance, (iii) **ferric -chelate reductase** activity and (iv) cupric-chelate reductase activity. It is also shown that in roots grown in iron supplemented medium MT transcripts accumulate in response to elevated exogenous zinc. However, contrary to expectations, depletion of exogenous copper below normal micronutrient levels also confers an increase in the abundance of MT transcripts. The hypothesis that the products of plant metallothionein genes could act as copper chaperones is discussed.

1997

6/3,AB/31 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11266470 BIOSIS NO.: 199800047802
The froh gene family from Arabidopsis thaliana: Putative iron-chelate reductases.
AUTHOR: Robinson Nigel J; Sadjuga; Groom Quentin J
AUTHOR ADDRESS: Dep. Biochem. Genet., Univ. Newcastle, Newcastle-upon-Tyne NE2 4HH**UK
JOURNAL: Plant and Soil 196 (2):p245-248 Oct., 1997
ISSN: 0032-079X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A group of b-type cytochromes play central roles in both the uptake of iron by yeast, exemplified by the products of the FRE1 and FRP1

genes, and in pathogen defence by animals, exemplified by gp91phox from humans. There has been speculation that related proteins have similar roles in plants. We have recently isolated a family of genes from *Arabidopsis thaliana*, designated froh, which encode deduced proteins which fall into the same class as FRE 1, FRP 1 and gp9 1 phox. This paper reports that root surface iron-chelate reductase activity was 2.7-fold greater in *A. thaliana* plants grown in 5 μ M, relative to plants grown in the presence of 25 μ M, Fe(III) EDDHA. Reversed transcriptase (RT) polymerase chain reactions (PCR) using RNA isolated from these plants detected increased accumulation of frohC transcripts in low iron. Products were RT-dependent and their identity confirmed by subsequent hybridisation to 32P-frohC probe and by sequence determination. The frohC transcripts accumulated in response to low iron in both roots and leaves while actin transcripts (control) remained constant. Exposure of leaves to salicylic acid (a potentiator of pathogen defense responses) led to an accumulation of transcripts encoding a pathogenesis-related protein, pr-1, but not frohC or actin transcripts. These observations suggest that FrohC is more likely to be involved in iron-reduction, either for uptake from the soil or retranslocation within the plant, than in pathogen defence.

1997

6/3,AB/32 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

11239791 BIOSIS NO.: 199800021123
Ascorbate stabilization at the plasma membrane of *Saccharomyces cerevisiae*.
AUTHOR: Navas P(a); Cordoba F; Villalba J M; Crane F L; Clarke C F;
Santos-Ocana C
AUTHOR ADDRESS: (a)Dep. Biol. Celular, Univ. Cordoba, 14004 Cordoba**Spain
JOURNAL: Molecular Biology of the Cell 8 (SUPPL.):p293A Nov., 1997
CONFERENCE/MEETING: 37th Annual Meeting of the American Society for Cell Biology Washington, D.C., USA December 13-17, 1997
SPONSOR: American Society for Cell Biology
ISSN: 1059-1524
RECORD TYPE: Citation
LANGUAGE: English
1997

6/3,AB/33 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11229385 BIOSIS NO.: 199800010717
Physiological responses of grapevine callus cultures to iron deficiency.
AUTHOR: Piagnani Claudia(a); Zocchi Graziano
AUTHOR ADDRESS: (a)Ist. Colt. Arboree, Univ. Studi Milano, via Celoria 2,
20133 Milano**Italy
JOURNAL: Journal of Plant Nutrition 20 (11):p1539-1549 Nov., 1997
ISSN: 0190-4167
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Grapevine is considered a 'Strategy I' plant because it performs some peculiar biochemical and physiological responses when grown under iron (Fe) deficiency stress conditions. Callus cultures were started from leaf and internode cuts of micropropagated plantlets of two grapevine genotypes well known for their Fe-chlorosis characteristic: *Vitis riparia* a very susceptible genotype and *Vitis berlandieri* a resistant one.

Modification of NADH: ferric (Fe²⁺) reductase activity was spectrophotometrically evaluated by following the formation of the complex ferrous (Fe²⁺-(BPDS)₃, while the malic and citric acid production were determined in callus cultures grown both in the presence (+Fe) and absence (-Fe) of Fe. Moreover, a microsomal fraction was isolated from the calli to evaluate the H⁺-ATPase and the Fe³⁺-EDTA reductase activities. As expected, calli of the Fe-efficient genotype (V. berlandieri) was able to enhance Fe³⁺-EDTA reductase activity when growing under Fe deficiency while the Fe-chlorosis susceptible V. riparia could not or did it with lower efficiency. Therefore, the H⁺-ATPase assay showed a higher enzymatic activity in the microsomal fraction isolated from Vitis berlandieri grown without Fe with respect to its control (+Fe). Organic acid determination gave quite contradictory results, specially regarding malic acid which, under our study conditions, seemed not to be linked with the strategies of response to Fe deficiency.

1997

6/3,AB/34 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11184631 BIOSIS NO.: 199799805776

A cytochemical method for light and electron microscopic demonstration of **ferric reductase**.

AUTHOR: Wang He Yi Cui-Lin; Zhang Fu-Suo

AUTHOR ADDRESS: Dep. Plant Nutr., China Agric. Univ., Beijing 100094**
China

JOURNAL: Acta Botanica Sinica 39 (5):p411-414 1997

ISSN: 0577-7496

RECORD TYPE: Abstract

LANGUAGE: Chinese; Non-English

SUMMARY LANGUAGE: Chinese; English

ABSTRACT: The soybean (Glycine max L.) root cultured under iron deficient condition was employed as the experimental material in order to raise the **ferric reductase** content in root. The method is chemically based on the reduction of ferricyanide by **ferric reductase** to ferrocyanide from which, in presence of cupric ions, an insoluble and electron-dense brownish precipitate is formed. For better observation under light microscope, the dull brown precipitate was converted into black silver precipitate of sharp-contrast using the sulfide-silver amplification method. With this method, accurate and specific localization of **ferric reductase** was obtained. Under electron microscope, the dense enzymic reaction product was found as fine granules covering the plasmalemma which was in consistent with the results obtained by biochemical method. The present method for the localization of **ferric reductase** is more accurate than the prussian blue staining method, because the brown precipitate in this method is finer than the prussian blue precipitate. Further, the pH 6.6 of the reaction medium is closer to the optimum pH of 5.5 to 6.5 of **ferric reductase** activity whereas the pH of the prussian blue staining solution is only 3.

1997

6/3,AB/35 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11076379 BIOSIS NO.: 199799697524

Induction of the root cell plasma membrane **ferric reductase**: An

exclusive role for Fe and Cu.
AUTHOR: Cohen Clark K; Norvell Wendell A; Kochian Leon V(a)
AUTHOR ADDRESS: (a)United States Plant Soil Nutr. Lab., United States Dep.
Agriculture-Agricultural Res. Serv., Cor**USA
JOURNAL: Plant Physiology (Rockville) 114 (3):p1061-1069 1997
ISSN: 0032-0889
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Induction of **ferric reductase** activity in dicots and nongrass monocots is a well-recognized response to Fe deficiency. Recent evidence has shown that Cu deficiency also induces plasma membrane Fe reduction. in this study we investigated whether other nutrient deficiencies could also induce **ferric reductase** activity in roots of pea (*Pisum sativum* L. cv Sparkle) seedlings. Of the nutrient deficiencies tested (K, Mg, Ca, Mn, Zn, Fe, and Cu), only Co and Fe deficiencies elicited a response. Cu deficiency induced an activity intermediate between Fe-deficient and control plant activities. To ascertain whether the same reductase is induced by Fe and Cu deficiency, concentration- and pH-dependent kinetics of root ferric reduction were compared in plants grown under control, -Fe, and -Cu conditions. Additionally, rhizosphere acidification, another process induced by Fe deficiency, was quantified in pea seedlings grown under the three regimes. Control, Fe-deficient, and Cu-deficient plants exhibited no major differences in pH optima or K-m for the kinetics of ferric reduction. However, the V-max for ferric reduction was dramatically influenced by plant nutrient status, increasing 16- to 38-fold under Fe deficiency and 1.5- to 4-fold under Cu deficiency, compared with that of control plants. These results are consistent with a model in which varying amounts of the same enzyme are deployed on the plasma membrane in response to plant Fe or Cu status. Rhizosphere acidification rates in the Cu-deficient plants were similarly intermediate between those of the control and Fe-deficient plants. These results suggest that Cu deficiency induces the same responses induced by Fe deficiency in peas.

1997

6/3,AB/36 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11058942 BIOSIS NO.: 199799680087
Metal ion effects on early growth and **ferric reductase** activity in wetland plants.
AUTHOR: Wadas Thaddeus(a); Witcher Lynis(a); Held Michael E; Jones-Held Susan(a)
AUTHOR ADDRESS: (a)King's Coll., Wilkes-Barre, PA 18711**USA
JOURNAL: Plant Physiology (Rockville) 114 (3 SUPPL.):p115-116 1997
CONFERENCE/MEETING: PLANT BIOLOGY '97: 1997 Annual Meetings of the American Society of Plant Physiologists and the Canadian Society of Plant Physiologists, Japanese Society of Plant Physiologists and the Australian Society of Plant Physiologists Vancouver, British Columbia, Canada August 2-6, 1997
ISSN: 0032-0889
RECORD TYPE: Citation
LANGUAGE: English
1997

6/3,AB/37 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

10962515 BIOSIS NO.: 199799583660
Enzyme reactions in *Moraxella bovis* contributing to metal detoxification.
AUTHOR: Vigil J R; Cardenas E; Baron L L
AUTHOR ADDRESS: Dep. Biol., Univ. New Mexico, Albuquerque, NM**USA
JOURNAL: Abstracts of the General Meeting of the American Society for
Microbiology 97 (0):p499 1997
CONFERENCE/MEETING: 97th General Meeting of the American Society for
Microbiology Miami Beach, Florida, USA May 4-8, 1997
ISSN: 1060-2011
RECORD TYPE: Citation
LANGUAGE: English
1997

6/3,AB/38 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10961123 BIOSIS NO.: 199799582268
Genetic and physiologic identity of loci involved in iron reduction and
oxidative stress in *Cryptococcus neoformans*.
AUTHOR: Nyhus K J; Jacobson E S
AUTHOR ADDRESS: McGuire VA Med. Ctr., Richmond, VA**USA
JOURNAL: Abstracts of the General Meeting of the American Society for
Microbiology 97 (0):p263 1997
CONFERENCE/MEETING: 97th General Meeting of the American Society for
Microbiology Miami Beach, Florida, USA May 4-8, 1997
ISSN: 1060-2011
RECORD TYPE: Citation
LANGUAGE: English
1997

6/3,AB/39 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10934453 BIOSIS NO.: 199799555598
Characterization of plasma membrane-bound Fe-3+-chelate reductase from
Fe-deficient and Fe-sufficient cucumber roots.
AUTHOR: Sueyoshi Kuni; Hirata Osamu; Oji Yoshiakiyo
AUTHOR ADDRESS: Dep. Agricultural Chemistry, Fac. Agric., Kobe Univ.,
Nada-ku, Kobe 657**Japan
JOURNAL: Soil Science and Plant Nutrition 43 (1):p149-156 1997
ISSN: 0038-0768
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: In vivo Fe-3+-chelate reductase (FeR) activity in cucumber roots
(*Cucumis sativus* L.) increased by transferring the plants from
Fe-sufficient (+Fe) conditions to Fe-deficient (-Fe) conditions. This
increase was inhibited by the protein synthesis inhibitor, cycloheximide.
The plasma membranes were isolated from the +Fe and -Fe roots and then
the enzymatic properties of plasma membrane-bound FeR were characterized.
The FeR in the plasma membranes from both the +Fe and -Fe roots reduced
Fe-3+-citrate using NADH as an electron donor in the presence of Triton
X-100. Plasma membrane-bound FeR from both types of roots showed similar
K-m values for Fe-3+-citrate and NADH at 70 and 100 μ M, respectively,
whereas V-max, of the enzyme from -Fe roots was three-fold higher than
that of the enzyme from +Fe roots. The enzyme was solubilized from plasma
membranes with 1.0% Triton X-100 and subsequently analyzed on an
isoelectric focusing gel. The activity staining of the gel after
electrophoresis showed that four FeR isozymes with different pIs of 5.3,
6.8, 7.5, and 8.7 were present on the plasma membranes of both the +Fe

and -Fe roots. Only the intensity of the pI 7.5 band was enhanced in the -Fe roots. These results suggested that the increase of FeR activity in the -Fe roots resulted from the increased synthesis of the FeR isoform which is constitutively present in the plasma membranes of +Fe roots.

1997

6/3,AB/40 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

10790357 BIOSIS NO.: 199799411502
Ferric iron reduction by *Cryptococcus neoformans*.
AUTHOR: Nyhus Karin J; Wilborn Amy T; Jacobson Eric S(a)
AUTHOR ADDRESS: (a)Res. Serv., Box 151, McGuire V.A.M.C., Richmond, VA
23249**USA
JOURNAL: Infection and Immunity 65 (2):p434-438 1997
ISSN: 0019-9567
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The pathogenic yeast *Cryptococcus neoformans* must reduce Fe(III) to Fe(II) prior to uptake. We investigated mechanisms of reduction using the chromogenic ferrous chelator bathophenanthroline disulfonate. Iron-depleted cells reduced 57 nmol of Fe(III) per 10⁻⁶ cells per h, while iron-replete cells reduced only 8 nmol of Fe(III). Exponential-phase cells reduced the most and stationary-phase cells reduced the least Fe(III), independent of iron status. Supernatants from iron-depleted cells reduced up to 2 nmol of Fe(III) per 10⁻⁶ cells per h, while supernatants from iron-replete cells reduced 0.5 nmol of Fe(III), implying regulation of the secreted reductant(s). One such reductant is 3-hydroxyanthranilic acid (3HAA), which was found at concentrations up to 29 μ -M in iron-depleted cultures but < 2 μ -M in cultures supplemented with iron. Moreover, when washed and resuspended in low iron medium, iron-depleted cells secreted 20.4 μ -M 3HAA, while iron-replete cells secreted only 4.5 μ -M 3HAA. Each mole of 3HAA reduced 3 mol of Fe(III), and increasing 3HAA concentrations correlated with increasing reducing activity of supernatants; however, 3HAA accounted for only half of the supernatant's reducing activity, indicating the presence of additional reductants. Finally, we found that melanized stationary-phase cells reduced 2 nmol of Fe(III) per 10⁻⁶ cells per h-16 times the rate of nonmelanized cells-suggesting that this redox polymer participates in reduction of Fe(III).

1997

6/3,AB/41 (Item 12 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10742154 BIOSIS NO.: 199799363299
Ferric-reductase activities in whole cells and cell fractions of *Vibrio (Listonella) anguillarum*.
AUTHOR: Mazoy Ramon; Lemos Manuel L(a)
AUTHOR ADDRESS: (a)Dep. Microbiol. Parasitol., Fac. Ciencias, Universidad Santiago de Compostela, Campus de Lugo, E**Spain
JOURNAL: Microbiology (Reading) 142 (11):p3187-3193 1996
ISSN: 1350-0872
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The ability of *Vibrio (Listonella) anguillarum* strains from

serotype groups O1 and O2 to reduce Fe-3+ in the form of different chelates was investigated. All strains, grown in M9 minimal medium supplemented with 0.2% Casamino acids, reduced Fe-3+ complexed by citrate, nitrilotriacetic acid and EDTA. In whole cells, the degree of reduction was dependent on the Fe-3+ ligand and on the strain, with the greatest values corresponding to ferric dicitrate and serotype group O1 strains, respectively. The **ferric-reductase** activity increased, over the basal levels, when the cells were grown with iron added as ferric dicitrate, haemin or haemoglobin. All strains also reduced ferricyanide, a compound that is not transported into the bacterial cells. Ferricyanide reduction was also increased when the cells were grown in the presence of an iron source. All of the cell fractions (periplasm, membranes and cytoplasm) showed Fe-3+-reducing activity, with the highest values observed in the presence of Mg-2+, NADH and FAD in the assay buffer. Cytoplasmic **ferric-reductase** could be visualized using native polyacrylamide or starch gel electrophoresis, whereas the periplasmic and membrane reductase(s) could only be detected on starch gels. The results indicate the presence of different **ferric-reductase** activities in *V. anguillarum*, which could be involved in the different iron-acquisition systems present in this micro-organism, i.e., siderophore-mediated systems and siderophore-independent mechanisms.

1996

6/3,AB/42 (Item 13 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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10631063 BIOSIS NO.: 199699252208
 Soluble maize root NADH **ferric-chelate reductase**.
 AUTHOR: Bagnaresi P(a); Basso B
 AUTHOR ADDRESS: (a)Dip. Biol., Univ. Bologna, Via Irnerio 42, I-40126 Bologna**Italy
 JOURNAL: Journal of Plant Nutrition 19 (8-9):p1171-1177 1996
 ISSN: 0190-4167
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: A combination of ammonium sulphate fractionation, Cibacron Blue 3 GA affinity chromatography and size exclusion chromatography was employed to partially purify a 28 kDa NADH Fe-3+-chelate reductase from maize root 110,000 g supernatants. This form was similar to a previously purified 28 kDa microsomal **ferric reductase**, showing the same chromatographic behavior, ratio of ferricyanide to ferric-chelate reduction (3:1 to 2:1, depending on the iron chelator) and high sensitivity to PHMB. The two forms were subjected to IEF in nondenaturing PAGE and the gel was activity-stained. Two bands of pI 8.5 and 7.6 were detected in both cases. A fainter pI 6.9 band was also present in the reductase from the supernatant. The supernatant form seems to be derived from the microsomal form, which was previously shown to be loosely bound to membranes and mainly hydrophilic.

1996

6/3,AB/43 (Item 14 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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10520590 BIOSIS NO.: 199699141735
 Iron uptake by symbiosomes from soybean root nodules.

AUTHOR: Levier Kristin; Day David A; Guerinot Mary Lou(a)
AUTHOR ADDRESS: (a)Dep. Biol. Sci., 6044 Gilman, Dartmouth Coll., Hanover,
NH 03755**USA
JOURNAL: Plant Physiology (Rockville) 111 (3):p893-900 1996
ISSN: 0032-0889
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: To identify possible iron sources for bacteroids in planta, soybean (*Glycine max* L. Merr.) symbiosomes (consisting of the bacteroid-containing peribacteroid space enclosed by the peribacteroid membrane (PBM)) and bacteroids were assayed for the ability to transport iron supplied as various ferric (Fe(III))-chelates. Iron presented as a number of Fe(III)-chelates was transported at much higher rates across the PBM than across the bacteroid membranes, suggesting the presence of an iron storage pool in the peribacteroid space. Pulse-chase experiments confirmed the presence of such an iron storage pool. Because the PBM is derived from the plant plasma membrane, we reasoned that it may possess a **ferric-chelate reductase** activity similar to that present in plant plasma membrane. We detected **ferric-chelate reductase** activity associated with the PBM and suggest that reduction of Fe(III) to ferrous (Fe(II)) plays a role in the movement of iron into soybean symbiosomes.

1996

6/3,AB/44 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10489090 BIOSIS NO.: 199699110235
Inhibition of *Azotobacter salinestris* growth by zinc under iron-limited conditions.
AUTHOR: Page William J(a); Manchak Janet; Yohemas Michael
AUTHOR ADDRESS: (a)Dep. Biol. Sci., Univ. Alberta, Edmonton, AB T6G 2E9**
Canada
JOURNAL: Canadian Journal of Microbiology 42 (7):p655-661 1996
ISSN: 0008-4166
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English; French

ABSTRACT: The growth yield of *Azotobacter salinestris*, a Na⁺-dependent, microaerophilic nitrogen-fixing bacterium, was inhibited more than 60% by 5 μ -M Zn-2+. This organism was much more sensitive to Zn-2+ than the obligate aerobe *Azotobacter vinelandii*. Inhibition of *A. salinestris* was most evident in iron-limited cells and exogenously added Fe-2+ was more effective than Fe-3+ in preventing inhibition by Zn-2+. While Zn-2+ decreased the Fe content of the cells, decreased the activity of the soluble cytoplasmic **ferric reductase**, and altered the intracellular Fe-2+/Fe-3+ ratio, which in turn increased siderophore production, none of these effects appeared severe enough to account for growth inhibition. However, Zn-2+ also was observed to be a powerful inhibitor of Fe-limited whole cell respiration. As the cells became more Fe sufficient, this inhibition of respiration was decreased. Growth of *A. salinestris* also was inhibited by Cd-2+ > Zn-2+ > Cu-2+ > Cr-2+ > Ni-2+ > Co-2+, and inhibition by these ions also was reversed by exogenous Fe-2+ or Fe-3+. Examination of isolated cell membranes showed that the sensitivity of *A. salinestris* NADH oxidase activity to Zn-2+ and other respiratory poisons changed as the cells became Fe sufficient, but a similar change did not occur in *A. vinelandii*. It is proposed that

Fe-limited *A. salinestris* cells present a sensitive target for Zn-2+ inhibition, possibly a sulfhydryl group in a terminal oxidase, but this target is lost or is of decreased importance in Fe-sufficient cells.

1996

6/3,AB/45 (Item 16 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10459380 BIOSIS NO.: 199699080525
Subcellular fractionation of nitrate and **ferric chelate reductase** activities in barley roots.
AUTHOR: Omholt Thomas E(a); Boyer Gregory L
AUTHOR ADDRESS: (a)Chemistry Dep., State University New York, Coll. Environ. Sci. Forestry, Syracuse, NY 13210**USA
JOURNAL: Plant Physiology (Rockville) 111 (2 SUPPL.):p102 1996
CONFERENCE/MEETING: Annual Meeting of the American Society of Plant Physiologists San Antonio, Texas, USA July 27-31, 1996
ISSN: 0032-0889
RECORD TYPE: Citation
LANGUAGE: English
1996

6/3,AB/46 (Item 17 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

10456749 BIOSIS NO.: 199699077894
Assessment of macrophage **ferric reductase** activity as a marker for genetic haemochromatosis.
AUTHOR: Partridge Jason; Wallace D F; Mistry P K; Dooley J S; Walker A P
AUTHOR ADDRESS: Royal Free Hosp. Sch. Med., London**UK
JOURNAL: European Journal of Human Genetics 4 (SUPPL. 1):p70 1996
CONFERENCE/MEETING: 28th Annual Meeting of the European Society of Human Genetics London, England, UK April 11-13, 1996
ISSN: 1018-4813
RECORD TYPE: Citation
LANGUAGE: English
1996

6/3,AB/47 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10424763 BIOSIS NO.: 199699045908
Direct measurement of ⁵⁹Fe-labeled Fe-2+ influx in roots of pea using a chelator buffer system to control free Fe-2+ in solution.
AUTHOR: Fox Tama C(a); Shaff Jon E; Grusak Michael A; Norvell Wendell A; Chen Yona; Chaney Rufus L; Kochian Leon V
AUTHOR ADDRESS: (a)United States Plant Soil Nutr. Lab., United States Dep. Agric.-Agric. Res. Serv., Cornell Univer**USA
JOURNAL: Plant Physiology (Rockville) 111 (1):p93-100 1996
ISSN: 0032-0889
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Fe-2+ transport in plants has been difficult to quantify because of the inability to control Fe" activity in aerated solutions and nonspecific binding of Fe to cell walls. In this study, a

Fe(II)-3-(2-pyridyl)-5,6-diphenyl-1,2,4-triazine-4'4'-disulfonic acid buffer system was used to control free Fe-2+ in uptake solutions. Additionally, desorption methodologies were developed to adequately remove nonspecifically bound Fe from the root apoplasm. This enabled us to quantify unidirectional Fe-2+ influx via radiotracer (⁵⁹Fe) uptake in roots of pea (*Pisum sativum* cv Sparkle) and its single gene mutant brz, an Fe hyperaccumulator. Fe influx into roots was dramatically inhibited by low temperature, indicating that the measured Fe accumulation in these roots was due to true influx across the plasma membrane rather than nonspecific binding to the root apoplasm. Both Fe-2+ influx and Fe translocation to the shoots were stimulated by Fe deficiency in Sparkle. Additionally, brz, a mutant that constitutively exhibits high **ferric reductase** activity, exhibited higher Fe-2+ influx rates than +Fe-grown Sparkle. These results suggest that either Fe deficiency triggers the induction of the Fe-2+ transporter or that the enhanced **ferric reductase** activity somehow stimulates the activity of the existing Fe-2+ transport protein.

1996

6/3,AB/48 (Item 19 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
 (c) 2002 BIOSIS. All rts. reserv.

10360903 BIOSIS NO.: 199698815821
 Purification of the cell-surface **ferric reductase** from
Trichomonas vaginalis.
 AUTHOR: Tarango M; Leherker M W
 AUTHOR ADDRESS: Univ. Texas at El Paso, El Paso, TX**USA
 JOURNAL: Abstracts of the General Meeting of the American Society for
 Microbiology 96 (0):p228 1996
 CONFERENCE/MEETING: 96th General Meeting of the American Society for
 Microbiology New Orleans, Louisiana, USA May 19-23, 1996
 ISSN: 1060-2011
 RECORD TYPE: Citation
 LANGUAGE: English
 1996

6/3,AB/49 (Item 20 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
 (c) 2002 BIOSIS. All rts. reserv.

10200186 BIOSIS NO.: 199698655104
 Formation of root epidermal transfer cells in *Plantago*.
 AUTHOR: Schmidt Wolfgang(a); Bartels Martin
 AUTHOR ADDRESS: (a)Carl von Ossietzky Univ. Oldenburg, Fachbereich
 Biologie, 26111 Oldenburg, Postfach 2503**Germany
 JOURNAL: Plant Physiology (Rockville) 110 (1):p217-225 1996
 ISSN: 0032-0889
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: The root ultrastructure and transmembrane electron transport activities of two *Plantago* species have been examined with respect to alterations in response to Fe deficiency, exogenously supplied auxin, and the presence of chromium in the external medium. Both species showed increased **ferric reductase** activity upon Fe starvation, but they differed in the maximum rates. The addition of chromium to the nutrient solution led to a further enhancement in Fe-ethylenediaminetetraacetate reduction by Fe-deficient plants. In roots of *Plantago lanceolata*, the enhanced redox activity is associated with

the formation of transfer cells in the epidermis. Similar characteristics of rhizodermal cells were observed in Fe-sufficient roots 3 d after application of the auxin analog 2,4-dichlorophenoxyacetic acid. No structural adaptations occurred in roots of *Plantago maritima*. A quantitative estimation of the frequencies of transfer cells in root segments of Fe-deficient plants that differ in reduction activity revealed no correlation between the two phenomena. It is concluded that the area of plasmalemma infoldings is not specialized for the enhanced reduction of extracytoplasmatic Fe in response to Fe deficiency. The role of transfer cells in the adaptation to suboptimal Fe availability and the mechanisms triggering their formation are discussed.

1996

6/3,AB/50 (Item 21 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10200016 BIOSIS NO.: 199698654934

The pH requirement for in vivo activity of the iron-deficiency-induced 'Turbo' **ferric chelate reductase**: A comparison of the iron-deficiency-induced iron reductase activities of intact plants and isolated plasma membrane fractions in sugar beet.

AUTHOR: Susin Santos; Abadia Anunciacion; Gonzalez-Reyes Jose Antonio; Lucena Juan Jose; Abadia Javier(a)

AUTHOR ADDRESS: (a)Departamento de Nutricion Vegetal, Estacion Experimental de Aula Dei, Consejo Superior de Invest**Spain

JOURNAL: Plant Physiology (Rockville) 110 (1):p111-123 1996

ISSN: 0032-0889

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The characteristics of the Fe reduction mechanisms induced by Fe deficiency have been studied in intact plants of *Beta vulgaris* and in purified plasma membrane vesicles from the same plants. in Fe-deficient plants the in vivo Fe(III)-ethylenediaminetetraacetic complex (Fe(III)-EDTA) reductase activity increased over the control values 10 to 20 times when assayed at a pH of 6.0 or below ('turbo' reductase) but increased only 2 to 4 times when assayed at a pH of 6.5 or above. The Fe(III)-EDTA reductase activity of root plasma membrane preparations increased 2 and 3.5 times over the controls, irrespective of the assay pH. The K-m for Fe(III)-EDTA of the in vivo **ferric chelate reductase** in Fe-deficient plants was approximately 510 and 240 μ M in the pH ranges 4.5 to 6.0 and 6.5 to 8.0, respectively. The K-m for Fe(III)-EDTA of the **ferric chelate reductase** in intact control plants and in plasma membrane preparations isolated from Fe-deficient and control plants was approximately 200 to 240 μ M. Therefore, the turbo **ferric chelate reductase** activity of Fe-deficient plants at low pH appears to be different from the constitutive **ferric chelate reductase**.

1996

6/3,AB/51 (Item 22 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10194006 BIOSIS NO.: 199698648924

Shoot-to-root signal transmission regulates root Fe(III) reductase activity in the dgl mutant of pea.

AUTHOR: Grusak Michael A(a); Pezeshgi Shahrbanu

AUTHOR ADDRESS: (a)United States Dep. Agric./Agric. Res. Service,
Children's Nutrition Res. Cent., Dep. Pediatrics,**USA
JOURNAL: Plant Physiology (Rockville) 110 (1):p329-334 1996
ISSN: 0032-0889
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: To understand the root, shoot, and Fe-nutritional factors that regulate root Fe-acquisition processes in dicotyledonous plants, Fe(III) reduction and net proton efflux were quantified in root systems of an Fe-hyperaccumulating mutant (dgl) and a parental (cv Dippes Gelbe Viktoria (DGV)) genotype of pea (*Pisum sativum*). Plants were grown with (+Fe treated) or without (-Fe treated) added Fe(III)-N,N'-ethylenebis(2-(2-hydroxyphenyl)-glycine) (2 μ M); root Fe(III) reduction was measured in solutions containing growth nutrients, 0.1 mM Fe(III)-ethylenediaminetetraacetic acid, and 0.1 mM Na-2-bathophenanthrolinedisulfonic acid. Daily measurements of Fe(III) reduction (d 10-20) revealed initially low rates in +Fe-treated and -Fe-treated dgl, followed by a nearly 5-fold stimulation in rates by d 15 for both growth types. In DGV, root Fe(III) reductase activity increased only minimally by d 20 in +Fe-treated plants and about 3-fold in -Fe-treated plants, beginning on d 15. Net proton efflux was enhanced in roots of -Fe-treated DGV and both dgl growth types, relative to +Fe-treated DGV. In dgl, the enhanced proton efflux occurred prior to the increase in root Fe(III) reductase activity. Reductase studies using plants with reciprocal shoot:root grafts demonstrated that shoot expression of the dgl gene leads to the generation of a transmissible signal that enhances Fe(III) reductase activity in roots. The dgl gene product may alter or interfere with a normal component of a signal transduction mechanism regulating Fe homeostasis in plants.

1996

6/3,AB/52 (Item 23 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10144555 BIOSIS NO.: 199698599473
Induction of **ferric reductase** activity in response to iron deficiency in *Arabidopsis*.
AUTHOR: Saleeba Jennifer A; Guerinot Mary Lou(a)
AUTHOR ADDRESS: (a)Dep. Biol. Sci., Dartmouth College, Hanover, NH
03755-3576**USA
JOURNAL: Biometals 8 (4):p297-300 1995
ISSN: 0966-0844
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The response to iron deficiency was investigated in 16 ecotypes of *Arabidopsis thaliana* (L.) Heynh. and in *Arabidopsis griffithiana*. An increase in root **ferric reductase** activity was observed under conditions of iron deficiency in these ecotypes and in both species. This observation is consistent with a Strategy I response which is typical for dicot plants. *A. griffithiana*, however, showed a lower induction of **ferric reductase** activity in response to iron deficiency than that of the commonly studied *A. thaliana* Columbia ecotypes.

1995

6/3,AB/53 (Item 24 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

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09897319 BIOSIS NO.: 199598352237
Investigation of the role of mineral nutrient deficiencies in induction of
the root-cell plasma membrane **ferric reductase**.
AUTHOR: Cohen Clara K; Norvell Wendell A; Kochian Leon V
AUTHOR ADDRESS: US Plant, Soil, Nutrition Lab., Cornell University,
Ithaca, NY 14853**USA
JOURNAL: Plant Physiology (Rockville) 108 (2 SUPPL.):p111 1995
CONFERENCE/MEETING: Annual Meeting of the American Society of Plant
Physiologists Charlotte, North Carolina, USA July 29-August 2, 1995
ISSN: 0032-0889
RECORD TYPE: Citation
LANGUAGE: English
1995

6/3,AB/54 (Item 25 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09896779 BIOSIS NO.: 199598351697
Uncoupling Fe-2+ influx from ferric reduction in Pisum sativum CV sparkle
and the Fe hyperaccumulator E107.
AUTHOR: Fox Tama C; Shaff Jon E; Norvell Wendell A; Kochian Leon V
AUTHOR ADDRESS: US Plant Soil, Nutrition Lab., USDA-ARS, Cornell Univ.,
Ithaca, NY 14853**USA
JOURNAL: Plant Physiology (Rockville) 108 (2 SUPPL.):p21 1995
CONFERENCE/MEETING: Annual Meeting of the American Society of Plant
Physiologists Charlotte, North Carolina, USA July 29-August 2, 1995
ISSN: 0032-0889
RECORD TYPE: Citation
LANGUAGE: English
1995

6/3,AB/55 (Item 26 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09850003 BIOSIS NO.: 199598304921
Trichomonas vaginalis ferric iron uptake is mediated by a cell surface
ferric reductase.
AUTHOR: Tarango M; Lecker M W
AUTHOR ADDRESS: Univ. Tex., El Paso, TX**USA
JOURNAL: Abstracts of the General Meeting of the American Society for
Microbiology 95 (0):p227 1995
CONFERENCE/MEETING: 95th General Meeting of the American Society for
Microbiology Washington, D.C., USA May 21-25, 1995
ISSN: 1060-2011
RECORD TYPE: Citation
LANGUAGE: English
1995

6/3,AB/56 (Item 27 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

09839271 BIOSIS NO.: 199598294189
AFT1: Activator of ferrous transport regulates iron uptake
transcriptionally in *S. cerevisiae*.
AUTHOR: Yamaguchi-Iwai Yuko; Yuan Daniel S; Dancis Andrew; Klausner Richard
D

AUTHOR ADDRESS: Cell Biol., Metabolism Branch, NICHD, NIH, Bethesda, MD
20892**USA
JOURNAL: Journal of Cellular Biochemistry Supplement 0 (21A):p251
1995
CONFERENCE/MEETING: Keystone Symposium on Metal and Oxygen Regulation of
Gene Expression Park City, Utah, USA March 18-24, 1995
ISSN: 0733-1959
RECORD TYPE: Citation
LANGUAGE: English
1995

6/3,AB/57 (Item 28 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09839257 BIOSIS NO.: 199598294175
The FRE1 and FRE2 *Saccharomyces cerevisiae* genes essential for iron uptake
participate also in copper metabolism.
AUTHOR: Georgatsou E(a); Mavrogiannis L; Alexandraki D(a)
AUTHOR ADDRESS: (a) Foundation Res. Technol.-HELLAS, Inst. Mol. Biol.
Biotechnol., PO Box 1527, Heraklion 711 10 Cre**Greece
JOURNAL: Journal of Cellular Biochemistry Supplement 0 (21A):p248
1995
CONFERENCE/MEETING: Keystone Symposium on Metal and Oxygen Regulation of
Gene Expression Park City, Utah, USA March 18-24, 1995
ISSN: 0733-1959
RECORD TYPE: Citation
LANGUAGE: English
1995

6/3,AB/58 (Item 29 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09839256 BIOSIS NO.: 199598294174
The involvement of stress-related transcription factors in the
iron-dependent regulation of the FRE2 **ferric reductase** gene
of *Saccharomyces cerevisiae*.
AUTHOR: Alexandraki D(a); Klinakis A; Georgatsou E(a)
AUTHOR ADDRESS: (a) Foundation Res. Technol.-HELLAS, Inst. Mol. Biol.
Biotechnol., PO Box 1527, Heraklion 711 10 Cre**Greece
JOURNAL: Journal of Cellular Biochemistry Supplement 0 (21A):p248
1995
CONFERENCE/MEETING: Keystone Symposium on Metal and Oxygen Regulation of
Gene Expression Park City, Utah, USA March 18-24, 1995
ISSN: 0733-1959
RECORD TYPE: Citation
LANGUAGE: English
1995

6/3,AB/59 (Item 30 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09721560 BIOSIS NO.: 199598176478
The effect of manganese oxides and manganese ion on growth and siderophore
production by *Azotobacter vinelandii*.
AUTHOR: Page William J
AUTHOR ADDRESS: Dep. Microbiol., Univ. Alberta, Edmonton, AB T6G 2E9**
Canada
JOURNAL: Biometals 8 (1):p30-36 1995

ISSN: 0966-0844
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The addition of manganese oxides to iron-limited medium promoted the formation of the pyoverdine siderophore azotobactin by *Azotobacter vinelandii*. When active-MnO₂ was used, there was greatly decreased iron uptake into the cells, hyperproduction of azotobactin and the abiotic, chemical destruction or adsorption of the catechol siderophores azotochelin and aminochelin by this strong oxidizing agent. Although the iron content of the cells was the same as iron-limited cells, the growth of cells in medium with active-MnO₂ was increased 1.5- to 2.5-fold over iron-limited controls. This growth promotion was not caused by iron contaminating the oxide or by manganese solubilized from the oxide. Soluble 0.05-4 mM Mn²⁺ inhibited the growth of iron-limited cells and had a minimal effect on iron uptake, but caused hyperproduction of azotobactin. This later effect was caused by the inhibition of soluble **ferric reductase**, in a manner identical to that previously observed for Zn²⁺. These results suggest that active-MnO₂ may interfere with a surface-localized iron uptake site, possibly another **ferric reductase**. The reason for the growth promotion by active-MnO₂ remains unknown, but is most likely related to decreased oxygen toxicity.

1995

6/3,AB/60 (Item 31 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09628693 BIOSIS NO.: 199598083611
A genetic approach to elucidating eukaryotic iron metabolism.
AUTHOR: Klausner Richard D; Dancis Andrew
AUTHOR ADDRESS: Cell Biol. Metabolism Branch, NICHD, NIH, Bethesda, MD
20892**USA
JOURNAL: FEBS Letters 355 (2):p109-113 1994
ISSN: 0014-5793
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Studies of mutants of the yeast *Saccharomyces cerevisiae* have led to the identification of genes required for high affinity iron uptake. Reduction of iron (III) outside the cell is accomplished by means of reductases encoded by FRE1 and FRE2, homologues of the gp91-phox component of the oxygen reductase of human granulocytes. High affinity iron (II) transport from the exterior to the interior of the cell occurs by means of a transport system that has not been molecularly characterized. However, the transport process requires the activity of a copper-containing oxidase encoded by FET3. The amino acid sequence of this protein resembles other multi-copper oxidases, including mammalian ceruloplasmin. High affinity copper uptake mediated by the copper transport protein encoded by CTR1 is required to provide the FET3 protein with copper, and thus copper uptake is indirectly required for ferrous iron uptake. These genetic elements of yeast and their relationships may be conserved in complex eukaryotic organisms.

1994

6/3,AB/61 (Item 32 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09344577 BIOSIS NO.: 199497352947

Investigating biophysical and molecular components of iron absorption in
Pisum sativum cv Sparkle roots.

AUTHOR: Fox Tama C; Garvin David F; Cohen Clara K; Kochian Leon V

AUTHOR ADDRESS: U.S. Plant Soil Nutr. Lab., Cornell Univ., Ithaca, NY
14853**USA

JOURNAL: Plant Physiology (Rockville) 105 (1 SUPPL.):p17 1994

CONFERENCE/MEETING: Annual Meeting of the American Society of Plant
Physiologists Portland, Oregon, USA July 30-August 3, 1994

ISSN: 0032-0889

RECORD TYPE: Citation

LANGUAGE: English

1994

6/3,AB/62 (Item 33 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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08905217 BIOSIS NO.: 199396056718

Iron uptake by leaf mesophyll cells: The role of the plasma membrane-bound
ferric-chelate reductase.

AUTHOR: Brueggemann Wolfgang(a); Maas-Kantel Klaudia; Moog Petra R

AUTHOR ADDRESS: (a)Bot. Inst. III, Heinrich-Heine-Universitaet,
Universitaetsstrasse 1, W-4000 Duesseldorf 1**Germany

JOURNAL: Planta (Heidelberg) 190 (2):p151-155 1993

ISSN: 0032-0935

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The uptake of ^{59}Fe from FeCl_3 , ferric (Fe^{3+}) citrate (FeCitr) and Fe^{3+} -EDTA (FeEDTA) was studied in leaf mesophyll of *Vigna unguiculata* (L.) Walp. Uptake rates decreased in the order FeCl_3 > FeCitr > FeEDTA , and uptake depended on an obligatory reduction step of Fe^{3+} to Fe^{2+} , after which the ion could be taken up independently of the chelator, citrate. Uptake was strongly increased by photosynthetically active light (λ > 630 nm), and kinetic analysis revealed saturation kinetics with a K_m (FeCitr) of 80-110 μM . In the presence of an external Fe^{2+} scavenger, bathophenanthroline disulfonate, the mesophyll also reduced external FeCitr with a K_m of approx. 50-60 μM . The reduction rates for FeCitr were five to eightfold higher than necessary for uptake. Purified plasma membranes from leaves revealed an NADH-dependent FeCitr - and FeEDTA -reductase activity, which had a pH optimum of 6.5-6.8 and a K_m of approx. 20 μM for NADH. Under anaerobic conditions, a K_m of 130-170 μM for ferric chelates was obtained, while in the presence of oxygen a K_m (FeCitr) of approx. 100 μM was found. It is concluded that the leaf plasma membrane provides a **ferric-chelate-reductase** activity, which plays a crucial role in iron uptake of leaf cells. Under in-vivo conditions, however, reactive oxygen species or strong (blue) light may also contribute to the obligatory reduction of Fe^{3+} prior to uptake.

1993

6/3,AB/63 (Item 34 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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08857877 BIOSIS NO.: 199396009378

Iron deficiency stress responses amongst citrus rootstocks.

AUTHOR: Treeby Michael(a); Uren Nick

AUTHOR ADDRESS: (a)CSIRO Div. Hortic., P.M.B., Merbein, VIC. 3505**
Australia
JOURNAL: Zeitschrift fuer Pflanzenernaehrung und Bodenkunde 156 (1):p75-81
1993
ISSN: 0044-3263
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: German; Non-English
SUMMARY LANGUAGE: German; English

ABSTRACT: Seedlings of citrus rootstocks is differing in time tolerance were grown in nutrient solutions with and without Fe. Proton efflux, release of phenolic compounds and Fe reducing substances and root-mediated reduction of Fe-III in FeEDTA and freshly precipitated Fe(OH)-3 in response to Fe deficiency were determined. Sweet orange, Carrizo citrange and trifoliolate orange, the three least tolerant rootstocks used in the study, did not decrease nutrient solution pH in response to Fe deficiency. The more time tolerant rootstocks, rough lemon, Cleopatra mandarin and sour orange, did decrease nutrient solution pH. But in CaSO₄ solution only sour orange increased H⁺ efflux significantly under Fe deficiency. In response to Fe deficiency, the release of phenolic compounds was increased significantly in rough lemon and Cleopatra mandarin seedlings, while the release of reducing substances was increased significantly in rough lemon, sour orange and trifoliolate orange. Rough lemon was the only rootstock to respond to Fe deficiency with an increase in root mediated reduction of chelated Fe-III at pH 6.5. At pH 8.0, both Fe-deficient rough lemon and Cleopatra mandarin roots reduced higher amounts of Fe-III from freshly precipitated Fe(OH)-3 than Fe-sufficient seedlings. Iron reduction by detached roots of Fe-deficient and Fe-sufficient rough lemon did not follow Michaelis-Menten kinetics at high substrate concentrations. Rates of Fe reduction at low substrate concentrations were inconsistent with the existence of an inducible **ferric reductase** in response to Fe deficiency.

1993

6/3,AB/64 (Item 35 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

08846097 BIOSIS NO.: 199395135448

Ferric reductase is associated with the membranes of anaerobically grown *Shewanella putrefaciens* MR-1.

AUTHOR: Myers Charles R(a); Myers Judith M
AUTHOR ADDRESS: (a)Dep. Pharmacol. Toxicol., Medical College Wisconsin,
8701 Watertown Plank Rd., Milwaukee, WI 532**USA
JOURNAL: FEMS (Federation of European Microbiological Societies)
Microbiology Letters 108 (1):p15-22 1993
ISSN: 0378-1097
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The expression and distribution of **ferric reductase** activity was examined in *Shewanella putrefaciens* MR-1. Formate-dependent **ferric reductase** was not detected in aerobically grown cells but was readily detectable in anaerobically grown cells. **Ferric reductase** activity was found exclusively in the membrane fractions, with 54-56% in the outer membrane. In contrast, the majority of formate dehydrogenase was in the soluble fraction with lesser amounts associated with the various membrane fractions. Outer membrane **ferric reductase** activity was markedly inhibited by

p-chloromercuriphenylsulfonate, 2-heptyl-4-hydroxyquinolone-N-oxide, and antimycin A, but was unaffected by the presence of alternate electron acceptors (nitrate, nitrite, fumarate, and trimethylamine N-oxide). Both formate and NADH served as electron donors for **ferric reductase**; activity with L-lactate or NADPH was poor. The addition of FMN markedly stimulated formate- and NADH-dependent **ferric reductase**.

1993

6/3,AB/65 (Item 36 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08623573 BIOSIS NO.: 199345041648
Membrane-associated **ferric reductase** and iron reduction-linked growth yields of *Shewanella putrefaciens* MR-1.
AUTHOR: Myers Charles R; Myers Judith M
AUTHOR ADDRESS: The Med. Coll. Wisconsin, Dep. Pharmacol. Toxicol., Milwaukee, WI 53226**USA
JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 93 (0):p253 1993
CONFERENCE/MEETING: 93rd General Meeting of the American Society for Microbiology Atlanta, Georgia, USA May 16-20, 1993
ISSN: 1060-2011
RECORD TYPE: Citation
LANGUAGE: English
1993

6/3,AB/66 (Item 37 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08242346 BIOSIS NO.: 000043031019
THE **FERRIC REDUCTASE** GENE OF *SCHIZOSACCHAROMYCES-POMBE*
TRANSCRIPTIONAL CONTROL BY IRON AND SEQUENCE SIMILARITY WITH HUMAN PHAGOCYTE NADPH OXIDASE
AUTHOR: ROMA D G; DANCIS A; ANDERSON G J; KLAUSNER R D
AUTHOR ADDRESS: CELL BIOL. METABOLISM BRANCH, NICHD, NATL. INST. HEALTH, BETHESDA, MD.
JOURNAL: THIRTY-SECOND ANNUAL MEETING OF THE AMERICAN SOCIETY FOR CLINICAL NUTRITION, BALTIMORE, MARYLAND, USA, APRIL 30-MAY 2, 1992. CLIN RES 40 (2). 1992. 168A. 1992
CODEN: CLREA
DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH
1992

6/3,AB/67 (Item 38 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

08204884 BIOSIS NO.: 000094017157
FERRIC REDUCTASE OF *SACCHAROMYCES-CEREVISIAE* MOLECULAR CHARACTERIZATION ROLE IN IRON UPTAKE AND TRANSCRIPTIONAL CONTROL BY IRON
AUTHOR: DANCIS A; ROMAN D G; ANDERSON G J; HINNEBUSCH A G; KLAUSNER R D
AUTHOR ADDRESS: CELL BIOL. METABOLISM BRANCH, LAB. MOL. GENETICS, NATIONAL INST. CHILD HEALTH, HUMAN DEVELOPMENT, BETHESDA, MD. 20892.
JOURNAL: PROC NATL ACAD SCI U S A 89 (9). 1992. 3869-3873. 1992
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the

United States of America .
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The principal iron uptake system of *Saccharomyces cerevisiae* utilizes a reductase activity that acts on ferric iron chelates external to the cell. The FRE1 gene product is required for this activity. The deduced amino acid sequence of the FRE1 protein exhibits hydrophobic regions compatible with transmembrane domains and has significant similarity to the sequence of the plasma membrane cytochrome b558 (the X-CGD protein), a critical component of a human phagocyte oxidoreductase suggesting that FRE1 is a structural component of the yeast **ferric reductase**. FRE1 mRNA levels are repressed by iron. Fusion of 977 base pairs of FRE1 DNA upstream from the translation start site of an *Escherichia coli* lacZ reporter gene confers iron-dependent regulation on expression of β -galactosidase in yeast. An 85-base-pair segment of FRE1 5' noncoding sequence contains a RAP1 binding site and a repeated sequence, TTTTGTCTCAYC; this segment is sufficient to confer iron-repressible transcriptional activity on heterologous downstream promoter elements.

1992

6/3,AB/68 (Item 39 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

08174810 BIOSIS NO.: 000042132883
IRON UPTAKE IN ARABIDOPSIS-THALIANA
AUTHOR: GUERINOT M L
AUTHOR ADDRESS: DEP. BIOL. SCI., DARTMOUTH COLL., HANOVER, N.H. 03755.
JOURNAL: 203RD ACS (AMERICAN CHEMICAL SOCIETY) NATIONAL MEETING, SAN FRANCISCO, CALIFORNIA, USA, APRIL 5-10, 1992. ABSTR PAP AM CHEM SOC 203 (1-3). 1992. AGFD69. 1992
CODEN: ACSRA
DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH
1992

6/3,AB/69 (Item 40 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08034864 BIOSIS NO.: 000042061687
CLONING OF THE **FERRIC REDUCTASE** GENE OF THE YEAST
SCHIZOSACCHAROMYCES-POMBE IMPLICATIONS FOR HUMAN IRON METABOLISM
AUTHOR: ROMAN D G; DANCIS A; ANDERSON G J; KLAUSNER R D
AUTHOR ADDRESS: CELL BIOL., METABOLISM BRANCH, NICHD, NATL. INST. HEALTH, BETHESDA, MD. 20892.
JOURNAL: PROCEEDINGS OF THE 8TH INTERNATIONAL CONGRESS OF HUMAN GENETICS, WASHINGTON, D.C., USA, OCTOBER 6-11, 1991. AM J HUM GENET 49 (4 SUPPL.). 1991. 417. 1991
CODEN: AJHGA
DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH
1991

6/3,AB/70 (Item 41 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
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07954502 BIOSIS NO.: 000093033600

IRON-III CHELATE REDUCTASE ACTIVITY OF PLASMA MEMBRANES ISOLATED FROM
TOMATO LYCOPERSICON-ESCULENTUM MILL. ROOTS COMPARISON OF ENZYMES FROM
IRON-DEFICIENT AND IRON-SUFFICIENT ROOTS

AUTHOR: HOLDEN M J; LUSTER D G; CHANEY R L; BUCKHOUT T J; ROBINSON C
AUTHOR ADDRESS: U.S. DEP. AGRIC., AGRIC. RES. SERV., FOREIGN DIS.-WEED SCI.
RES. UNIT, FT. DETRICK, FREDERICK, MD. 21702.

JOURNAL: PLANT PHYSIOL (BETHESDA) 97 (2). 1991. 537-544. 1991

FULL JOURNAL NAME: Plant Physiology (Bethesda)

CODEN: PLPHA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Reduction of Fe^{3+} to Fe^{2+} is a prerequisite for Fe uptake by tomato roots. **Ferric chelate reductase** activity in plasma membranes (PM) isolated from roots of both iron-sufficient (+Fe) and iron-deficient (-Fe) tomatoes (*Lycopersicon esculentum* Mill.) was measured as NADH-dependent ferric citrate reductase and exhibited simple Michaelis-Menten kinetics for the substrates, NADH and Fe^{3+} (citrate³⁻)₂. NADH and Fe^{3+} (citrate³⁻)₂ Km values for reductase in PM from +Fe and -Fe tomato roots were similar, whereas Vmax values were two- to threefold higher for reductase from -Fe tomatoes. The pH optimum for Fe-chelate reductase was 6.5. Fe-chelate reductases from -Fe and +Fe tomato roots were equally sensitive to several triazine dyes. Reductase was solubilized with n-octyl .beta.-D-glucopyranoside and electrophoresed in nondenaturing isoelectric focusing gels. Three bands, with isoelectric points of 5.5 to 6.2, were resolved by enzyme activity staining of electrofocused PM proteins isolated from +Fe and -Fe tomato roots. Activity staining was particularly enhanced in the isoelectric point 5.5 and 6.2 bands solubilized from -Fe PM. We conclude that PM from roots of +Fe and -Fe plants contain Fe-chelate reductases with similar characteristics. The response to iron deficiency stress likely involves increased expression of constitutive Fe-chelate reductase isoforms in expanding epidermal root PM.

1991

6/3,AB/71 (Item 42 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07764003 BIOSIS NO.: 000041062254

TOMATO LYCOPERSICON-ESCULENTUM MILL. ROOT PLASMA MEMBRANE **FERRIC-
CHELATE REDUCTASE** PURIFICATION AND SEPARATION FROM OTHER PM
ELECTRON TRANSPORT COMPLEXES

AUTHOR: HOLDEN M J; LUSTER D G; CHANEY R L; BUCKHOUT T J
AUTHOR ADDRESS: U.S.D.A.-AGRICULTURAL RESEARCH SERVICE, FOREIGN
DISEASE-WEED SCIENCE, FREDERICK, MD. 21702.

JOURNAL: ANNUAL MEETING OF THE AMERICAN SOCIETY OF PLANT PHYSIOLOGISTS,
ALBUQUERQUE, NEW MEXICO, USA, JULY 28-AUGUST 1, 1991. PLANT PHYSIOL
(BETHESDA) 96 (1 SUPPL.). 1991. 35. 1991

CODEN: PLPHA

DOCUMENT TYPE: Meeting

RECORD TYPE: Citation

LANGUAGE: ENGLISH

1991

6/3,AB/72 (Item 43 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

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07627612 BIOSIS NO.: 000040127821

FERRIC REDUCTASE ACTIVITY IN RAT DUODENAL LUMEN AND MUCOSA

AUTHOR: WIEN E M; VAN CAMPEN D R

AUTHOR ADDRESS: DIV. NUTR. SCI., CORNELL UNIV., ITHACA, N.Y. 14853.

JOURNAL: 75TH ANNUAL MEETING OF THE FEDERATION OF AMERICAN SOCIETIES FOR EXPERIMENTAL BIOLOGY, ATLANTA, GEORGIA, USA, APRIL 21-25, 1991. FASEB (FED AM SOC EXP BIOL) J 5 (4). 1991. A559. 1991

CODEN: FAJOE

RECORD TYPE: Citation

LANGUAGE: ENGLISH

1991

6/3,AB/73 (Item 44 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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07521438 BIOSIS NO.: 000091084567

GONADAL DEVELOPMENT IN THE JAPANESE QUAIL COTURNIX-COTURNIX-JAPONICA OF SEX-LINKED ALBINISM

AUTHOR: YAMAMOTO N; ARAKI Y

AUTHOR ADDRESS: 1ST DEP. PHYSIOL., GIFU UNIV. SCHOOL MED., GIFU-SHI, GIFU 500, JPN.

JOURNAL: ACTA SCH MED UNIV GIFU 38 (2). 1990. 170-180. 1990

FULL JOURNAL NAME: Acta Scholae Medicinalis Universitatis in Gifu

CODEN: GDIKA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: The gonadal development in a sex-linked albino variant of a Japanese quail (*Coturnix coturnix japonica*) was studied with respect to changes in gonadal size and the histological findings. The changes in the size of the entire gonads (E), their cortex (C) and medulla (M) were estimated. The male (m) and the female (f) gonads after 4, 6, 9, 11, 13 and 15 days of incubation, 7 days after hatching (A. H.) and the adult were investigated. The maximum dimension of the transverse section was used to indicate gonadal size. In the male, 4 days after incubation (A. I.), the size of the left (L) and the right (R) cortex (mLC and mRC) was comparable to those of the left and right medulla (mLM and mRM), respectively (mLC/mLM = 0.82, mRC/mRM = 0.85). However, from 6 days A. I., mLM and mRM, which developed into the testes, became much larger than mLC and mRC (mLC/mLM = 0.38, mRC/mRM = 0.16, 6 days A. I.). In addition, the mLM size was not so different from that of mRM throughout the experimental stages (mLM/mRM = 1.03-1.66). In the female, throughout the experimental stages, the left entire gonad (fLE) was obviously larger than the right one (fRE), undergoing atrophy (fLE/fRE = 1.31-13.22). The left cortex (fLC), which becomes the ovary, was much more developed than the right one (fRC) (fLC/fRC = 1.38-30.58). Although the left cortex (fLC) was smaller than the left medulla (fLM) until 13 days A. I., the size ratio of the two tissues was reversed later, because fLC became markedly developed (fLC/fLM = 2.72, 7 days A. H.). Comparison of male and female gonadal size showed that mLM and mRM were comparable to or somewhat smaller than fLM and fRM, respectively, in the early embryonic stage (mLM/fLM = 0.86, mRM/fRM = 0.89, 4 days A. I.). However, the size ratio of the two tissues in each side was reversed later, as mLM and mRM developed markedly (mLM/fLM = 2.08, mRM/fRM = 2.34, 7 days A. H.). But fLC was much larger than mLC throughout the experimental stages (mLC/fLC = 0.09-0.83). It was observed histologically that 6 days A. I., the male gonads were already distinguishable from the female; mLM and mRM, which were more developed than mLC and mRC, formed the primary sex cords, containing numerous spermatogonia. On the other hand, fLC in this stage was much thicker than fLM, showing more oogonia than fLM. From 9

days A. I., mLM and mRM similarly presented spermatogonia in the primary sex cords; these male gonads were called the testes. Although both fLC and mLC in this stage showed germ cell clusters, fLC had more clusters in the ovarian cord than mLC; the female left gonad was called the ovary. From 11 days A. I., the oocytes in the clusters in fLC became pre-mitotic, and the clusters developed into follicles after hatching. On the other hand, the germ cell clusters in mLC, fewer than those of fLC, disappeared after hatching.

1990

6/3,AB/74 (Item 45 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07299958 BIOSIS NO.: 000090079845
PLASMA MEMBRANE-BOUND NADH IRON EDTA REDUCTASE AND IRON DEFICIENCY IN
TOMATO LYCOPERSICON-ESCULENTUM IS THERE A TURBO REDUCTASE?
AUTHOR: BRUEGGEMANN W; MOOG P R; NAKAGAWA H; JANIESCH P; KUIPER P J C
AUTHOR ADDRESS: LAB. PLANT PHYSIOLOGY, UNIV. GRONINGEN, POB 14, NL-9750 AA
HAREN, THE NETHERLANDS.
JOURNAL: PHYSIOL PLANT 79 (2). 1990. 339-346. 1990
FULL JOURNAL NAME: Physiologia Plantarum
CODEN: PHPLA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The properties of NADH-dependent Fe³⁺-EDTA reductase in plasma membranes (PM) from roots of iron-deficient and -sufficient tomato plants [*Lycopersicon esculentum* L. (Mill.) cv. Abunda] were examined. Iron deficiency resulted in a 3-fold increase of in vivo root iron-chelate reductase activity with a K_m (Fe³⁺-EDTA) of 230 μM. In purified root PM, average specific activities of **ferric chelate reductase** of 410 and 254 nmol Fe (mg protein)⁻¹ min⁻¹ were obtained for iron-deficient and -sufficient plants, respectively. In both cases, the PM-bound activity showed a pH optimum at pH 6.8. Activity depended on NADH and not on NADPH and on the presence of detergent. The activity was inhibited 40-50% by superoxide dismutase (EC 1.15.1.1.) and ca 30% by oxygen. Kinetic analysis of the membrane-bound enzyme revealed a K_m (Fe³⁺-EDTA) of ca 200 μM for both iron-stressed and -sufficient plants. For NADH, K_m values around 230 μM were obtained. The **ferric chelate reductase** could be solubilized from salt-washed PM with Triton X-100 at a protein:detergent ratio of 1:2.8 (w/w). The Triton-soluble fraction revealed one enzyme-stained band in native polyacrylamide electrophoresis. Although the membranes showed no nitrate reductase (NR; EC 1.6.6.1) activity, anti-spinach NR immunoglobulin G (IgG) recognized a 54 kDa band both in the PM and the Triton-soluble fraction, but not in the enzymatically active material obtained from the native gel. No evidence could be found for the synthesis of a new, biochemically distinct PM-bound **ferric chelate reductase** under iron deficiency, which might be identified as the so-called Turbo reductase. It is concluded that iron deficiency in tomato induces increased expression of a **ferric chelate reductase** in root PM, which is already present in iron-sufficient plants and probably also in plants, which do not contain the Turbo reductase, like the grasses. The iron reductase is not identical with the recently reported PM-associated nitrate reductase.

1990

6/3,AB/75 (Item 46 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07117517 BIOSIS NO.: 000039054211

THE EFFECTS OF CHELATOR STRENGTH ON THE MEASUREMENT OF **FERRIC**
CHELATE REDUCTASE ACTIVITY

AUTHOR: OMHOLT T E; BOYER G L

AUTHOR ADDRESS: FAC. CHEM., SUNY COLL. ENVIRON. SCI. FORESTRY, SYRACUSE,
N.Y. 13210.

JOURNAL: ANNUAL MEETING OF THE AMERICAN SOCIETY OF PLANT PHYSIOLOGISTS,
INDIANAPOLIS, INDIANA, USA, JULY 29-AUGUST 2, 1990. PLANT PHYSIOL
(BETHESDA) 93 (1 SUPPL.). 1990. 65. 1990

CODEN: PLPHA

DOCUMENT TYPE: Meeting

RECORD TYPE: Citation

LANGUAGE: ENGLISH

1990

6/3,AB/76 (Item 47 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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06888161 BIOSIS NO.: 000089042090

PHYSIOLOGICAL DISORDERS OF THE NICOTIANAMINE-AUXOTROPH TOMATO MUTANT
CHLORONERVA AT DIFFERENT LEVELS OF IRON NUTRITION II. IRON DEFICIENCY
RESPONSE AND HEAVY METAL METABOLISM

AUTHOR: STEPHAN U W; GRUEEN M

AUTHOR ADDRESS: ZENTRALINSTITUT GENETIK AND KULTURPFLANZENFORSCHUNG DER
AKADEMIE DER WISSENSCHAFTEN DER DDR, CORRENSSTRASSE 3, GATERSLABEN,
DDR-4325.

JOURNAL: BIOCHEM PHYSIOL PFLANZ (BPP) 185 (3-4). 1989. 189-200. 1989

FULL JOURNAL NAME: Biochemie und Physiologie der Pflanzen (Bpp)

CODEN: BPPFA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: The tomato mutant chloronerva exhibits typical symptoms of iron deficiency. Iron deficiency-induced proton secretion occurs up to 10 μM FeEDTA in the nutrient medium (wild-type only at iron supply lower than 1 μM). Thickened root tips and root hair zones are formed up to 20 μM Fe (wild-type root hairs up to 5 μM). The **ferric reductase** activity of the rhizodermis remains higher than in the wild-type up to 100 μM Fe supply. In the concentration range of 5 to 10 μM Fe supply the mutant accumulates the 2- to 3-fold amount of iron in the shoot compared with the wild-type. The increased uptake of certain heavy metals (e.g. Cu, Mn, Zn) by the wild-type under iron deficiency is extended to a higher iron supply range in the mutant. All these deviations from the wild-type behaviour are overcome by the supply with nicotianamine (NA) to the leaves. The role of NA as the intracellular transporter for Fe(II) in the regulation of iron metabolism and iron deficiency response mechanisms is discussed.

1989

6/3,AB/77 (Item 48 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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06756931 BIOSIS NO.: 000088066364

FERRIC REDUCTASE ACTIVITY IN AZOTOBACTER-VINELANDII AND ITS
INHIBITION BY ZINC

AUTHOR: HUYER M; PAGE W J

AUTHOR ADDRESS: DEP. MICROBIOL., UNIV. ALBERTA, EDMONTON, ALBERTA, CANADA
T6G 2E9.

JOURNAL: J BACTERIOL 171 (7). 1989. 4031-4037. 1989
FULL JOURNAL NAME: Journal of Bacteriology
CODEN: JOBAA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: **Ferric reductase** activity was examined in *Azotobacter vinelandii* and was found to be located in the cytoplasm. The specific activities of soluble cell extracts were not affected by the iron concentration of the growth medium; however, activity was inhibited by the presence of Zn^{2+} during cell growth and also by the addition of Zn^{2+} to the enzyme assays. Intracellular Fe^{2+} levels were lower and siderophore production was increased in Zn^{2+} -grown cells. The **ferric reductase** was active under aerobic conditions, had an optimal pH of approximately 7.5, and required flavin mononucleotide and Mg^{2+} for maximum activity. The enzyme utilized NADH to reduce iron supplied as a variety of iron chelates, including the ferrisiderophores of *A. vinelandii*. The enzyme was purified by conventional protein purification techniques, and the final preparation consisted of two major proteins with molecular weights of 44,600 and 69,000. The apparent K_m values of the **ferric reductase** for Fe^{3+} (supplied as ferric citrate) and NADH were 10 and 15.8 μM , respectively, and the data for the enzyme reaction were consistent with Ping Pong Bi Bi kinetics. The approximate K_i values resulting from inhibition of the enzyme by Zn^{2+} , which was a hyperbolic (partial) mixed-type inhibitor, were 25 μM with respect to iron and 1.7 μM with respect to NADH. These results suggested that **ferric reductase** activity may have a regulatory role in the processes of iron assimilation in *A. vinelandii*.

1989

6/3,AB/78 (Item 49 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06567594 BIOSIS NO.: 000087009755
FERRIC REDUCING ACTIVITY IN ROOTS OF IRON-DEFICIENT PHASEOLUS-VULGARIS
SOURCE OF REDUCING EQUIVALENTS
AUTHOR: LUBBERDING H J; DE GRAAF F H J M; BIENFAIT H F
AUTHOR ADDRESS: DEP. MICROBIOL., UNIV. NIJMEGEN, TOERNOOIVELD, NIJMEGEN, NETHERLANDS.
JOURNAL: BIOCHEM PHYSIOL PFLANZ (BPP) 183 (4). 1988. 271-276. 1988
FULL JOURNAL NAME: Biochemie und Physiologie der Pflanzen (Bpp)
CODEN: BPPFA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Fe deficiency activates a system in the roots of dicotyledons which can reduce extracellular ferric chelates (**ferric reductase**); this system is located in the plasma membranes of the epidermal cells. In order to identify the source of reducing equivalents for the reduction of ferric chelates by roots of bean (*Phaseolus vulgaris* L. var. Prelude), properties of NADP⁺ reducing enzymes were studied and incubations were performed with glucose labeled with ^{14}C at positions C1 and C6. NADP-dependent isocitrate dehydrogenase was the most active of the enzymes tested in root protein extracts and it could reduce NADP⁺ even at very high NADPH/NADP⁺ ratios. It is concluded that citrate, which accumulates in roots upon Fe deficiency, via transformation into isocitrate by mitochondrial aconitase, drives cytosolic NADP in bean roots to a strongly reduced state through isocitrate dehydrogenase. Upon addition of reducible ferric salts, the NADP couple becomes more oxidized making it possible for the oxidative pentose phosphate pathway to contribute to NADP⁺ reduction.

1988

6/3,AB/79 (Item 50 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.

05638566 BIOSIS NO.: 000083111712
CONTROL OF THE DEVELOPMENT OF IRON-EFFICIENCY REACTIONS IN POTATO AS A
RESPONSE TO IRON DEFICIENCY IS LOCATED IN THE ROOTS
AUTHOR: BIENFAIT H F; DE WEGER L A; KRAMER D
AUTHOR ADDRESS: DEP. PLANT PHYSIOL., UNIV. AMSTERDAM, KRUISLAAN 318, 1098
SM AMSTERDAM, NETHERLANDS.
JOURNAL: PLANT PHYSIOL (BETHESDA) 83 (2). 1987. 244-247. 1987
FULL JOURNAL NAME: Plant Physiology (Bethesda)
CODEN: PLPHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Roots of potato plants (*Solanum tuberosum* cc. Bintje) growing on low Fe nutrient solution developed the characteristic Fe efficiency reactions, such as high **ferric reductase** activity, proton extrusion and increased root hair formation. Roots from a tuber with sprout removed, when grown on Fe-free nutrient solution, also expressed these reactions; transfer to iron-containing medium resulted in their complete disappearance within 10 days. Roots growing on 2% sucrose in sterile Murashige-Skoog medium increased their **ferric reductase** activity upon withholding Fe and formed transfer cells. It is concluded that potato roots themselves control the development of Fe-efficiency reactions, and that the shoot may exert a modulating influence on their expression.

1987

6/3,AB/80 (Item 51 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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05552686 BIOSIS NO.: 000083025826
ISOLATION OF A LENTIVIRUS FROM A MACAQUE WITH LYMPHOMA COMPARISON WITH
HUMAN T CELL LYMPHOTROPIC VIRUS TYPE III-LYMPHADENOPATHY-ASSOCIATED VIRUS
AND OTHER LENTIVIRUSES
AUTHOR: BENVENISTE R E; ARTHUR L O; TSAI C-C; SOWDER R; COPELAND T D;
HENDERSON L E; OROSZLAN S
AUTHOR ADDRESS: LAB. OF VIRAL CARCINOGENESIS, NATL. CANCER INST.,
NCI-FREDERICK CANCER RES. FACILITY, FREDERICK, MD. 21701-1013.
JOURNAL: J VIROL 60 (2). 1986. 483-490. 1986
FULL JOURNAL NAME: Journal of Virology
CODEN: JOVIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A retrovirus has been isolated on the human T-cell line HuT 78 after cocultivation of a lymph node from a pig-tailed macaque (*Macaca nemestrina*) that had died with malignant lymphoma in 1982 at the University of Washington primate center. This isolate, designated MnIV (WPRC-1) (*M. nemestrina* immunodeficiency virus, Washington Primate Research Center) shows the characteristic morphology of a lentivirus and replicates to high titers in various lymphocyte lines of human and primate origin. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis of purified MnIV revealed multiple bands of structural proteins, including a major viral gag protein of 28 kilodaltons, that did not

comigrate with the viral proteins of a human immunodeficiency virus (HIV [FRE-1]) that was also isolated on HuT 78 cells. The relatedness of MnIV to other lentiviruses (HTLV-III/LAV, EIAV, and visna) was examined in radioimmunoassays, by immunoblot techniques, and by N-terminal amino acid sequence analysis of the viral p28 gag protein. The immunoassays revealed cross-reactivity only between MnIV p28 and HTLV-III/LAV p24, and sequence analysis showed that 14 of the 24 N-terminal residues of MnIV p28 and HTLV-III/LAV p24 are identical. These results indicate that MnIV belongs to the same lentivirus family as HTLV-III/LAV but is only partially related to these human acquired immune deficiency syndrome retroviruses.

1986

6/3,AB/81 (Item 52 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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05383413 BIOSIS NO.: 000032106542
FERRIC REDUCTASE ACTIVITY IN NEISSERIA-GONORRHOEAE
AUTHOR: LEFAOU A E; MORSE S A
AUTHOR ADDRESS: LAB. BACTERIOLOGIE, FAC. MED., STRASBOURG, FRANCE.
JOURNAL: 87TH ANNUAL MEETING OF THE AMERICAN SOCIETY FOR MICROBIOLOGY,
ATLANTA, GEORGIA, USA, MARCH 1-6, 1987. ABSTR ANNU MEET AM SOC MICROBIOL 87
(0). 1987. 75. 1987
CODEN: ASMAC
DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH
1987

6/3,AB/82 (Item 53 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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03866371 BIOSIS NO.: 000075044444
NITROGEN-15 NMR INVESTIGATION OF NITRITE REDUCTASE SUBSTRATE INTERACTION
AUTHOR: TIMKOVICH R; CORK M S
AUTHOR ADDRESS: DEP. CHEM., ILL. INST. TECHNOL., CHICAGO, ILL. 60616.
JOURNAL: BIOCHEMISTRY 21 (16). 1982. 3794-3797. 1982
FULL JOURNAL NAME: Biochemistry
CODEN: BICHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: ¹⁵N NMR spectroscopy at 30.4 MHz was employed to determine the interaction of the substrate nitrite (97.2% enriched) with bacterial nitrite reductase, denoted cytochrome cd1, from *Pseudomonas aeruginosa*. The addition of ferric enzyme to nitrite did not alter the chemical shift of the bulk nitrite resonance, nor was it possible to observe a new resonance from a hypothetical bound form. The spin-lattice relaxation time (T₁) was lowered from 13.2 to 2.7 s, and the spin-spin relaxation time (T₂) was halved. Values of T₁ were measured by progressive saturation and values of T₂ by line widths. Control experiments involving ferric cytochrome c and metmyoglobin demonstrated that the perturbations did not arise from the bulk paramagnetic properties of the protein solutions. Variable enzyme/substrate ratios were measured to assess the strength of interaction. The most reasonable model consistent with the data proposes a weak association between nitrite and **ferric reductase** with a value of 1.3 M⁻¹ for the association constant.

1982

6/3,AB/83 (Item 1 from file: 6)
DIALOG(R)File 6:NTIS
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2023710 NTIS Accession Number: ERS-TB-1843/XAB

Measuring the Economywide Effect of the Farm Sector: Two Methods
(Technical bulletin)

Edmondson, W. ; Petrulis, M. ; Somwaru, A.

Economic Research Service, Washington, DC. Rural Economy Div.

Corp. Source Codes: 010371021

Jul 95 43p

Languages: English

Journal Announcement: GRAI9723

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Farm-Related (FRE) series estimates the number of jobs in farming and in
industries directly and indirectly related to agriculture. In terms of
relative employment shares (percent of the domestic economy), the FFS
declined 2 percent and the FRE 1.9 percent in 1990, the last
year for which both data sets are available.

6/3,AB/84 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06542680 Genuine Article#: ZA144 Number of References: 11

Title: Cytochrome P-450 reductase is responsible for the ferriredutase
activity associated with isolated plasma membranes of *Saccharomyces*
cerevisiae (ABSTRACT AVAILABLE)

Author(s): Lesuisse E (REPRINT) ; CasterasSimon M; Labbe P

Corporate Source: UNIV PARIS 07, INST JACQUES MONOD, LAB BIOCHIM

PORPHYRINES, TOUR 43, 2 PL JUSSIEU/F-75251 PARIS 05//FRANCE/ (REPRINT)

Journal: FEMS MICROBIOLOGY LETTERS, 1997, V156, N1 (NOV 1), P147-152

ISSN: 0378-1097 Publication date: 19971101

Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS

Language: English Document Type: ARTICLE

Abstract: Cytochrome P-450 reductase (encoded by the NCP1 gene) was found
to catalyse all the NADPH-dependent ferriredutase activities
associated with isolated plasma membranes of the yeast *Saccharomyces*
cerevisiae. We therefore examined the contribution of this enzyme to
the ferriredutase activity of cells in vivo. Cytochrome P-450
reductase was shown to be not essential for the cell ferriredutase
activity, but it influenced this activity, with different effects on
the Fre1- and the Fre2-dependent reductase systems. Overexpression of
FRE1 did not lead to an increased ferriredutase activity of the cells
when NCP1 was repressed. In contrast, cells that overexpressed FRE2 had
maximal ferriredutase activity when NCP1 was repressed. The degree of
NCP1 expression also affected the amount of iron and copper accumulated
by the cells during growth. The biochemical implications and the
physiological significance of these observations are discussed.

6/3,AB/85 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06334656 Genuine Article#: YK389 Number of References: 37
Title: *Saccharomyces cerevisiae* mutants altered in vacuole function are defective in copper detoxification and iron-responsive gene transcription (ABSTRACT AVAILABLE)
Author(s): Szczypka MS; Zhu ZW; Silar P; Thiele DJ (REPRINT)
Corporate Source: UNIV MICHIGAN, SCH MED, DEPT BIOL CHEM/ANN ARBOR//MI/48109 (REPRINT); UNIV MICHIGAN, SCH MED, DEPT BIOL CHEM/ANN ARBOR//MI/48109
Journal: YEAST, 1997, V13, N15 (DEC), P1423-1435
ISSN: 0749-503X Publication date: 19971200
Publisher: JOHN WILEY & SONS LTD, BAFFINS LANE CHICHESTER, W SUSSEX, ENGLAND PO19 1UD

Language: English Document Type: ARTICLE

Abstract: The metal ions, Cu^{2+} and $\text{Fe}^{3+}/2+$, are essential co-factors for a wide variety of enzymatic reactions. However, both metal ions are toxic when hyper-accumulated or maldistributed within cells due to their ability to generate damaging free radicals or through the displacement of other physiological metal ions from metalloproteins. Although copper transport into yeast cells is apparently independent of iron, the known dependence on Cu^{2+} for high affinity transport of Fe^{2+} into yeast cells has established a physiological link between these two trace metal ions. In this study we demonstrate that proteins encoded by genes previously demonstrated to play critical roles in vacuole assembly or acidification, PEP3, PEP5 and VMA3, are also required for normal copper and iron metal ion homeostasis. Yeast cells lacking a functional PEP3 or PEP5 gene are hypersensitive to copper and render the normally iron-repressible FET3 gene, encoding a multi-copper Fe(II) oxidase involved in Fe^{2+} transport, also repressible by exogenous copper ions. The inability of these same vacuolar mutant strains to repress FET3 mRNA levels in the presence of an iron-unresponsive allele of the AFT1 regulatory gene are consistent with alterations in the intracellular distribution or redox states of $\text{Fe}^{3+}/2+$ in the presence of elevated extracellular concentrations of copper ions. Therefore, the yeast vacuole is an important organelle for maintaining the homeostatic convergence of the essential yet toxic copper and iron ions. (C) 1997 John Wiley & Sons, Ltd.

6/3,AB/86 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05993995 Genuine Article#: XM844 Number of References: 28
Title: Molecular biology of iron and zinc uptake in eukaryotes (ABSTRACT AVAILABLE)
Author(s): Eide D (REPRINT)
Corporate Source: UNIV MISSOURI, NUTR SCI PROGRAM, 217 GWYNN HALL/COLUMBIA//MO/65211 (REPRINT)
Journal: CURRENT OPINION IN CELL BIOLOGY, 1997, V9, N4 (AUG), P 573-577
ISSN: 0955-0674 Publication date: 19970800
Publisher: CURRENT BIOLOGY LTD, 34-42 CLEVELAND STREET, LONDON, ENGLAND W1P 6LB

Language: English Document Type: ARTICLE

Abstract: Recent studies of iron uptake in *Saccharomyces cerevisiae* have provided insights into the role of multicopper oxidases in eukaryotic metal transport. These studies have also led to the identification of a novel iron transporter in plants and the recognition of a new family of transporter proteins that may participate in metal uptake in a diverse array of eukaryotic species.

6/3,AB/87 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05958160 Genuine Article#: XK165 Number of References: 41
Title: Homeostatic regulation of copper uptake in yeast via direct binding of MAC1 protein to upstream regulatory sequences of FRE1 and CTR1 (ABSTRACT AVAILABLE)
Author(s): YamaguchiIwai Y; Serpe M; Haile D; Yang WM; Kosman DJ; Klausner RD; Dancis A (REPRINT)
Corporate Source: UNIV PENN, STELLAR CHANCE LABS 1009, DEPT MED, DIV HEMATOL ONCOL, 422 CURIE BLVD/PHILADELPHIA//PA/19104 (REPRINT); NICHHD, CELL BIOL & METAB BRANCH, NIH/BETHESDA//MD/20892; SUNY ALBANY, SCH MED & BIOMED SCI, DEPT BIOCHEM/BUFFALO//NY/14214; NCI, BIOCHEM LAB, NIH/BETHESDA//MD/20892
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1997, V272, N28 (JUL 11), P 17711-17718
ISSN: 0021-9258 Publication date: 19970711
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814
Language: English Document Type: ARTICLE
Abstract: Copper deprivation of *Saccharomyces cerevisiae* induces transcription of the FRE1 and CTR1 genes, FRE1 encodes a surface reductase capable of reducing and mobilizing copper chelates outside the cell, and CTR1 encodes a protein mediating copper uptake at the plasma membrane. In this paper, the protein encoded by MAC1 is identified as the factor mediating this homeostatic control. A novel dominant allele of MAC1, MAC1(up2), is mutated in a Cys-rich domain that may function in copper sensing (a G to A change of nucleotide 812 resulting in a Cys-271 to Tyr substitution). This mutant is functionally similar to the MAC1(up1) allele in which His-279 in the same domain has been replaced by Gin. Both mutations confer constitutive copper-independent expression of FRE1 and CTR1. A sequence including the palindrome TTTGCTCA,, TGAGCAAA, appearing within the 5'-flanking region of the CTR1 promoter, is necessary and sufficient for the copper- and MAC1-dependent CTR1 transcriptional regulation. An identical sequence appears as a direct repeat in the FRE1 promoter. The data indicate that the signal resulting from copper deprivation is transduced via the Cys-rich motif of MAC1 encompassing residues 264-279, MAC1 then binds directly and specifically to the CTR1 and FRE1 promoter elements, inducing transcription of those target genes. This model defines the homeostatic mechanism by which yeast regulates the cell acquisition of copper in response to copper scarcity or excess.

6/3,AB/88 (Item 5 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05887040 Genuine Article#: XE435 Number of References: 62
Title: The AFT1 transcriptional factor is differentially required for expression of high-affinity iron uptake genes in *Saccharomyces cerevisiae* (ABSTRACT AVAILABLE)
Author(s): Casas C; Aldea M; Espinet C; Gallego C; Gil R; Herrero E (REPRINT)
Corporate Source: UNIV LLEIDA, FAC MED, DEPT CIENCIAS MED BASIQUES, ROVIRA ROURE 44/LLEIDA 25198//SPAIN/ (REPRINT); UNIV LLEIDA, FAC MED, DEPT CIENCIAS MED BASIQUES/LLEIDA 25198//SPAIN/
Journal: YEAST, 1997, V13, N7 (JUN 15), P621-637
ISSN: 0749-503X Publication date: 19970615
Publisher: JOHN WILEY & SONS LTD, BAFFINS LANE CHICHESTER, W SUSSEX, ENGLAND PO19 1UD
Language: English Document Type: ARTICLE

Abstract: High-affinity iron uptake in *Saccharomyces cerevisiae* involves the extracytoplasmic reduction of ferric ions by FRE1 and FRE2 reductases. Ferrous ions are then transported across the plasma membrane through the FET3 oxidase-FTR1 permease complex. Expression of the high-affinity iron uptake genes is induced upon iron deprivation. We demonstrate that Aft1 is differentially involved in such regulation. Aft1 protein is required for maintaining detectable non-induced levels of FET3 expression and for induction of FRE1 in iron starvation conditions. On the contrary, FRE1 mRNA induction is normal in the absence of Aft1, although the existence of AFT1 point mutations causing constitutive expression of FRE1 (Yamaguchi-Iwai et al., EMBO J. 14: 1231-1239, 1995) indicates that Aft1 may also participate in FRE1 expression in a dispensable way. The alterations in the basal levels of expression of the high-affinity iron uptake genes may explain why the AFT1 mutant is unable to grow on respirable carbon sources. Overexpression of AFT1 leads to growth arrest at the G(1) stage of the cell cycle. Aft1 is a transcriptional activator that would be part of the different transcriptional complexes interacting with the promoter of the high-affinity iron uptake genes. Aft1 displays phosphorylation modifications depending on the growth stage of the cells, and it might link induction of genes for iron uptake to other metabolically dominant requirements for cell growth. (C) 1997 by John Wiley & Sons, Ltd.

6/3,AB/89 (Item 6 from file: 34)
 DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05824988 Genuine Article#: WZ944 Number of References: 52

Title: *Escherichia coli* flavohaemoglobin (Hmp) reduces cytochrome c and Fe(III)-hydroxamate K by electron transfer from NADH via FAD: Sensitivity of oxidoreductase activity to haem-bound dioxygen (ABSTRACT AVAILABLE)

Author(s): Poole RK (REPRINT) ; Rogers NJ; Dmello RAM; Hughes MN; Orii Y
 Corporate Source: UNIV SHEFFIELD, KREBS INST BIOMOLEC RES, DEPT MOL BIOL & BIOTECHNOL, FIRTH COURT, WESTERN B/SHEFFIELD S10 2TN/S YORKSHIRE/ENGLAND/ (REPRINT); UNIV LONDON KINGS COLL, DIV LIFE SCI/LONDON W8 7AH//ENGLAND/; UNIV LONDON KINGS COLL, DEPT CHEM/LONDON WC2R 2LS//ENGLAND/; KYOTO UNIV, GRAD SCH MED, DEPT PUBL HLTH/KYOTO 606//JAPAN/

Journal: MICROBIOLOGY-UK, 1997, V143, 5 (MAY), P1557-1565

ISSN: 1350-0872 Publication date: 19970500

Publisher: SOC GENERAL MICROBIOLOGY, HARVEST HOUSE 62 LONDON ROAD, READING, BERKS, ENGLAND RG1 5AS

Language: English Document Type: ARTICLE

Abstract: *Escherichia coli* flavohaemoglobin (Hmp) reduced purified mitochondrial cytochrome c aerobically in a reaction that was not substantially inhibited by superoxide dismutase, demonstrating that superoxide anion, the product of O₂ reduction by Hmp, did not contribute markedly to cytochrome c reduction. Cytochrome c was reduced by Hmp even in the presence of 0.5 mM CO, when the haem B was locked in the ferrous, low-spin state, demonstrating that electron transfer to cytochrome c from NADH was via FAD, not haem. Hmp also reduced the ferrisiderophore complex Fe(III)-hydroxamate K from *Rhizobium leguminosarum* by. *viciae* anaerobically in a CO-insensitive manner, but at low rates and with low affinity for this substrate. The NADH-cytochrome c oxidoreductase activity of Hmp was slightly sensitive to the binding and reduction of O₂ at the haem. The V-max of cytochrome c reduction fell from 7.1 s⁻¹ in the presence of 0.5 mM CO to 5.0 s⁻¹ in the presence of 100 μM O₂, with no significant change in K_m for cytochrome c (6.8 to 7.3 μM, respectively). O₂ at near-micromolar concentrations diminished cytochrome c reduction to a similar extent as did 100 μM O₂. Thus, Hmp acts as a reductase of broad specificity, apparently without involvement of electron transfer

via the globin-like haem. These data are consistent with the hypothesis that Hmp could act as an intracellular sensor of O-2 since, in the absence of O-2, electron flux from FAD to other electron accepters increases. However, the nature of such accepters in vivo is not known and alternative models for O-2 sensing are also considered.

6/3,AB/90 (Item 7 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05790026 Genuine Article#: WX569 Number of References: 54
Title: Characterization of the FET4 protein of yeast - Evidence for a direct role in the transport of iron (ABSTRACT AVAILABLE)
Author(s): Dix D; Bridgham J; Broderius M; Eide D (REPRINT)
Corporate Source: UNIV MISSOURI,DEPT FOOD SCI & HUMAN NUTR/COLUMBIA//MO/65211 (REPRINT); UNIV MINNESOTA,DEPT BIOCHEM & MOL BIOL/DULUTH//MN/55812
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1997, V272, N18 (MAY 2), P 11770-11777

ISSN: 0021-9258 Publication date: 19970502
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814

Language: English Document Type: ARTICLE

Abstract: The low affinity Fe²⁺ uptake system of *Saccharomyces cerevisiae* requires the FET4 gene. In this report, we present evidence that FET4 encodes the Fe²⁺ transporter protein of this system. Antibodies prepared against FET4 detected two distinct proteins with molecular masses of 63 and 68 kDa. In vitro synthesis of FET4 suggested that the 68-kDa form is the primary translation product, and the 63-kDa form may be generated by proteolytic cleavage of the full-length protein. Consistent with its role as an Fe²⁺ transporter, FET4 is an integral membrane protein present in the plasma membrane. The level of FET4 closely correlated with uptake activity over a broad range of expression levels and is itself regulated by iron. Furthermore, mutations in FET4 can alter the kinetic properties of the low affinity uptake system, suggesting a direct interaction between FET4 and its Fe²⁺ substrate. Mutations affecting potential Fe²⁺ ligands located in the predicted transmembrane domains of FET4 significantly altered the apparent K_m and/or V_{max} of the low affinity system. These mutations may identify residues involved in Fe²⁺ binding during transport.

6/3,AB/91 (Item 8 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05463514 Genuine Article#: WA564 Number of References: 15
Title: AN OXIDASE-PERMEASE-BASED IRON TRANSPORT-SYSTEM IN SCHIZOSACCHAROMYCES-POMBE AND ITS EXPRESSION IN SACCHAROMYCES-CEREVISIAE (Abstract Available)
Author(s): ASKWITH C; KAPLAN J
Corporate Source: UNIV UTAH,SCH MED,DEPT PATHOL,DIV CELL BIOL & IMMUNOL,50 N MED DR/SALT LAKE CITY//UT/84132; UNIV UTAH,SCH MED,DEPT PATHOL,DIV CELL BIOL & IMMUNOL/SALT LAKE CITY//UT/84132
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1997, V272, N1 (JAN 3), P 401-405

ISSN: 0021-9258

Language: ENGLISH Document Type: ARTICLE

Abstract: Genetic studies have demonstrated that high affinity ferrous transport in *Saccharomyces cerevisiae* requires an oxidase (Fet3p) and a permease (Ftr1p). Using an iron-independent galactose-based expression system, we show that expression of these two genes can mediate high affinity ferrous iron transport, indicating that these two genes are

not only necessary, but sufficient for high affinity iron transport. *Schizosaccharomyces pombe* also employ an oxidase-permease system for high affinity iron transport. The *S. pombe* genes, *fiol(+)* (ferrous iron oxidase) and *fipl(+)* (ferriferous permease), share significant similarity to *FET3* and *FTR1* hom *S. cerevisiae*. Both *fiol(+)* and *fipl(+)* are transcriptionally regulated by iron need, and disruption of *fiol(+)* results in a loss of high affinity iron transport. Expression of *fiol(+)* alone in an *S. cerevisiae* *fet3* disruption strain does not result in high affinity iron transport. This result indicates that the *S. pombe* ferroxidase, while functionally homologous to the *S. cerevisiae* ferroxidase, does not have enough similarity to interact with the *S. cerevisiae* permease. Simultaneous expression of both *S. pombe* genes, *fiol(+)* and *fipl(+)*, in *S. cerevisiae* can reconstitute high affinity iron transport. These results demonstrate that the oxidase and permease are all that is required to reconstitute high affinity iron transport and suggest that such transport systems are found in other eukaryotes.

6/3,AB/92 (Item 9 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05407223 Genuine Article#: VW686 Number of References: 27
Title: INTRAMEMBRANE BIS-HEME MOTIF FOR TRANSMEMBRANE ELECTRON-TRANSPORT
CONSERVED IN A YEAST IRON REDUCTASE AND THE HUMAN NADPH OXIDASE (Abstract Available)
Author(s): FINEGOLD AA; SHATWELL KP; SEGAL AW; KLAUSNER RD; DANCIS A
Corporate Source: UNIV PENN,DEPT MED,DIV HEMATOL ONCOL,1009 STELLAR CHANCE
LABS,422 CURIE BLVD/PHILADELPHIA//PA/19104; NICHHD,CELL BIOL & METAB
BRANCH,NIH/BETHESDA//MD/20892; UNIV LONDON UNIV COLL,SCH MED,DEPT
MED/LONDON WC1E 6JJ//ENGLAND/
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1996, V271, N49 (DEC 6), P
31021-31024
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE
Abstract: A plasma membrane iron reductase, required for cellular iron acquisition by *Saccharomyces cerevisiae*, and the human phagocytic NADPH oxidase, implicated in cellular defense, contain low potential plasma membrane b cytochromes that share elements of structure and function. Four critical histidine residues in the *FRE1* protein of the iron reductase were identified by site-directed mutagenesis. Individual mutation of each histidine to alanine eliminated the entire heme spectrum without affecting expression of the apoprotein, documenting the specificity of the requirement for the histidine residues. These critical residues are predicted to coordinate a bis-heme structure between transmembrane domains of the *FRE1* protein. The histidine residues are conserved in the related *gp91(phox)* protein of the NADPH oxidase of human granulocytes, predicting the sites of heme coordination in that protein complex. Similarly spaced histidine residues have also been implicated in heme binding by organelle b cytochromes with little overall sequence similarity to the plasma membrane b cytochromes. This bis-heme motif may play a role in transmembrane electron transport by distinct families of polytopic b cytochromes.

6/3,AB/93 (Item 10 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05206227 Genuine Article#: VH089 Number of References: 39
Title: RBOHA A RICE HOMOLOG OF THE MAMMALIAN GP91PHOX RESPIRATORY BURST
OXIDASE GENE (Abstract Available)

Author(s): GROOM QJ; TORRES MA; FORDHAMSKELTON AP; HAMMONDKOSACK KE;
ROBINSON NJ; JONES JDG
Corporate Source: UNIV NEWCASTLE,DEPT BIOCHEM & GENET/NEWCASTLE TYNE NE2
4HH/TYNE & WEAR/ENGLAND//; JOHN INNES CTR PLANT SCI RES,SAINSBURY
LAB/NORWICH NR4 7UH/NORFOLK/ENGLAND/
Journal: PLANT JOURNAL, 1996, V10, N3 (SEP), P515-522
ISSN: 0960-7412

Language: ENGLISH Document Type: ARTICLE

Abstract: It has been hypothesized that plants contain respiratory burst oxidases which, upon activation, oxidize NADPH and generate extracellular superoxide, O₂(.-). These proteins are proposed to play a central role in defence against pathogens. However, plant DNA sequences that encode proteins with similarity to components of respiratory burst oxidases have not previously been reported. This paper describes the complete cDNA and genomic DNA sequence of the rice rbohA (for respiratory burst oxidase homologue) gene. The predicted RbohA product is most similar to the main catalytic subunit, gp91phox, of the respiratory burst oxidase of neutrophils. Reverse transcriptase PCR detects rbohA transcripts in both roots and shoots of healthy rice plants.

6/3,AB/94 (Item 11 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05098438 Genuine Article#: VA205 Number of References: 25

Title: EXTRACELLULAR IRON REDUCTASE-ACTIVITY PRODUCED BY

LISTERIA-MONOCYTOGENES (Abstract Available)

Author(s): BARCHINI E; COWART RE

Corporate Source: UNIV TEXAS,MD ANDERSON CANC CTR,DEPT MED
SPECIALTIES,INFECT DIS SECT,1515 HOLCOMBE BLVD/HOUSTON//TX/77030; UNIV
TEXAS,MD ANDERSON CANC CTR,DEPT MED SPECIALTIES,INFECT DIS
SECT/HOUSTON//TX/77030; ORAL ROBERTS UNIV,SCH MED,DEPT IMMUNOL
MICROBIOL/TULSA//OK/74137

Journal: ARCHIVES OF MICROBIOLOGY, 1996, V166, N1 (JUL), P51-57
ISSN: 0302-8933

Language: ENGLISH Document Type: ARTICLE

Abstract: Little is known about how pathogenic microorganisms that do not produce low-molecular-weight iron-chelating agents, termed siderophores, acquire iron from their environment. We have identified an extracellular enzyme produced by *Listeria monocytogenes* that can mobilize iron from a variety of iron-chelate complexes via reduction of the metal. The iron reductase requires Mg²⁺, flavin mononucleotide (FMN), and reduced nicotinamide adenine dinucleotide (NADH) for activity. Saturation kinetics were found when initial velocity studies of iron reduction were carried out as a function of variable FMN concentrations in the presence of 100 μ M NADH and 10 mM Mg²⁺. Hyperbolic kinetics were also found when these studies were repeated as a function of variable NADH concentrations along with 20 μ M FMN and 10 mM Mg²⁺. This process of extracellular reduction, in all likelihood, could be involved in the mobilization of iron from soils and aqueous environments and from host tissues in pathogenic processes. This is the first report of the extracellular enzymic reduction of iron by microorganisms.

6/3,AB/95 (Item 12 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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05040312 Genuine Article#: TL436 Number of References: 29

Title: EXTRACELLULAR ASCORBATE STABILIZATION AS A RESULT OF TRANSPLASMA
ELECTRON-TRANSFER IN SACCHAROMYCES-CEREVISIAE (Abstract Available)

Author(s): SANTOSOCANA C; NAVAS P; CRANE FL; CORDOBA F
Corporate Source: UNIV CORDOBA, DEPT BIOL CELULAR/E-14004 CORDOBA//SPAIN/;
PURDUE UNIV, DEPT BIOL SCI/W LAFAYETTE//IN/47907; UNIV HUELVA, DEPT
CIENCIAS AGROFORESTALES/E-21819 HUELVA//SPAIN/
Journal: JOURNAL OF BIOENERGETICS AND BIOMEMBRANES, 1995, V27, N6 (DEC), P597-603
ISSN: 0145-479X
Language: ENGLISH Document Type: ARTICLE
Abstract: The presence of yeast cells in the incubation medium prevents the oxidation of ascorbate catalyzed by copper ions. Ethanol increases ascorbate retention. Pyrazole, an alcohol dehydrogenase inhibitor, prevents ascorbate stabilization by cells. Chelation of copper ions does not account for stabilization, since oxidation rates with broken or boiled cells or conditioned media are similar to control rates in the absence of cells. Protoplast integrity is needed to reach optimal values of stabilization. Chloroquine, a known inhibitor of plasma membrane redox systems, inhibits the ascorbate stabilization, the inhibition being partially reversed by coenzyme Q(6). Chloroquine does not inhibit ferricyanide reduction. Growth of yeast in iron-deficient media to increase ferric ion reductase activity also increases the stabilization. In conclusion, extracellular ascorbate stabilization by yeast cells can reflect a coenzyme Q dependent transplasmalemma electron transfer which uses NADH as electron donor. Iron deficiency increases the ascorbate stabilization but the transmembrane ferricyanide reduction system can act independently of ascorbate stabilization.

6/3, AB/96 (Item 13 from file: 34)
DIALOG(R) File 34: SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04875082 Genuine Article#: UP385 Number of References: 31
Title: EVIDENCE FOR THE SACCHAROMYCES-CEREVISIAE FERRIREDUCTASE SYSTEM BEING A MULTICOMPONENT ELECTRON-TRANSPORT CHAIN (Abstract Available)
Author(s): LESUISSE E; CASTERASSIMON M; LABBE P
Corporate Source: UNIV PARIS 07, INST JACQUES MONOD, LAB BIOCHIM PORPHYRINES, TOUR 43, 2 PL JUSSIEU/F-75251 PARIS 05//FRANCE/
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1996, V271, N23 (JUN 7), P 13578-13583
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE
Abstract: We have studied the relationships between in vivo (whole cells) and in vitro (plasma membranes) ferriredutase activity in *Saccharomyces cerevisiae*. Isolated plasma membranes were enriched in the product of the *FRE1* gene and had NADPH dehydrogenase activity that was, increased when the cells were grown in iron/copper-deprived medium. The diaphorase activity was, however, independent of *Frelp*, and *Frelp* itself had pro ferriredutase activity in vitro. There were striking similarities between the yeast ferriredutase system and the neutrophil NADPH oxidase: oxygen could act as an electron acceptor in the ferriredutase system, and *Frelp*, like gp91, is a glycosylated hemoprotein with a b-type cytochrome spectrum. The ferriredutase system was sensitive to the NADPH oxidase inhibitor diphenyleneiodonium (DPI). DPI inhibition proceeded with two apparent *K_i* values (high and low affinity binding) in whole wild-type and *Delta fre2* cells and with one apparent *K_i* in *Delta fre1* cells (high affinity binding) and in plasma membranes (low affinity binding). These results suggest that the *Frel*-dependent ferriredutase system involves at least two components (*Frelp* and an NADPH dehydrogenase component) differing in their sensitivities to DBH, as in the neutrophil NAPBPH oxidase. A third component, the product of the *UTR1* gene, was shown to act synergistically with *Frelp* to increase the cell ferriredutase activity.

6/3,AB/97 (Item 14 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04826306 Genuine Article#: UK843 Number of References: 22
Title: DIRECT MEASUREMENT OF FE-59-LABELED FE²⁺ INFLUX IN ROOTS OF PEA
USING A CHELATOR BUFFER SYSTEM TO CONTROL FREE FE²⁺ IN SOLUTION (Abstract Available)
Author(s): FOX TC; SHAFF JE; GRUSAK MA; NORVELL WA; CHEN Y; CHANEY RL; KOCHIAN LV
Corporate Source: CORNELL UNIV,USDA ARS,US PLANT SOIL & NUTR LAB/ITHACA//NY/14853; BAYLOR COLL MED,DEPT PEDIAT,CHILDRENS NUTR RES CTR,USDA ARS/HOUSTON//TX/77030; HEBREW UNIV JERUSALEM,FAC AGR,DEPT SOIL & WATERSCI/IL-76100 REHOVOT//ISRAEL/; USDA ARS,ENVIRONM CHEM LAB/BELTSVILLE//MD/20705
Journal: PLANT PHYSIOLOGY, 1996, V111, N1 (MAY), P93-100
ISSN: 0032-0889

Language: ENGLISH Document Type: ARTICLE

Abstract: Fe²⁺ transport in plants has been difficult to quantify because of the inability to control Fe²⁺ activity in aerated solutions and nonspecific binding of Fe to cell walls. In this study, a Fe(II)-3-(2-pyridyl)-5,6-diphenyl-1,2,4-triazine-4'4''-disulfonic acid buffer system was used to control free Fe²⁺ in uptake solutions. Additionally, desorption methodologies were developed to adequately remove nonspecifically bound Fe from the root apoplasm. This enabled us to quantify unidirectional Fe²⁺ influx via radiotracer (Fe-59) uptake in roots of pea (*Pisum sativum* cv Sparkle) and its single gene mutant *brz*, an Fe hyperaccumulator. Fe influx into roots was dramatically inhibited by low temperature, indicating that the measured Fe accumulation in these roots was due to true influx across the plasma membrane rather than nonspecific binding to the root apoplasm. Both Fe²⁺ influx and Fe translocation to the shoots were stimulated by Fe deficiency in Sparkle. Additionally, *brz*, a mutant that constitutively exhibits high **ferric reductase** activity, exhibited higher Fe²⁺ influx rates than +Fe-grown Sparkle. These results suggest that either Fe deficiency triggers the induction of the Fe²⁺ transporter or that the enhanced **ferric reductase** activity somehow stimulates the activity of the existing Fe²⁺ transport protein.

6/3,AB/98 (Item 15 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04773243 Genuine Article#: UG238 Number of References: 54
Title: MOLECULAR-BIOLOGY OF IRON ACQUISITION IN SACCHAROMYCES-CEREVISIAE (Abstract Available)
Author(s): ASKWITH CC; DESILVA D; KAPLAN J
Corporate Source: UNIV UTAH,MED CTR,DEPT PATHOL,DIV CELL BIOL & IMMUNOL/SALT LAKE CITY//UT/84132; UNIV UTAH,MED CTR,DEPT PATHOL,DIV CELL BIOL & IMMUNOL/SALT LAKE CITY//UT/84132
Journal: MOLECULAR MICROBIOLOGY, 1996, V20, N1 (APR), P27-34
ISSN: 0950-382X

Language: ENGLISH Document Type: REVIEW

Abstract: In recent years, significant advances have been made in our understanding of the mechanism and regulation of elemental iron transport in the eukaryote *Saccharomyces cerevisiae*. This organism employs two distinct iron-transport systems, depending on the bioavailability of the metal. In iron-replete environments, a low-affinity transport system ($K_m = 30 \mu M$) is used to acquire iron. This system may also be used to acquire other metals including cobalt and cadmium. When environmental iron is limiting, a high-affinity (K_m

= 0.15 μ M) iron-transport system is induced. Genetic studies in *S. cerevisiae* have identified multiple genes involved in both iron-transport systems. Cell-surface reductases, FRE1 and FRE2, provide ferrous iron for both systems. A non-ATP-dependent transmembrane transporter (FET4) has been identified as the main component of low-affinity transport. One gene identified to date as part of the high-affinity transport system is FET3, which shows high sequence and functional homology to multicopper oxidases. Accessory genes required for the functioning of this transport system include a plasma-membrane copper transporter (CTR1), an intracellular copper transporter (CCC2), and a putative transcription factor (AFT1). The mechanism by which these genes act in concert to ensure iron accumulation in *S. cerevisiae* presents an intriguing picture, drawing parallels with observations made in the human system almost 40 years ago.

6/3,AB/99 (Item 16 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04755243 Genuine Article#: UF024 Number of References: 21
Title: PARTIAL CHARACTERIZATION AND IDENTIFICATION OF A TRANSFERRIN-LIKE MOLECULE OF PATHOGENIC YEAST CRYPTOCOCCUS-NEOFORMANS (Abstract Available)
Author(s): TESFAELASE F; HAY RJ
Corporate Source: UNIV BATH,DEPT BIOCHEM/BATH BA2 7AY/AVON/ENGLAND/; GUYS HOSP,ST JOHNS INST DERMATOL/LONDON SE1 9RT//ENGLAND/
Journal: JOURNAL OF GENERAL AND APPLIED MICROBIOLOGY, 1996, V42, N1 (FEB), P61-70
ISSN: 0022-1260
Language: ENGLISH Document Type: ARTICLE
Abstract: We have partially characterized, purified, and N-terminal amino acid sequenced a protein of approximately 80 kDa from *Cryptococcus neoformans*. Of the 15 N-terminal amino acids sequenced, 12 are identical to those found in ovotransferrin. Polyclonal antisera raised against ovotransferrin crossreacted with the 80kDa protein. In addition, incorporation of Fe-55 indicated the presence of iron binding by the 80 kDa protein. Because *Cryptococcus neoformans* does not possess an iron-scavenging ligand, siderophore, we suggest that an alternative transferrin-like molecule (the 80 kDa protein) may play a role in iron uptake by this organism.

6/3,AB/100 (Item 17 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04644962 Genuine Article#: TZ983 Number of References: 57
Title: A PERMEASE-OXIDASE COMPLEX INVOLVED IN HIGH-AFFINITY IRON UPTAKE IN YEAST (Abstract Available)
Author(s): STEARMAN R; YUAN DS; YAMAGUCHIIWAI Y; KLAUSNER RD; DANCIS A
Corporate Source: NICHHD,CELL BIOL & METAB BRANCH,NIH/BETHESDA//MD/20892; NICHHD,CELL BIOL & METAB BRANCH,NIH/BETHESDA//MD/20892
Journal: SCIENCE, 1996, V271, N5255 (MAR 15), P1552-1557
ISSN: 0036-8075
Language: ENGLISH Document Type: ARTICLE
Abstract: Iron must cross biological membranes to reach essential intracellular enzymes. Two proteins in the plasma membrane of yeast-a multicopper oxidase, encoded by the FET3 gene, and a permease, encoded by the FTR1 gene-were shown to mediate high-affinity iron uptake. FET3 expression was required for FTR1 protein to be transported to the plasma membrane. FTR1 expression was required for apo-FET3 protein to be loaded with copper and thus acquire oxidase activity. FTR1 protein also played a direct role in iron transport. Mutations in a conserved

sequence motif of FTR1 specifically blocked iron transport.

6/3,AB/101 (Item 18 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04488026 Genuine Article#: TF713 Number of References: 26
Title: TOPOGRAPHY OF THE 27-AND 31-KDA ELECTRON-TRANSPORT PROTEINS IN THE
ONION ROOT PLASMA-MEMBRANE (Abstract Available)
Author(s): CORDOBA MC; SERRANO A; CORDOBA F; GONZALEZREYES JA; NAVAS P;
VILLALBA JM
Corporate Source: UNIV CORDOBA,FAC CIENCIAS,DEPT BIOL CELULAR,AVDA SAN
ALBERTO MAGNO S-N/E-14004 CORDOBA//SPAIN/; UNIV CORDOBA,FAC
CIENCIAS,DEPT BIOL CELULAR/E-14004 CORDOBA//SPAIN/
Journal: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, 1995, V
216, N3 (NOV 22), P1054-1059
ISSN: 0006-291X
Language: ENGLISH Document Type: ARTICLE

Abstract: Plasma membranes purified from onion roots contain two distinct
NAD(P)H-dehydrogenases dehydrogenases of 27 and 31 kDa that differ in
their physicochemical properties, substrate specificities and
inhibitors sensitivities. The 27-kDa enzyme used both NADH and NADPH as
electron donors. The 31-kDa enzyme was fully specific for NADH and
accounted for the bulk of NADH-ferricyanide oxidoreductase. We have
used NADPH- and NADH-ferricyanide oxidoreductase activities as markers
for investigating the orientation of the 27- and 31-kDa enzymes at the
plasma membrane, respectively. These activities were assayed in
right-side-out vesicles isolated by two-phase partition, inside-out
vesicles obtained by treatment with the detergent Brij 58 and membranes
permeabilized with Triton X-100. Upon addition of Brij 58 to
right-side-out plasma membrane vesicles, both NADPH- and
NADH-ferricyanide oxidoreductases were activated to the same degree as
the plasma membrane H⁺-ATPase. Redox activities were similar when
measured in the presence of either Brij 58 or Triton X-100. Our results
demonstrate that both enzymes expose their catalytic sites toward the
cytoplasmic side of the plasma membrane. (C) 1995 Academic Press, Inc.

6/3,AB/102 (Item 19 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04469768 Genuine Article#: TG210 Number of References: 51
Title: MOLECULAR CHARACTERIZATION OF A PUTATIVE ARABIDOPSIS-THALIANA COPPER
TRANSPORTER AND ITS YEAST HOMOLOG (Abstract Available)
Author(s): KAMPFENKEL K; KUSHNIR S; BABIYCHUK E; INZE D; VANMONTAGU M
Corporate Source: STATE UNIV GHENT,GENET LAB,KL LEDEGANCKSTRAAT 35/B-9000
GHENT//BELGIUM/; STATE UNIV GHENT,INRA LAB/B-9000 GHENT//BELGIUM/
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1995, V270, N47 (NOV 24), P
28479-28486
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE

Abstract: At the molecular level, little is known about the transport of
copper across plant membranes. We have isolated an Arabidopsis thaliana
cDNA by complementation of a mutant (ctrl-3) of Saccharomyces
cerevisiae defective in high affinity copper uptake. This cDNA codes
for a highly hydrophobic protein (COPT1) of 169 amino acid residues and
with three putative transmembrane domains. Most noteworthy, the first
44 residues display significant homology to the methionine- and
histidine-rich copper binding domain of three bacterial copper binding
proteins, among these a copper transporting ATPase. Mutant yeast cells
expressing COPT1 exhibit nearly wild type behavior with regard to
growth on a nonfermentable carbon source and resistance to copper and

iron starvation. Expression of COPT1 is also associated with an increased sensitivity to copper toxicity. Additionally, COPT1 shows significant homology to an open reading frame of 189 amino acid residues on yeast chromosome VIII. This gene (CTR2) may encode an additional yeast metal transporter able to mediate the uptake of copper. A mutation in CTR2 displays a higher level of resistance to toxic copper concentrations. Overexpression of CTR2 provides increased resistance to copper starvation and is also associated with an increased sensitivity to copper toxicity. The amino acid sequence of CTR2, like Arabidopsis COPT1, contains three potential transmembrane domains. Taken together, the data suggest that a plant metal transporter, which is most likely involved in the transport of copper, has been identified.

6/3,AB/103 (Item 20 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04469221 Genuine Article#: TF217 Number of References: 22
Title: EFFECTS OF CADMIUM AND OF YAP1 AND CAD1/YAP2 GENES ON
IRON-METABOLISM IN THE YEAST SACCHAROMYCES-CEREVISIAE (Abstract
Available)

Author(s): LESUISSE E; LABBE P
Corporate Source: UNIV PARIS 07, INST JACQUES MONOD, BIOCHIM PORPHYRINES
LAB, TOUR 43, 2 PL JUSSIEU/F-75251 PARIS 05//FRANCE/
Journal: MICROBIOLOGY-UK, 1995, V141, NOV (NOV), P2937-2943
ISSN: 1350-0872
Language: ENGLISH Document Type: ARTICLE

Abstract: Saccharomyces cerevisiae was more resistant to cadmium when the growth medium contained excess iron. Cadmium reduced the amount of iron taken up by cells during growth, and the cell ferrireductase activity was also strongly inhibited. These effects depended on the YAP1 and CAD1/YAP2 gene dosage. The growth rate of cells in iron-deficient conditions and their ferrireductase activity in the absence of added cadmium were also strongly affected by the dosage of YAP1 and CAD1/YAP2 genes. Our results suggest an indirect influence of these genes on iron metabolism, possibly via modification of the cell redox status.

6/3,AB/104 (Item 21 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04391108 Genuine Article#: RZ986 Number of References: 24
Title: CELLULAR MECHANISMS UNDERLYING THE INCREASED DUODENAL
IRON-ABSORPTION IN RATS IN RESPONSE TO PHENYLHYDRAZINE-INDUCED
HEMOLYTIC-ANEMIA (Abstract Available)

Author(s): ORIORDAN DK; SHARP P; SYKES RM; SRAI SK; EPSTEIN O; DEBNAM ES
Corporate Source: ROYAL FREE HOSP, SCH MED, DEPT PHYSIOL, ROWLAND HILL
ST/LONDON NW3 2PF//ENGLAND//; ROYAL FREE HOSP, SCH MED, DEPT
PHYSIOL/LONDON NW32PF//ENGLAND//; ROYAL FREE HOSP, SCH MED, DEPT
MED/LONDON NW3 2PF//ENGLAND//; ROYAL FREE HOSP, SCH MED, DEPT BIOCHEM &
MOLEC BIOL/LONDON NW3 2PF//ENGLAND/
Journal: EUROPEAN JOURNAL OF CLINICAL INVESTIGATION, 1995, V25, N10 (OCT), P722-727
ISSN: 0014-2972

Language: ENGLISH Document Type: ARTICLE
Abstract: Haemolytic anaemia induced by phenylhydrazine (PZ) promotes iron absorption across rat small intestine. This present study investigates the role of the brush border potential difference (V-m) and mucosal reducing activity in the response. In addition, quantitative autoradiography was used to assess PZ-induced changes in the villus localization of brush border iron uptake. Iron transfer from duodenum

to blood was increased significantly 5 days after treatment with PZ. Autoradiography showed that most brush border iron uptake occurred at the upper villus region and the maximal rate was increased fourfold by PZ. Duodenal villus length was increased in PZ-treated rats. PZ treatment did not influence mucosal reducing activity but V-m, measured using duodenal sheets, increased from -50 to -57 mV ($P < 0.001$) and this was due to a reduced brush border sodium permeability. Thus, an expanded absorptive surface and an enhanced electrical driving force for iron uptake across the duodenal brush border are important adaptations for increased iron absorption in PZ-induced haemolytic anaemia.

6/3,AB/105 (Item 22 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

04184046 Genuine Article#: RL538 Number of References: 26
Title: CHARACTERIZATION AND PARTIAL-PURIFICATION OF A FERRIREDUCTASE FROM HUMAN DUODENAL MICROVILLUS MEMBRANES (Abstract Available)
Author(s): RIEDEL HD; REMUS AJ; FITSCHER BA; STREMMEL W
Corporate Source: UNIV HEIDELBERG HOSP,DEPT MED,BERGHEIMER STR 58/D-69115 HEIDELBERG//GERMANY//; UNIV HEIDELBERG HOSP,DEPT MED/D-69115 HEIDELBERG//GERMANY/

Journal: BIOCHEMICAL JOURNAL, 1995, V309, AUG (AUG 1), P745-748
ISSN: 0264-6021

Language: ENGLISH Document Type: ARTICLE

Abstract: Reduction of ferric iron in the presence of HuTu 80 cells or duodenal microvillus membranes (MVMs) was investigated. With both systems, NADH-dependent reduction of Fe^{3+} /NTA (nitrilotriacetic acid) was demonstrated, using the ferrous iron chelator ferrozine. Uptake of Fe^{3+} from Fe^{3+} /NTA by HuTu 80 cells was strongly inhibited by addition of ferrozine, indicating that Fe^{2+} is the substrate for the iron uptake system. With isolated plasma membranes it is shown that the reductase activity is sensitive to trypsin and incubation at 65 degrees C. The reductase activity could be extracted from the plasma membrane and partially purified by ammonium sulphate precipitation and isoelectric focusing. From the purification and inhibition characteristics we conclude that reduction of ferric iron on the surface of duodenal plasma membranes is catalysed by a membrane protein.

6/3,AB/106 (Item 23 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03916283 Genuine Article#: QR536 Number of References: 13
Title: FERRIREDUCTASE ACTIVITY IN SACCHAROMYCES-CEREVISIAE AND OTHER FUNGI - COLORIMETRIC ASSAYS ON AGAR PLATES

Author(s): LESUISSE E; CASTERASSIMON M; LABBE P
Corporate Source: UNIV PARIS 07,INST JACQUES MONOD,BIOCHIM PORPHYRINES LAB,TOUR 43,2 PL JUSSIEU/F-75251 PARIS 05//FRANCE/

Journal: ANALYTICAL BIOCHEMISTRY, 1995, V226, N2 (APR 10), P375-377
ISSN: 0003-2697

Language: ENGLISH Document Type: NOTE

6/3,AB/107 (Item 24 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03901674 Genuine Article#: QR037 Number of References: 41
Title: AFT1 - A MEDIATOR OF IRON-REGULATED TRANSCRIPTIONAL CONTROL IN SACCHAROMYCES-CEREVISIAE (Abstract Available)

Author(s): YAMAGUCHIIWAI Y; DANCIS A; KLAUSNER RD
Corporate Source: NICHHD, CELL BIOL & METAB BRANCH/BETHESDA//MD/20892;
NICHHD, CELL BIOL & METAB BRANCH/BETHESDA//MD/20892
Journal: EMBO JOURNAL, 1995, V14, N6 (MAR 15), P1231-1239
ISSN: 0261-4189

Language: ENGLISH Document Type: ARTICLE

Abstract: Using a scheme for selecting mutants of *Saccharomyces cerevisiae* with abnormalities of iron metabolism, we have identified a gene, AFT1, that mediates the control of iron uptake. AFT1 encodes a 78 kDa protein with a highly basic amino terminal domain and a glutamine-rich C-terminal domain, reminiscent of transcriptional activators. The protein also contains an amino terminal and a C-terminal region with 10% His residues. A dominant mutant allele of this gene, termed AFT1-1(up), results in high levels of **ferric reductase** and ferrous iron uptake that are not repressed by exogenous iron. The increased iron uptake is associated with enhanced susceptibility to iron toxicity. These effects may be explained by the failure of iron to repress transcription of FRE1, FRE2 and FET3. FRE1 and FRE2 encode plasma membrane **ferric reductases**, obligatory for ferric iron assimilation, and FET3 encodes a copper-dependent membrane-associated oxidase required for ferrous iron uptake. Conversely, a strain with interruption of the AFT1 gene manifests low **ferric reductase** and ferrous iron uptake and is susceptible to iron deprivation, because of deficient expression of FRE1 and negligible expression of FRE2 and FET3. Thus, AFT1 functions to activate transcription of target genes in response to iron deprivation and thereby plays a central role in iron homeostasis.

6/3,AB/108 (Item 25 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03885689 Genuine Article#: QP889 Number of References: 40
Title: THE MENKES-WILSON-DISEASE GENE HOMOLOG IN YEAST PROVIDES COPPER TO A CERULOPLASMIN-LIKE OXIDASE REQUIRED FOR IRON UPTAKE (Abstract Available)

Author(s): YUAN DS; STEARMAN R; DANCIS A; DUNN T; BEELER T; KLAUSNER RD
Corporate Source: NICHHD, CELL BIOL & METAB BRANCH/BETHESDA//MD/20892;
NICHHD, CELL BIOL & METAB BRANCH/BETHESDA//MD/20892; UNIFORMED SERV UNIV
HLTH SCI, DEPT BIOCHEM/BETHESDA//MD/20814
Journal: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, 1995, V92, N7 (MAR 28), P2632-2636
ISSN: 0027-8424

Language: ENGLISH Document Type: ARTICLE

Abstract: The CCC2 gene of the yeast *Saccharomyces cerevisiae* is homologous to the human genes defective in Wilson disease and Menkes disease. A biochemical hallmark of these diseases is a deficiency of copper in ceruloplasmin and other copper proteins found in extracytosolic compartments. Here we demonstrate that disruption of the yeast CCC2 gene results in defects in respiration and iron uptake. These defects could be reversed by supplementing cells with copper, suggesting that CCC2 mutant cells were copper deficient. However, cytosolic copper levels and copper uptake were normal. Instead, CCC2 mutant cells lacked a copper-dependent oxidase activity associated with the extracytosolic domain of the FET3-encoded protein, a ceruloplasmin homologue previously shown to be necessary for high-affinity iron uptake in yeast. Copper restored oxidase activity both in vitro and in vivo, paralleling the ability of copper to restore respiration and iron uptake. These results suggest that the CCC2-encoded protein is required for the export of copper from the cytosol into an extracytosolic compartment, supporting the proposal that intracellular copper transport is impaired in Wilson disease and Menkes disease.

6/3,AB/109 (Item 26 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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03742674 Genuine Article#: QC018 Number of References: 86
Title: IRON REDUCTASE SYSTEMS ON THE PLANT PLASMA-MEMBRANE - A REVIEW (Abstract Available)
Author(s): MOOG PR; BRUGGEMANN W
Corporate Source: UNIV GRONINGEN,CENTRUM BIOL,DEPT PLANT
BIOL,POB14,KERKLAAN 30/9750 AA HAREN//NETHERLANDS/
Journal: PLANT AND SOIL, 1994, V165, N2, P241-260
ISSN: 0032-079X
Language: ENGLISH Document Type: ARTICLE
Abstract: Higher plant roots, leaf mesophyll tissue, protoplasts as well as green algae are able to reduce extra-cellular ferricyanide and ferric chelates. In roots of dicotyledonous and nongraminaceous, monocotyledonous plants, the rate of ferric reduction is increased by iron deficiency. This reduction is an obligatory prerequisite for iron uptake and is mediated by redox systems localized on the plasma membrane. Plasma membrane-bound iron reductase systems catalyze the transmembrane electron transport from cytosolic reduced pyridine nucleotides to extracellular iron compounds. Natural and synthetic ferric complexes can act as electron acceptors.

This paper gives an overview about the present knowledge on iron reductase systems at the plant plasma membrane with special emphasis on biochemical characteristics and localisation.

6/3,AB/110 (Item 27 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03740872 Genuine Article#: QB967 Number of References: 53
Title: POTENTIAL MOLECULAR TARGETS OF METABOLIC PATHWAYS
Author(s): BOYLE SM; SZANISZLO PJ; NOZAWA Y; JACOBSON ES; COLE GT
Corporate Source: UNIV TEXAS,DEPT BOT/AUSTIN//TX/78713; UNIV TEXAS,DEPT
BOT/AUSTIN//TX/78713; VIRGINIA MARYLAND REG COLL VET
MED/BLACKSBURG//VA/24061; GIFU UNIV,SCH MED/GIFU 500//JAPAN/; MCGUIRE
DEPT VET AFFAIRS MED CTR/RICHMOND//VA/23298
Journal: JOURNAL OF MEDICAL AND VETERINARY MYCOLOGY, 1994, V32, S1, P
79-89
ISSN: 0268-1218
Language: ENGLISH Document Type: ARTICLE

6/3,AB/111 (Item 28 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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03709253 Genuine Article#: QA287 Number of References: 38
Title: EVIDENCE FOR CU(II) REDUCTION AS A COMPONENT OF COPPER UPTAKE BY
SACCHAROMYCES-CEREVISIAE (Abstract Available)
Author(s): HASSETT R; KOSMAN DJ
Corporate Source: SUNY BUFFALO,SCH MED & BIOMED SCI,DEPT
BIOCHEM/BUFFALO//NY/14214; SUNY BUFFALO,SCH MED & BIOMED SCI,DEPT
BIOCHEM/BUFFALO//NY/14214
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1995, V270, N1 (JAN 6), P
128-134
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE
Abstract: The yeast *Saccharomyces cerevisiae* contains a plasma membrane reductase activity associated with the gene product of the FRE1 locus.

This reductase is required for Fe(III) uptake by this yeast; transcription from FRE1 is repressed by iron (Dancis, A., Klausner, R. D., Hinnebusch, A. G., and Barriocanal, J. G. (1990) Mol. Cell. Biol. 10, 2294-2301). We show here that Cu(II) is equally efficient at repressing FRE1 transcription and is an excellent substrate for the Frelp reductase. This reductase activity is required for 50-70% of the uptake of Cu-64 by wild type cells. Under conditions of low Fre1-dependent activity, cells retain 30-70% of Cu(II) reductase activity but only 8-25% of Fe(III) reductase activity. While Frelp-dependent activity is 100% inhibitable by Pt(II), this residual Cu(II) reduction is insensitive to this inhibitor. The data suggest the presence of a Frelp-independent reductase activity in the yeast plasma membrane which is relatively specific for Cu(II) and which supports copper uptake in the absence of FRE1 expression. The gene product of MAC1, which is required for regulation of FRE1 transcription, is also required for expression of Cu(II) reduction activity. This is due in part to its role in the regulation of FRE1; however, it is required for expression of the putative Cu(II) reductase, as well. Similarly, a gain-of function mutation, MAC1(up1), which causes elevated and unregulated transcription from FRE1 and elevated Fe(III) reduction and Fe-59 uptake exhibits a similar phenotype with respect to Cu(II) reduction and Cu-64 uptake. Ascorbate, which reduces periplasmic Cu(II) to Cu(I), suppresses the dependence of Cu-64 uptake on plasma membrane reductase activity as is the case for ascorbate-supported Fe-59 uptake. The close parallels between Cu(II) and Fe(III) reduction, and Cu-64 and Fe-59 uptake, strongly suggest that Cu(II) uptake by yeast involves a Cu(I) intermediate. This results in the reductive mobilization of the copper from periplasmic chelating agents, making the free ion available for translocation across the plasma membrane.

6/3,AB/112 (Item 29 from file: 34)
 DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
 (c) 2002 Inst for Sci Info. All rts. reserv.

03608102 Genuine Article#: PQ930 Number of References: 41
 Title: THE FET4 GENE ENCODES THE LOW-AFFINITY FE(II) TRANSPORT PROTEIN OF SACCHAROMYCES-CEREVISIAE (Abstract Available)
 Author(s): DIX DR; BRIDGHAM JT; BRODERIUS MA; BYERSDORFER CA; EIDE DJ
 Corporate Source: UNIV MINNESOTA,DEPT BIOCHEM & MOLEC BIOL/DULUTH//MN/55812 ; UNIV MINNESOTA,DEPT BIOCHEM & MOLEC BIOL/DULUTH//MN/55812
 Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1994, V269, N42 (OCT 21), P 26092-26099
 ISSN: 0021-9258
 Language: ENGLISH Document Type: ARTICLE
 Abstract: Previous studies on Fe(II) uptake in *Saccharomyces cerevisiae* suggested the presence of two uptake systems with different affinities for this substrate. We demonstrate that the FET3 gene is required for high affinity uptake but not for the low affinity system. This requirement has enabled a characterization of the low affinity system. Low affinity uptake is time-, temperature-, and concentration-dependent and prefers Fe(II) over Fe(III) as substrate. We have isolated a new gene, FET4, that is required for low affinity uptake, and our results suggest that FET4 encodes an Fe(II) transporter protein. FET4's predicted amino acid sequence contains six potential transmembrane domains. Overexpressing FET4 increased low affinity uptake, whereas disrupting this gene eliminated that activity. In contrast, overexpressing FET4 decreased high affinity activity, while disrupting FET4 increased that activity. Therefore, the high affinity system may be regulated to compensate for alterations in low affinity activity. These analyses, and the analysis of the iron-dependent regulation of the plasma membrane Fe(III) reductase, demonstrate that the low affinity system is a biologically relevant mechanism of iron uptake in yeast. Furthermore, our results indicate that the high and low affinity

systems are separate uptake pathways.

6/3,AB/113 (Item 30 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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03601129 Genuine Article#: PQ491 Number of References: 44
Title: THE SACCHAROMYCES-CEREVISIAE COPPER TRANSPORT PROTEIN (CTR1P) -
BIOCHEMICAL, CHARACTERIZATION, REGULATION BY COPPER, AND
PHYSIOLOGICAL-ROLE IN COPPER UPTAKE (Abstract Available)
Author(s): DANCIS A; HAILE D; YUAN DS; KLAUSNER RD
Corporate Source: NICHHD,CELL BIOL & METAB BRANCH/BETHESDA//MD/20892;
NICHHD,CELL BIOL & METAB BRANCH/BETHESDA//MD/20892
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1994, V269, N41 (OCT 14), P
25660-25667
ISSN: 0021-9258

Language: ENGLISH Document Type: ARTICLE

Abstract: The CTR1 gene of *Saccharomyces cerevisiae* encodes a protein required for high affinity copper uptake. The protein is expressed on the plasma membrane, is heavily glycosylated with O-linkages, and exists as an oligomer in vivo. The transcript abundance is strongly regulated by copper availability, being induced by copper deprivation and repressed by copper excess. Regulation occurs at very low, nontoxic levels of available copper and is independent of ACE1, the trans-inducer of yeast metallothionein. Expression of Ctr1p is limiting for copper uptake, since overexpression from a 2 mu high copy number plasmid increases copper uptake. Mutations in CTR1 result in altered cellular responses to extracellular copper, demonstrating a physiologic role for CTR1 in the delivery of copper to the cytosol. A copper dependent reporter gene construct, CUP1-lacZ, is not expressed in CTR1 mutants to the same level as in wild-type strains, and Cu,Zn superoxide dismutase activity is deficient in these mutants. The growth arrest that occurs in CTR1 mutants grown aerobically in copper-deficient media is attributable to the defect in Cu,Zn superoxide dismutase activity.

6/3,AB/114 (Item 31 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03350644 Genuine Article#: NZ044 Number of References: 18
Title: THE YELLOW-STRIPE-1 AND YELLOW-STRIPE-3 MUTANTS OF MAIZE -
NUTRITIONAL AND BIOCHEMICAL-STUDIES (Abstract Available)
Author(s): BASSO B; BAGNARESI P; BRACALE M; SOAVE C
Corporate Source: CNR,CTR STUDIO BIOL CELLULARE & MOLEC PIANTE,VIA CELORIA
26/I-20133 MILAN//ITALY//; UNIV MILAN,DIPARTIMENTO BIOL/I-20133
MILAN//ITALY//; UNIV BOLOGNA,DIPARTIMENTO BIOL/I-40126 BOLOGNA//ITALY/
Journal: MAYDICA, 1994, V39, N2, P97-105
ISSN: 0025-6153

Language: ENGLISH Document Type: ARTICLE

Abstract: Plants acquire iron from soil by two specific mechanisms: i) reduction of Fe³⁺ to Fe²⁺, a reaction catalyzed by a transmembrane reductase activity, followed by Fe²⁺ uptake; ii) release of Fe³⁺-chelating compounds -phytosiderophores- which are taken up by roots in the ferrated form. The first mechanism is typical for dicots, while the second is used by gramineous species. Both mechanisms are induced by iron starvation. ys1 and ys3 maize mutants display an iron chlorosis in field or in hydroponic culture in the presence of ferric chelates (Fe-EDTA), but both mutants turn green if supplied with Fe²⁺. Greening takes also place when the mutants are grown in a culture tube together with wt plants in a solution with Fe-EDTA. For ys1 (but not for ys3), even cultivation in an exhausted nutrient solution in which a wt plant had been previously grown induces greening. wt plants produce

a diffusible factor restoring iron uptake capability in the mutants; in the case of ysl1, this factor is likely to be the phytosiderophore.

Iron starvation induces in roots of wt an increase of in vito Fe³⁺-reductase activity as well as changes in the microsomal protein pattern; both mutants behave as starved wt even when grown in the presence of Fe³⁺-EDTA. **Ferric-chelate-reductase** zymograms of root microsomal proteins electrofocused on polyacrylamide gels reveal the presence of several isozymes one of which, with an apparent pI of 6.4, is predominant in plasma membrane enriched fractions. In segregating progenies from Ysl1/ysl1 and Ys3/ys3 plants, normal and mutant seedlings show a similar IEF pattern; however the pI 6.4 isozyme present in the Ysl1 background is missing in Ys3 and it is replaced by an isozyme with a pI of about 7.3. It could be that the two isoforms represent alleles of a gene encoding the **ferric-reductase**.

6/3,AB/115 (Item 32 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03215083 Genuine Article#: NM944 Number of References: 20
Title: SEQUENCING OF A 13.2-KB SEGMENT NEXT TO THE LEFT TELOMERE OF YEAST CHROMOSOME-XI REVEALED 5 OPEN READING FRAMES AND RECENT RECOMBINATION EVENTS WITH THE RIGHT ARMS OF CHROMOSOME-III AND CHROMOSOME-V (Abstract Available)
Author(s): ALEXANDRAKI D; TZERMIA M
Corporate Source: INST MOLEC BIOL & BIOTECHNOL,FDN RES & TECHNOL HELLAS,POB 1527/GR-71110 IRAKLION//GREECE//; UNIV CRETE,DEPT BIOL/GR-71110 IRAKLION//GREECE/
Journal: YEAST, 1994, V10, SA (APR), PS81-S91
ISSN: 0749-503X
Language: ENGLISH Document Type: ARTICLE
Abstract: We report the entire sequence of a 13.2 kb segment next to the left telomere of chromosome XI of *Saccharomyces cerevisiae*. A 1.2 kb fragment near one end is 91% homologous to the right arm of chromosome III and 0.7 kb of that are 77% homologous to the right arm of chromosome V. Five open reading frames are included in the sequenced segment. Two of them are almost identical to the known YCR104W and YCR103C hypothetical proteins of chromosome III. A third one contains a region homologous to the Zn (2)-Cys (6) binuclear cluster pattern of fungal transcriptional activators. The fourth one, part of which is similar to the mammalian putative transporter of mevalonate, has the structure of membrane transporters. The fifth one is similar to yeast **ferric reductase**. The sequence has been deposited in the EMBL data library under Accession Number X75950.

6/3,AB/116 (Item 33 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03077925 Genuine Article#: NA966 Number of References: 31
Title: IRON - NUTRITIOUS, NOXIOUS, AND NOT READILY AVAILABLE
Author(s): GUERINOT ML; YI Y
Corporate Source: DARTMOUTH COLL,DEPT BIOL SCI/HANOVER//NH/03755
Journal: PLANT PHYSIOLOGY, 1994, V104, N3 (MAR), P815-820
ISSN: 0032-0889
Language: ENGLISH Document Type: EDITORIAL

6/3,AB/117 (Item 34 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

(c) 2002 Inst for Sci Info. All rts. reserv.

02943453 Genuine Article#: MU678 Number of References: 40

Title: THE FET3 GENE OF SACCHAROMYCES-CEREVISIAE ENCODES A MULTICOPPER
OXIDASE REQUIRED FOR FERROUS IRON UPTAKE (Abstract Available)

Author(s): ASKWITH C; EIDE D; VANHO A; BERNARD PS; LI LT; DAVISKAPLAN S;
SIPE DM; KAPLAN J

Corporate Source: UNIV UTAH, DEPT PATHOL, DIV CELL BIOL & IMMUNOL/SALT LAKE
CITY//UT/84132; UNIV MINNESOTA, SCH MED, DEPT BIOCHEM & MOLEC
BIOL/DULUTH//MN/55812

Journal: CELL, 1994, V76, N2 (JAN 28), P403-410

ISSN: 0092-8674

Language: ENGLISH Document Type: ARTICLE

Abstract: *S. cerevisiae* accumulate iron by a process requiring a ferrireductase and a ferrous transporter. We have isolated a mutant, *fet3*, defective for high affinity Fe(II) uptake. The wild-type FET3 gene was isolated by complementation of the mutant defect. Sequence analysis of the gene revealed the presence of an open reading frame coding for a protein with strong similarity to the family of blue multicopper oxidoreductases. Consistent with the role of copper in iron transport, growth of wild-type cells in copper-deficient media resulted in decreased ferrous iron transport. Addition of copper, but not other transition metals (manganese or zinc), to the assay media resulted in the recovery of Fe(II) transporter activity. We suggest that the catalytic activity of the Fet3 protein is required for cellular iron accumulation.

6/3,AB/118 (Item 35 from file: 34)

DIALOG(R) File 34:SciSearch(R) Cited Ref Sci

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02943452 Genuine Article#: MU678 Number of References: 43

Title: MOLECULAR CHARACTERIZATION OF A COPPER TRANSPORT PROTEIN IN
SACCHAROMYCES-CEREVISIAE - AN UNEXPECTED ROLE FOR COPPER IN IRON
TRANSPORT (Abstract Available)

Author(s): DANCIS A; YUAN DS; HAILE D; ASKWITH C; EIDE D; MOEHLE C; KAPLAN J;
KLAUSNER RD

Corporate Source: NICHHD, CELL BIOL & METAB BRANCH/BETHESDA//MD/20892; UNIV
UTAH, COLL MED, DEPT PATHOL, DIV CELL BIOL & IMMUNOL/SALT LAKE
CITY//UT/84132; UNIV MINNESOTA, SCH MED, DEPT BIOCHEM & MOLEC
BIOL/DULUTH//MN/55812; NICHHD, MOLEC GENET LAB/BETHESDA//MD/20892

Journal: CELL, 1994, V76, N2 (JAN 28), P393-402

ISSN: 0092-8674

Language: ENGLISH Document Type: ARTICLE

Abstract: We report the identification and characterization of CTR1, a gene in the yeast *S. cerevisiae* that encodes a multispreading plasma membrane protein specifically required for high affinity copper transport into the cell. The predicted protein contains a methionine- and serine-rich domain that includes 11 examples of the sequence Met-X₂-Met, a motif noted in proteins involved in bacterial copper metabolism. CTR1 mutants and deletion strains have profound deficiency in ferrous iron uptake, thus revealing a requirement for copper in mediating ferrous transport into the cell. Genetic evidence suggests that the target for this requirement is the FET3 gene (detailed in a companion study), predicted to encode a copper-containing protein that acts as a cytosolic ferro-oxidase. These findings provide an unexpected mechanistic link between the uptake of copper and iron.

6/3,AB/119 (Item 36 from file: 34)

DIALOG(R) File 34:SciSearch(R) Cited Ref Sci

(c) 2002 Inst for Sci Info. All rts. reserv.

02875407 Genuine Article#: MM120 Number of References: 29
 Title: MAC1, A NUCLEAR REGULATORY PROTEIN RELATED TO CU-DEPENDENT
 TRANSCRIPTION FACTORS IS INVOLVED IN CU/FE UTILIZATION AND STRESS
 RESISTANCE IN YEAST (Abstract Available)
 Author(s): JUNGMAHN J; REINS HA; LEE JW; ROMEO A; HASSETT R; KOSMAN D;
 JENTSCH S
 Corporate Source: MAX PLANCK GESELL, FRIEDRICH MIESCHER LAB, SPEMANNSTR
 37-39/D-72076 TUBINGEN//GERMANY//; MAX PLANCK GESELL, FRIEDRICH MIESCHER
 LAB, SPEMANNSTR 37-39/D-72076 TUBINGEN//GERMANY/
 Journal: EMBO JOURNAL, 1993, V12, N13 (DEC 15), P5051-5056
 ISSN: 0261-4189
 Language: ENGLISH Document Type: ARTICLE
 Abstract: The related transcription factors ACE1 of *Saccharomyces*
cerevisiae and AMT1 of *Candida glabrata* are involved in copper
 metabolism by activating the transcription of copper metallothionein
 genes. ACE1 and AMT1 are 'copper-rist' transcription factors which
 possess a conserved cysteine-rich copper binding domain required for
 DNA binding. Here we report the identification of a nuclear protein
 from *S. cerevisiae*, MAC1, whose N-terminal region is highly similar to
 the copper and DNA binding domains of ACE1 and AMT1. Loss-of-function
 mutants of MAC1 have a defect in the plasma membrane Cu(II) and Fe(III)
 reductase activity, are slow growing, respiratory deficient, and
 hypersensitive to heat and exposure to cadmium, zinc, lead and H₂O₂.
 Conversely, a dominant gain-of-function mutant of MAC1 shows an
 elevated reductase activity and is hypersensitive to copper. We have
 identified two target genes of MAC1 whose altered expression in mutants
 of MAC1 can account for some of the observed mutant phenotypes. First,
 MAC1 is involved in basal level transcription of FRE1, encoding a
 plasma membrane component associated with both Cu(II) and Fe(III)
 reduction. Second, MAC1 is involved in the H₂O₂-induced transcription
 of CTT1, encoding the cytosolic catalase. This suggests that MAC1 may
 encode a novel metal-fist transcription factor required for both basal
 and regulated transcription of genes involved in Cu/Fe utilization and
 the stress response.

6/3, AB/120 (Item 37 from file: 34)
 DIALOG(R) File 34:SciSearch(R) Cited Ref Sci
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02872505 Genuine Article#: ML714. Number of References: 45
 Title: THE GEF1 GENE OF SACCHAROMYCES-CEREVISIAE ENCODES AN INTEGRAL
 MEMBRANE-PROTEIN - MUTATIONS IN WHICH HAVE EFFECTS ON RESPIRATION AND
 IRON-LIMITED GROWTH (Abstract Available)
 Author(s): GREENE JR; BROWN NH; DIDOMENICO BJ; KAPLAN J; EIDE DJ
 Corporate Source: SCHERING PLOUGH CORP, RES INST, 2015 GALLOPING HILL
 RD/KENILWORTH//NJ/07033; UNIV UTAH, MED CTR, DEPT PATHOL/SALT LAKE
 CITY//UT/84132; UNIV MINNESOTA, DEPT BIOCHEM & MOLEC
 BIOL/DULUTH//MN/55812
 Journal: MOLECULAR & GENERAL GENETICS, 1993, V241, N5-6 (DEC), P
 542-553
 ISSN: 0026-8925
 Language: ENGLISH Document Type: ARTICLE
 Abstract: We have isolated a new class of respiration-defective, i.e
 petite, mutants of the yeast *Saccharomyces omq, ces cel cerevisiae*.
 Mutations in the GEF1 gene cause cells to grow slowly on rich media
 containing carbon sources utilized by respiration. This phenotype is
 suppressed by adding high concentrations of iron to the growth medium.
 Gef(1-) mutants also fail to grow on a fermentable carbon source,
 glucose, when iron is reduced to low concentrations in the medium,
 suggesting that the GEF1 gene is required for efficient metabolism of
 iron during growth on fermentable as well as respired carbon sources.
 However, activity of the iron uptake system appears to be unaffected in
 gef1(-) mutants. Fe(II) transporter activity and regulation is normal

in *gef1(-)* mutants. Fe(III) reductase induction during iron-limited growth is disrupted, but this appears to be a secondary effect of growth rate alterations. The wild-type *GEF1* gene was cloned and sequenced; it encodes a protein of 779 amino acids, 13 possible transmembrane domains, and significant similarity to chloride channel proteins from fish and mammals, suggesting that *GEF1* encodes an integral membrane protein. A *gef1(-)* deletion mutation generated in vitro and introduced into wild-type haploid strains by gene transplacement was not lethal. Oxygen consumption by intact *gef1(-)* cells and by mitochondrial fractions isolated from *gef1(-)* mutants was reduced 25-50% relative to wild type, indicating that mitochondrial function is defective in these mutants. We suggest that *GEF1* encodes a transport protein that is involved in intracellular iron metabolism.

6/3,AB/121 (Item 38 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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02234754 Genuine Article#: KM326 Number of References: 38
Title: REDUCTION AND MOBILIZATION OF IRON BY A NAD(P)H - FLAVIN
OXIDOREDUCTASE FROM ESCHERICHIA-COLI (Abstract Available)
Author(s): COVES J; FONTECAVE M
Corporate Source: UNIV JOSEPH FOURIER,ETUDES DYNAM & STRUCT SELECTIVITE
LAB,CNRS,URA 332,BP 53X/F-38041 GRENOBLE//FRANCE//; UNIV JOSEPH
FOURIER,ETUDES DYNAM & STRUCT SELECTIVITE LAB,CNRS,URA 332,BP
53X/F-38041 GRENOBLE//FRANCE/
Journal: EUROPEAN JOURNAL OF BIOCHEMISTRY, 1993, V211, N3 (FEB 1), P
635-641

ISSN: 0014-2956

Language: ENGLISH Document Type: ARTICLE

Abstract: Iron is an essential element in all living cells. Solubilization, uptake and transport of iron by microorganisms is controlled by highly efficient and specific Fe³⁺-chelating agents named siderophores. However, mechanisms of mobilization of iron from ferrisiderophores are still enigmatic. Here, we demonstrate that *Escherichia coli* contains a powerful enzymatic system for the reduction of ferrisiderophores. Siderophores have a much lower affinity for ferrous iron, which then can be liberated. This system has been previously purified and characterized as a NAD(P)H:flavin oxidoreductase [Fontecave, M., Eliasson, R. and Reichard, P. (1987) J. Biol. Chem. 262, 12325-12331]]. It catalyzes the reduction of free flavins, FMN, FAD or riboflavin by NADH or NADPH. Reduced flavins, in turn transfer their electrons to physiological ferric complexes: ferrisiderophores, ferric citrate and ferritins. The reaction is inhibited by molecular oxygen and greatly stimulated by Fe²⁺-acceptors such as ferrozine or the iron-free form of ribonucleotide reductase subunit R2. We suggest that the reduction and the mobilization of iron from ferrisiderophores in the cell might be regulated by the presence of physiological ferrous traps such as apoproteins.

6/3,AB/122 (Item 39 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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02050239 Genuine Article#: JW945 Number of References: 16
Title: PHYSIOLOGICAL-CHARACTERISTICS OF RHIZOBIUM-MELILOTI 1021-TN5 MUTANTS
WITH ALTERED RHIZOBACTIN ACTIVITIES (Abstract Available)
Author(s): BARTON LL; FEKETE FA; VESTER CR; GILL PR; NEILANDS JB
Corporate Source: UNIV NEW MEXICO,DEPT BIOL,MICROBIAL CHEM
LAB/ALBUQUERQUE//NM/87131; INRA,PATHOL VEGETALE LAB/F-75231 PARIS
05//FRANCE//; UNIV CALIF BERKELEY,DEPT MOLEC & CELLULAR
BIOL/BERKELEY//CA/94720

Journal: JOURNAL OF PLANT NUTRITION, 1992, V15, N10, P2145-2156

ISSN: 0190-4167

Language: ENGLISH Document Type: ARTICLE

Abstract: Rhizobium meliloti 1021 and several Tn5 generated mutants were examined for physiological activities which would reflect the capacity of these strains for efficient iron metabolism. Rhizobactin production in liquid culture, as measured by CAS reactivity, was greatest in R. meliloti 1021 with lesser amounts formed by strains PRR 63 and PRR 62. Examination of the various strains of R. meliloti grown under different levels of iron revealed that all strains tested were constitutive for **ferric reductase**. Evaluation of Medicago sativa L. cultivated in peat pots and inoculated with R. meliloti revealed that greatest levels of growth was with R. meliloti 1021, the only strain in this study with an efficient rhizobactin system. Evaluation of dinitrogen fixed by nodulated plants grown in a hydroponic system indicated that the amount of nitrogen fixed per bacteroid in the nodule was not constant but was correlated with the rhizobactin producing capability of the R. meliloti strains. Levels of dinitrogen fixed per unit of viable bacteroids was greater with R. meliloti 1021 than with PRR 29 or PRR

6/3,AB/123 (Item 40 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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01638427 Genuine Article#: HN741 Number of References: 0
Title: THE **FERRIC REDUCTASE** GENE OF SCHIZOSACCHAROMYCES-POMBE -
TRANSCRIPTIONAL CONTROL BY IRON AND SEQUENCE SIMILARITY WITH HUMAN
PHAGOCYTE NADPH OXIDASE
Author(s): ROMAN DG; DANCIS A; ANDERSON GJ; KLAUSNER RD
Corporate Source: NICHHD,CELL BIOL & METAB BRANCH/BETHESDA//MD/20892
Journal: CLINICAL RESEARCH, 1992, V40, N2 (APR), PA168
Language: ENGLISH Document Type: MEETING ABSTRACT

6/3,AB/124 (Item 41 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

01353863 Genuine Article#: GR309 Number of References: 0
Title: CLONING OF THE **FERRIC REDUCTASE** GENE OF THE YEAST
SAHIZOSACCHAROMYCES-POMBE - IMPLICATIONS FOR HUMAN IRON-METABOLISM
Author(s): ROMAN DG; DANCIS A; ANDERSON GJ; KLAUSNER RD
Corporate Source: NICHHD,CELL BIOL & METAB BRANCH/BETHESDA//MD/20892
Journal: AMERICAN JOURNAL OF HUMAN GENETICS, 1991, V49, N4, P417
Language: ENGLISH Document Type: MEETING ABSTRACT

6/3,AB/125 (Item 1 from file: 50)
DIALOG(R)File 50:CAB Abstracts
(c) 2002 CAB International. All rts. reserv.

03216243 CAB Accession Number: 961301133
Reduction of exogenous ferric iron by a surface-associated **ferric reductase** of Listeria species.
Deneer, H. G.; Healey, V.; Boychuk, I.
Department of Microbiology, University of Saskatchewan, Saskatoon, Canada, S7N 5E5.
Microbiology (Reading) vol. 141 (8): p.1985-1992
Publication Year: 1995
ISSN: 1350-0872 --
Language: English
Document Type: Journal article

Details of the mechanisms involved in iron acquisition by *Listeria* species were investigated. Whole cells of *L. monocytogenes* were shown to reduce many forms of ferric iron efficiently. Reduction only occurred after direct contact between the bacteria and the iron source. The reducing activity was strongly influenced by culture conditions such as growth temperature and aerobiosis and was seen in all species of *Listeria*, though to varying degrees. 32 ref.

6/3,AB/126 (Item 2 from file: 50)
DIALOG(R)File 50:CAB Abstracts
(c) 2002 CAB International. All rts. reserv.

03200966 CAB Accession Number: 960703773

The pH requirement for in vivo activity of the iron-deficiency-induced "turbo" **ferric chelate reductase**. A comparison of the iron-deficiency-induced iron reductase activities in intact plants and isolated plasma membrane fractions in sugar beet.

Susin, S.; Abadia, A.; Gonzalez-Reyes, J. A.; Lucena, J. J.; Abadia, J.
Departamento de Nutricion Vegetal, Estacion Experimental de Aula Dei,
Consejo Superior de Investigaciones Cientificas, Apdo. 202, 50080
Zaragoza, Spain.

Plant Physiology vol. 110 (1): p.111-123

Publication Year: 1996

ISSN: 0032-0889 --

Language: English

Document Type: Journal article

The characteristics of the Fe reduction mechanisms induced by Fe deficiency were studied in intact sugarbeet plants and in purified plasma membrane vesicles from the same plants. In Fe-deficient plants the in vivo Fe(III)-ethylenediaminetetraacetic complex (Fe(III)-EDTA) reductase activity increased over the control values 10-20 times when assayed at a pH of 6.0 or below ("turbo" reductase) but increased only 2-4 times when assayed at a pH of 6.5 or above. The Fe(III)-EDTA reductase activity of root plasma membrane preparations increased 2 and 3.5 times over the controls, irrespective of the assay pH. The Km for Fe(III)-EDTA of the in vivo **ferric chelate reductase** in Fe-deficient plants was approximately 510 and 240 micro M in the pH ranges 4.5-6.0 and 6.5-8.0, respectively. The Km for Fe(III)-EDTA of the **ferric chelate reductase** in intact control plants and in plasma membrane preparations isolated from Fe-deficient and control plants was about 200-240 micro M. Therefore, the turbo **ferric chelate reductase** activity of Fe-deficient plants at low pH appears to be different from the constitutive **ferric chelate reductase**.
. 29 ref.

6/3,AB/127 (Item 3 from file: 50)
DIALOG(R)File 50:CAB Abstracts
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02925238 CAB Accession Number: 941610924

The yellow-stripe-1 and -3 mutants of maize: nutritional and biochemical studies.

Basso, B.; Bagnaresi, P.; Bracale, M.; Soave, C.

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Maydica vol. 39 (2): p.97-105

Publication Year: 1994

ISSN: 0025-6153 --

Language: English

Document Type: Journal article

Plants acquire iron from soil by two specific mechanisms: (1) reduction of Fe³⁺ to Fe²⁺, a reaction catalysed by a transmembrane reductase

activity, followed by Fe²⁺ uptake; and (2) release of Fe³⁺-chelating compounds (phytosiderophores) which are taken up by roots in the ferrated form. The first mechanism is typical for dicots, while the second is used by gramineous species. Both mechanisms are induced by iron starvation. The ys1 and ys3 maize mutants displayed iron chlorosis in the field or in hydroponic culture in the presence of ferric chelates (Fe-EDTA), but both mutants turned green if supplied with Fe²⁺. Greening also took place when the mutants were grown in culture together with wild-type plants in a solution with Fe-EDTA. For ys1 (but not for ys3), even cultivation in an exhausted nutrient solution in which a wild-type plant had been previously grown induced greening. Wild-type plants produced a diffusible factor restoring iron uptake capability in the mutants; in the case of ys1, this factor is likely to be the phytosiderophore. Iron starvation induced in roots of the wild-type an increase of in vivo Fe³⁺-reductase activity as well as changes in the microsomal protein pattern; both mutants behaved as starved wild-types even when grown in the presence of Fe³⁺-EDTA. **Ferric-chelate-reductase** zymograms of root microsomal proteins electrofocused on polyacrylamide gels revealed the presence of several isoenzymes one of which, with an apparent pI of 6.4, was predominant in plasma membrane enriched fractions. In segregating progenies from Ys1/ys1 and Ys3/ys3 plants, normal and mutant seedlings showed a similar isoelectric focusing pattern; however the pI 6.4 isoenzyme present in the Ys1 background was missing in Ys3 and it was replaced by an isoenzyme with a pI of about 7.3. It could be that the two isoforms represent alleles of a gene encoding the **ferric-reductase**. 18 ref.

6/3,AB/128 (Item 4 from file: 50)
 DIALOG(R)File 50:CAB Abstracts
 (c) 2002 CAB International. All rts. reserv.

02719176 CAB Accession Number: 930764505
 Nicotianamine - a common constituent of strategies I and II of iron acquisition by plants: a review.
 Scholz, G.; Becker, R.; Pich, A.; Stephan, U. W.
 Institute of Genetics and Crop Plant Research, 4325 Gatersleben, Germany.
 Journal of Plant Nutrition vol. 15 (10): p.1647-1665
 Publication Year: 1992
 ISSN: 0190-4167 --
 Language: English
 Document Type: Conference paper; Journal article
 Nicotianamine is an intermediate in the biosynthesis of phytosiderophores from L-methionine in Fe-deficient plants. This review examines, in particular, its role in the regulation of iron deficiency response mechanisms, **ferric reductase**, and phloem loading/unloading of iron. References to tomato (in particular), Phaseolus vulgaris, peas and tobacco are made. 44 ref.

6/3,AB/129 (Item 5 from file: 50)
 DIALOG(R)File 50:CAB Abstracts
 (c) 2002 CAB International. All rts. reserv.

02524614 CAB Accession Number: 920311655
 Physiological disorders of the nicotianamine-auxotroph tomato mutant chloronerva at different levels of iron nutrition. II. Iron deficiency response and heavy metal metabolism.
 Stephan, U. W.; Grun, M.
 Zentralinstitut für Genetik und Kulturpflanzenforschung, Akademie der Wissenschaften, Gatersleben, Germany.
 Biochemie und Physiologie der Pflanzen vol. 185 (3-4): p.189-200
 Publication Year: 1989

ISSN: 0015-3796 --

Language: English

Document Type: Journal article

A mutant of cv. Bonner Beste, chloronerva, exhibits not only abnormal visible characteristics but also an abnormally high intake of Fe which is translocated to the shoots. Seedlings of the normal cultivar and its mutant were grown in Hoagland's nutrient solution (composition given) and when 14 days old were placed for 2 days in nutrient solution containing Fe at 0 (less than 0.1), 2, 5, 10, 20, 50 or 100 micro M. Iron deficiency-induced proton secretion occurred at up to 10 micro M FeEDTA in the nutrient solution for the mutant, but at up to 5 micro M for the normal, wild-type, cultivar. Thickened root tips and root hair zones were observed at up to 20 micro M for the mutant, whereas the root hairs were formed at up to 5 micro M for the normal cultivar. The **ferric reductase** activity of the rhizodermis remained higher in the mutant than in the normal cultivar at up to 100 micro M Fe. Over the concentration range of 5-10 micro M, the mutant accumulated 2 to 3 times more Fe in its shoots than did the normal cultivar. The increased uptake of certain heavy metals (e.g. Cu, Mn and Zn) by the normal cultivar observed under Fe-deficient conditions extended to a higher Fe supply range for the mutant. All these deviations from the wild-type behaviour were overcome when nicotianamine (NA) was supplied to the leaves of the mutant. The role of NA as an intracellular transporter for Fe(II) in the regulation of Fe metabolism and Fe deficiency response mechanisms is discussed. 47 ref.

6/3,AB/130 (Item 6 from file: 50)

DIALOG(R)File 50:CAB Abstracts

(c) 2002 CAB International. All rts. reserv.

02134862 CAB Accession Number: 891414495

Influences of weight reduction on aerobic power and body composition of middle-aged women.

Atomi, Y.; Miyashita, M.

Dep. Sports Sciences, College of Arts and Sciences, Univ. Tokyo, 3-8-1, Komaba, Meguro-ku, Tokyo 153, Japan.

Journal of Sports Medicine and Physical Fitness vol. 27 (4): p.501-509

Publication Year: 1987

ISSN: 0022-4707 --

Language: English

Document Type: Journal article

Sixteen moderately obese women (33.4 plus or minus 4.9% body fat) 31 to 51 years old completed 10-week weight reduction programmes. Two programmes were used: one group performed the food restriction programme only (FR) and another performed both food and exercise programmes (FRE); 8 women served as a control group. Mean total energy intake estimated from food records was 5065 plus or minus 209 kJ daily for FR and 4923 plus or minus 727 and 5844 plus or minus 229 kJ daily for FRE for non-exercising and exercising days, respectively. The exercise was conducted on a bicycle ergometer at 60% VO2max 5 days per week. Mean body weight decreased from 60.95 plus or minus 3.42 kg to 57.11 plus or minus 4.63 kg for FR and from 58.38 plus or minus 7.17 kg to 54.85 plus or minus 5.58 kg for FRE. There was no significant difference between the 2 groups in changes of body weight, lean body mass or body fat. The significant inverse changes in VO2max were observed (increase for FRE 1.341 plus or minus 0.185 to 1.618 plus or minus 0.241 litres/min and decrease for FR 1.559 plus or minus 0.281 to 1.410 plus or minus 0.324 litres/min). Although moderate weight reduction by either food restriction or food restriction and physical exercise have similar effects on the changes of body weight and body composition, they might influence aerobic power inversely. 26 ref.

6/3,AB/131 (Item 7 from file: 50)
DIALOG(R)File 50:CAB Abstracts
(c) 2002 CAB International. All rts. reserv.

02064692 CAB Accession Number: 890353869
Reduction of iron in squash callus cultures.
Omholt, T. E.; Boyer, G. L.
State University of New York, College of Environmental Science &
Forestry, Syracuse, NY 13210, USA.
Journal of Plant Nutrition vol. 11 (6-11): p.1227-1235
Publication Year: 1988
ISSN: 0190-4167 --
Language: English
Document Type: Conference paper; Journal article
Purified nitrate reductase (NR) from squash has been shown to reduce Fe(III) bound with different chelators (see Biochemical and Biophysical Research Communications (1984) 125, 52-58). To investigate the relationship between NR and iron reduction in plant cells, callus cultures were propagated from cotyledons of squash (*Cucurbita maxima*) on MS medium containing 5 μ M each of kinetin and 2,4-D. Friable callus was transferred to plates containing 3 levels of iron: (a) normal (100 μ M Fe(II) chelated with 100 μ M EDTA), (b) 1 μ M Fe(III) as FeCl₃, or (c) 1 μ M Fe(II) as FeSO₄. At 24-h intervals, duplicate plates were harvested and assayed for NR, nitrite reductase and **ferric reductase** activities. Callus grown on low Fe(III) medium showed a marked increase in NR activity, compared with control callus. Callus grown on low Fe(II) showed a slight, but much less pronounced, increase in NR activity. **Ferric reductase** activity did not differ between the 3 iron treatments. Ammonium sulphate precipitation of control and low Fe(II)-grown callus indicated that it was possible to separate NR activity from the endogenous iron reductase activity. These results suggest that NR is not the major enzyme responsible for the reduction of iron in crude callus homogenates. 19 ref.

6/3,AB/132 (Item 1 from file: 65)
DIALOG(R)File 65:Inside Conferences
(c) 2002 BLDSC all rts. reserv. All rts. reserv.

01513339 INSIDE CONFERENCE ITEM ID: CN015023468
Characterization of a Cell Surface **Ferric Reductase** in
Trichomonas vaginalis
Tarango, M.
CONFERENCE: International Society for STD Research-Meeting; 11th
MEETING- INTERNATIONAL SOCIETY FOR STD RESEARCH, 1995; 11th P: 124
ISSTD, 1995
LANGUAGE: English DOCUMENT TYPE: Conference Abstracts
CONFERENCE SPONSOR: International Society for STD Research
CONFERENCE LOCATION: New Orleans, LA
CONFERENCE DATE: Aug 1995 (19950) (19950)

6/3,AB/133 (Item 1 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
(c) 2002 Cambridge Sci Abs. All rts. reserv.

02095639 3993495
Morphological and metabolic responses to starvation by the dissimilatory
metal-reducing bacterium *Shewanella alga* BrY
Caccavo, F., Jr.; Ramsing, N.B.; Costerton, J.W.
Cent. for Biofilm Eng., Montana State Univ., 409 Cobleigh Hall, Bozeman, MT
59717, USA
APPL. ENVIRON. MICROBIOL. vol. 62, no. 12, pp. 4678-4682 (1996)
ISSN: 0099-2240

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Microbiology Abstracts A: Industrial & Applied Microbiology

The response of the dissimilatory metal-reducing bacterium *Shewanella* alga BrY to carbon and nitrogen starvation was examined. Starvation resulted in a gradual decrease in the mean cell volume from 0.48 to 0.2 μm^3 and a dramatic decrease in Fe(III) reductase activity. Growth of starved cultures was initiated with O_2 , ferric oxyhydroxide, Co(III)-EDTA, or Fe(III)-bearing subsurface materials as the sole electron acceptor. Microbially reduced subsurface materials reduced CrO_4^{2-} . Starvation of dissimilatory metal-reducing bacteria may provide a means of delivering this metabolism to contaminated subsurface environments for in situ bioremediation.

6/3,AB/134 (Item 2 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
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02047561 3926485

Effect of heme and vacuole deficiency on FRE1 gene expression and ferrireductase activity in *Saccharomyces cerevisiae*
Amillet, J. M.; Galianzo, F.; Labbe Bois, R.
Lab. Biochimie des Porphyrines, Inst. Jacques Monod, Univ. Paris 7, 2 Place Jussieu, 75251 Paris Cedex 05, France
FEMS MICROBIOL. LETT. vol. 137, no. 1, pp. 25-29 (1996)
ISSN: 0378-1097
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Microbiology Abstracts C: Algology, Mycology & Protozoology;
Biochemistry Abstracts 2: Nucleic Acids

We have examined the effects of heme or vacuole deficiency on the kinetics of induction of cell surface ferrireductase activity and expression of the FRE1 gene encoding a component of ferrireductase, in response to iron or copper deprivation in *S. cerevisiae*. Heme deficiency caused a small decrease in the basal expression of FRE1, but did not impair its induction by Fe or Cu limitation. Thus, the absence of ferrireductase activity and its non-inducibility in heme-less cells is not due to the absence of FRE1 expression. Vacuole deficiency led to constitutively high ferrireductase activity slightly induced by Cu limitation, and to high levels of FRE1 expression further inducible by Fe or Cu deprivation. Thus, the vacuole might be a component of the iron signalling pathway.

6/3,AB/135 (Item 3 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
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01911822 3725990

AFT1: A mediator of iron regulated transcriptional control in *Saccharomyces cerevisiae*
Yamaguchi Iwai, Y.; Dancis, A.; Klausner, R.D.
Cell Biol. and Metab. Branch, NICHD and Hum. Dev., NIH, Bethesda, MD, USA
EMBO J. vol. 14, no. 6, pp. 1231-1239 (1995)
ISSN: 0261-4189
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Biochemistry Abstracts 2: Nucleic Acids; Genetics Abstracts;
Microbiology Abstracts C: Algology, Mycology & Protozoology

Using a scheme for selecting mutants of *Saccharomyces cerevisiae* with abnormalities of iron metabolism, we have identified a gene, AFT1, that mediates the control of iron uptake. AFT1 encodes a 78 kDa protein with a highly basic amino terminal domain and a glutamine-rich C-terminal domain, reminiscent of transcriptional activators. The protein also contains an

amino terminal and a C-terminal region with 10% His residues. A dominant mutant allele of this gene, termed AFT1-1 super(up), results in high levels of **ferric reductase** and ferrous iron uptake that are not repressed by exogenous iron. The increased iron uptake is associated with enhanced susceptibility to iron toxicity. These effects may be explained by the failure of iron to repress transcription of FRE1, FRE2 and FET3. FRE1 and FRE2 encode plasma membrane **ferric reductases**, obligatory for ferric iron assimilation, and FET3 encodes a copper-dependent membrane-associated oxidase required for ferrous iron uptake. Conversely, a strain with interruption of the AFT1 gene manifests low **ferric reductase** and ferrous iron uptake and is susceptible to iron deprivation, because of deficient expression of FRE1 and negligible expression of FRE2 and FET3. Thus, AFT1 functions to activate transcription of target genes in response to iron deprivation and thereby plays a central role in iron homeostasis.

6/3,AB/136 (Item 4 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
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01715998 2996674

The fission yeast **ferric reductase** gene *frp1* super(+) is required for ferric iron uptake and encodes a protein that is homologous to the gp91-phox subunit of the human NADPH phagocyte oxidoreductase.

Roman, D.G.; Dancis, A.; Anderson, G.J.; Klausner, R.D.
Cell Biol. and Metab. Branch, Natl. Inst. Child Health and Hum. Dev.,
Bethesda, MD 20892, USA

MOL. CELL. BIOL. vol. 13, no. 7, pp. 4342-4350 (1993.)

ISSN: 0270-7306

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH

SUBFILE: Microbiology Abstracts Section C: Algology, Mycology and
Protozoology; Biochemistry Abstracts Part 2: Nucleic Acids; Genetics
Abstracts

We have identified a cell surface **ferric reductase** activity in the fission yeast *Schizosaccharomyces pombe*. A mutant strain deficient in this activity was also deficient in ferric iron uptake, while ferrous iron uptake was not impaired. We have cloned *frp1* super(+), the wild-type allele of the mutant gene. *frp1* super(+) mRNA levels were repressed by iron addition to the growth medium. Fusion of 138 nucleotides of *frp1* super(+) promoter sequences to a reporter gene, the bacterial chloramphenicol acetyltransferase gene, conferred iron-dependent regulation upon the latter when introduced into *S. pombe*. The predicted amino acid sequence of the *frp1* super(+) gene exhibits hydrophobic regions compatible with transmembrane domains. It shows similarity to the *Saccharomyces cerevisiae* FRE1 gene product and the gp91-phox protein, a component of the human NADPH phagocyte oxidoreductase that is deficient in X-linked chronic granulomatous disease.

6/3,AB/137 (Item 5 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
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01556589 2676455

Fe super(3+)-chelate reductase activity of plasma membranes isolated from tomato (*Lycopersicon esculentum* Mill.) roots. Comparison of enzymes from Fe-deficient and Fe-sufficient roots.

Holden, M.J.; Luster, D.G.; Chaney, R.L.; Buckhout, T.J.; Robinson, C.
U.S. Dep. Agric., Agric. Res. Serv., Foreign Dis. - Weed Sci. Res. Unit,
Ft. Detrick, Frederick, MD 21702, USA

PLANT PHYSIOL. vol. 97, no. 2, pp. 537-544 (1991.)

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH

SUBFILE: Biochemistry Abstracts Part 1: Biological Membranes

Reduction of Fe super(3+) to Fe super(2+) is a prerequisite for Fe uptake by tomato roots. **Ferric chelate reductase** activity in plasma membranes isolated from roots of both iron-sufficient (+Fe) and iron-deficient (-Fe) tomatoes (*Lycopersicon esculentum* Mill.) was measured as NADH-dependent ferric citrate reductase and exhibited simple Michaelis-Menten kinetics for the substrates, NADH and Fe super(3+) (citrate super(3-)) sub(2). NADH and Fe super(3+) (citrate super(3-)) sub(2) K sub(m) values for reductase in PM from +Fe and -Fe tomato roots were similar, whereas V sub(max) values were two- to threefold higher for reductase from -Fe tomatoes.

6/3,AB/138 (Item 6 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
(c) 2002 Cambridge Sci Abs. All rts. reserv.

01295231 2102321

Ferric reductase activity in *Azotobacter vinelandii* and its inhibition by Zn super(2+).

Huyer, M.; Page, W.J.
Dep. Microbiol., Univ. Alberta, Edmonton, Alta. T6G 2E9, Canada
J. BACTERIOL. vol. 171, no. 7, pp. 4031-4037 (1989.)
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Microbiology Abstracts Section B: Bacteriology

Ferric reductase activity was examined in *Azotobacter vinelandii* and was found to be located in the cytoplasm. The specific activities of soluble cell extracts were not affected by the iron concentration of the growth medium however, activity was inhibited by the presence of Zn super(2+) during cell growth and also by the addition of Zn super(2+) to the enzyme assays. Intracellular Fe super(2+) levels were lower and siderophore production was increased in Zn super(2+)-grown cells. The **ferric reductase** was active under the aerobic conditions, had an optimal pH of approximately 7.5, and required flavin mononucleotide and Mg super(2+) for maximum activity. These results suggested that **ferric reductase** activity may have a regulatory role in the processes of iron assimilation in *A. vinelandii*.

6/3,AB/139 (Item 1 from file: 94)
DIALOG(R)File 94:JICST-EPlus
(c)2002 Japan Science and Tech Corp(JST). All rts. reserv.

02423060 JICST ACCESSION NUMBER: 96A0461174 FILE SEGMENT: PreJICST-E
Induction of **ferric reductase** activity of green alga

Chlorococcum littorale in high CO2 and ferrous ion deficient conditions.

SASAKI TAKAYUKI (1); KURANO NORIHIDE (1); MIYAJI SHIGEO (1)
(1) Kaiyobaiotekunorojikenkyusho
Nippon Shokubutsu Seiri Gakkai Nenkai oyobi Shinpojiumu Koen Yoshishu,
1996, VOL.36th(1996), PAGE.153
JOURNAL NUMBER: L1736AAU
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Conference Proceeding
MEDIA TYPE: Printed Publication

6/3,AB/140 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal
(c) 2002 INIST/CNRS. All rts. reserv.

13460125 PASCAL No.: 98-0155813

Contribution a l'etude du mecanisme d'acquisition du fer chez *Listeria monocytogenes* : role des catechols et des catecholamines
(Iron acquisition mechanism in *Listeria monocytogenes* : role of catechol and catecholamines)

COULANGES Valerie; VIDON Dominique, dir

Universite de Strasbourg 1, Strasbourg, Francee

Univ.: Universite de Strasbourg 1. Strasbourg. FRA Degree: Th. doct.

1997-09; 1997 24 p.

Language: French Summary Language: French; English

Listeria monocytogenes est un pathogene opportuniste ayant besoin de fer pour sa croissance et sa virulence. *L. monocytogenes* ne produit pas de siderophore mais est capable d'utiliser certains siderophores exogenes d'origine bacterienne ou fongique, ainsi qu'un grand nombre de substances naturelles a noyau catechol, pour reserver l'effet inhibiteur provoque par la tropolone et la 8-hydroxyquinoline, deux chelateurs du fer. L'esculine peut etre hydrolysee par *L. monocytogenes* en liberant la fraction aglycone a structure o-diphenol, l'esculetine. Celle-ci neutralise in vitro l'inhibition de croissance induite par les chelateurs du fer. De plus, l'injection d'esculetine augmente, de maniere dose-dependante, le taux de mortalite et l'invasion de la rate chez la souris infectee par des doses subletales de *L. monocytogenes*. L'esculetine agit donc comme un siderophore pour *L. monocytogenes* in vivo, chez la souris. D'autre part, les catecholamines levent aussi l'inhibition de croissance de *L. monocytogenes* induite par la tropolone ou l'hydroxyquinoline, quelque soit le stereoisomere utilise. En outre, la noradrenaline potentialise l'effet stimulateur de croissance induit par la transferrine dans un milieu deplete en fer. Enfin, la dopamine et la noradrenaline permettent l'incorporation de $5 \text{ } ^{55}\text{Fe}$ par des bacteries carencees en fer par un processus exigeant de l'energie. La captation du fer ainsi que l'activite reductasique de la bacterie sont inhibees par PtCl_2 . Les catecholamines semblent fonctionner comme des siderophores grace a leur fonction ortho-diphenol. L'acquisition du fer ne parait pas impliquer de recepteurs specifiques aux catecholamines mais une reductase ferrique membranaire.

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6/3,AB/141 (Item 2 from file: 144)
DIALOG(R) File 144:Pascal
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13165319 PASCAL No.: 97-0427080

The NADH-dependent Fe SUP 3 SUP + -chelate reductases of tomato roots

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Journal: Planta, 1997, 202 (4) 427-434

Language: English

The NADH-dependent Fe SUP 3 SUP + -chelate reductase (NFCHR) of tomato (*Lycopersicon esculentum* L.) roots, a strategy I species, was investigated. The Fe SUP 3 SUP + -citrate reductase (FeCitR) assay was strongly inhibited by p-hydroxymercuribenzoic acid (PHMB); moreover, the inhibitor was found to be more specific to the FeCitR assay than to the Fe SUP 3 SUP + -EDTA reductase assay, which was catalyzed by at least another reductase of 46 kDa. After high-speed centrifugation of tomato root membranes, high FeCitR activities were detected in pellets and lower activities in supernatants. After two-phase partitioning of microsomes, FeCitR activity (91 nmol min SUP - SUP 1 . mg SUP - SUP 1) was less active in the upper phase (plasma membrane) than in the lower phase (277 nmol min SUP - SUP 1 . mg SUP - SUP 1). However, only the activity of the plasma-membrane-associated NFCHR (FeCitR) was significantly enhanced (2.6-fold) in iron-deficient tomato plants, whereas that of NFCHR in non-plasma-membrane rich fractions was

unaffected by this treatment. The NFCHR obtained from lysophosphatidylcholine-solubilized plasma membrane was present as a 200-kDa protein complex following fast protein liquid chromatography on Superdex 200, or as a 28-kDa form following Blue Sepharose CL-6B chromatography. Both preparations were more active following iron starvation. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis showed that the 28-kDa protein purified from solubilized tomato microsomes or supernatant fractions by a final Mono Q step consisted of a single band of 32 kDa. Tomato root NFCHR resembled the NFCHR of maize (a strategy II plant, P Bagnaresi and P Pupillo, 1995, J Exp Bot 46: 1497-1503) in several properties: relative molecular mass, hydrophilicity, chromatographic behaviour, sensitivity to mercurials, specificity for electron donors and acceptors (e.g. cytochrome c), and a ferricyanide reductase-to-FeCitR ratio of 2.5. Preincubation with NADH partially protected NFCHR from PHMB-induced inactivation. Our data show that strategy I and II plants seem to share similar NFCHR proteins, which appear to belong to the cytochrome b SUB 5 reductase flavoprotein group.

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6/3,AB/142 (Item 3 from file: 144)
DIALOG(R)File 144:Pascal
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12825541 PASCAL No.: 97-0042393
Trans-plasma membrane reduction of Fe SUP 3 SUP + -EDTA or hexachloroiridate IV by cultured cells of *Acer pseudoplatanus* L. induces an ethylene response

MALERBA M; BIANCHETTI R
Centro di Studio del C.N.R. per la Biologia Cellulare e Molecolare delle Piante, Dipartimento di Biologia, Sezione Botanica Generale, Universita degli Studi di Milano, Via Celoria 26, 20133 Milano, Italy

Journal: Journal of plant physiology, 1996, 149 (6) 753-756
Language: English
Addition of Fe SUP 3 SUP + -EDTA or hexachloroiridate IV (HCl), two electron acceptors involving different plasma membrane (PM) reductases, induced ethylene production in sycamore (*Acer pseudoplatanus* L.) cells. Comparison of action curves and time-courses of ethylene response, as well as the difference in superoxide dismutase (SOD, EC 1.15.1.1) sensitivity, indicate that the two compounds induced ethylene through mechanisms at least partially different.

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6/3,AB/143 (Item 4 from file: 144)
DIALOG(R)File 144:Pascal
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12818007 PASCAL No.: 97-0034399
Ferric-reductase activities in whole cells and cell fractions in *Vibrio* (*Listonella*) *anguillarum*

MAZOY R; LEMOS M L
Departamento de Microbiologia y Parasitologia, Facultad de Ciencias, Universidad de Santiago de Compostela, Campus de Lugo, 27002 Lugo, Spain
Journal: Microbiology : (Spencers Wood), 1996, 142 (p.11)
3187-3193

Language: English
The ability of *Vibrio* (*Listonella*) *anguillarum* strains from serotype groups O1 and O2 to reduce Fe SUP 3 SUP + in the form of different chelates was investigated. All strains, grown in M9 minimal medium supplemented with 0.2% Casamino acids, reduced Fe SUP 3 SUP + complexed by citrate, nitrilotriacetic acid and EDTA. In whole cells, the degree of reduction was

dependent on the Fe SUP 3 SUP + ligand and on the strain, with the greatest values corresponding to ferric dicitrate and serotype group O1 strains, respectively. The **ferric-reductase** activity increased, over the basal levels, when the cells were grown with iron added as ferric dicitrate, haemin or haemoglobin. All strains also reduced ferricyanide, a compound that is not transported into the bacterial cells. Ferricyanide reduction was also increased when the cells were grown in the presence of an iron source. All of the cell fractions (periplasm, membranes and cytoplasm) showed Fe SUP 3 SUP + -reducing activity, with the highest values observed in the presence of Mg SUP 2 SUP + , NADH and FAD in the assay buffer. Cytoplasmic **ferric-reductase** could be visualized using native polyacrylamide or starch gel electrophoresis, whereas the periplasmic and membrane reductase(s) could only be detected on starch gels. The results indicate the presence of different **ferric-reductase** activities in *V. onguillarum*, which could be involved in the different iron-acquisition systems present in this micro-organism, i.e. siderophore-mediated systems and siderophore-independent mechanisms.

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6/3,AB/144 (Item 5 from file: 144)
DIALOG(R)File 144:Pascal
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12602565 PASCAL No.: 96-0290027
Ferric chelate reduction by sunflower (*Helianthus annuus* L.) leaves : influence of light, oxygen, iron-deficiency and leaf age
DE LA GUARDIA M D; ALCANTARA E
Department of Agronomy, Escuela T.S. Ingenieros Agronomos y de Montes, University of Cordoba, Apdo. 3048, 14080 Cordoba, Spain
Journal: Journal of experimental botany, 1996, 47 (298) 669-676 (7 p.)

Language: English
The presence of ferric chelate reducing activity in sunflower (*Helianthus annuus* L.) leaves has been studied by submerging leaf discs in a solution with Fe(III)-ethylenediaminetetra-acetate (FeEDTA), bathophenanthroline disulphonate (BPDS) and vacuum infiltration. The effect of different factors on the Fe(III) reduction rate was studied. Ferric reduction rate was about 10-fold higher in the light than in darkness. The light effect was greatly inhibited by 3-(3,4-dichlorophenyl)-1,1-dimethylurea (DCMU), a photosystem II inhibitor. Several inhibitors of redox systems (cis-platinum (II) diamine dichloride (cis-platin), p-nitrophenylacetate (p-NPA) and p-hydroxymercuribenzoic acid (pHMB)) decreased the FeEDTA reduction rate. The greatest inhibition was produced by the -SH group reagent pHMB (17% of control, in light). The FeEDTA reduction rate was much higher in the absence of O SUB 2 than with air or 100% O SUB 2 . Superoxide dismutase (SOD) decreased FeEDTA reduction with air in the light. Young leaves reduced Fe(III)-chelate at a higher rate than did older leaves. In iron-deficient plants, leaves did not exhibit enhanced ferric chelate-reducing activity as was observed in roots. It is suggested that at least two different redox systems or two states of the same redox system work in the light and in darkness.

6/3,AB/145 (Item 6 from file: 144)
DIALOG(R)File 144:Pascal
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12351511 PASCAL No.: 95-0593913
Characterization of NADH-dependent Fe SUP 3 SUP + -chelate reductases of maize roots
BAGNARESI P; PUPILLO P
Univ. Bologna, dip. biologia, 40126 Bologna, Italy

Journal: Journal of experimental botany, 1995, 46 (291) 1497-1503

Language: English

iron-deficient maize seedlings exhibit a starvation syndrome characterized by an increase in different parameters such as root fresh weight (+30%), protein -25%) and plasma membrane-associated NADH Fe SUP 3 SUP - -EDTA reductase (NFR; +45%). NFR activity was found associated with 9000 g (20 min) and 110000 g 1 h) sediments, purified plasma membrane and 110000 g supernatants. No differences were observed between the properties of reductases from Fe-starved versus Fe-sufficient roots. The characterization of NFR was undertaken. Low M SUB r forms (46 and 28 kDa, as detected by size-exclusion chromatography) were present in all fractions whereas 210 and 110 kDa forms were unique in membranes and 110000 g supernatants respectively. The 210 kDa form was solubilized from microsomes and characterized. The enzyme is acetone-resistant and appears to be comprised largely if not totally of the low M SUB r forms (46 and 28 kDa, corresponding to 30 and 32kDa bands, respectively, in SDS-PAGE). The 210 kDa form tended to break down to subunits follow-mg dilution, and the effect could be prevented by addition of 10% (v/v) glycerol. A three-step purification procedure for microsomal NFR was devised, consisting of acetone fractionation of lysophosphatidylcholine solubilized microsomes, Blue Sepharose CL-6B affinity chromatography and a final size exclusion chromatography in the absence of detergent, resulting in a 700-fold purification of the 28 kDa protein. The best electron acceptor for the purified 28 kDa form was ferricyanide (400 mu mol min SUP - SUP 1 mg SUP - SUP 1 protein) followed by Fe SUP 3 SUP - -chelates (up to 200 mu mol min SUP - SUP 1 mg SUP - SUP 1 protein) and other compounds to a lesser extent (cyt c, DCPIP). The 46 kDa form, on the other hand, had high ferricyanide reductase activity (about 300 mu mol min SUP - SUP 1 mg SUP - SUP 1 protein) and relatively low Fe SUP 3 SUP + -chelate reductase activity. The properties of NFR (high M SUB r active forms, dono

6/3,AB/146 (Item 7 from file: 144)

DIALOG(R) File 144:Pascal

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12135117 PASCAL No.: 95-0367329

Mechanisms of Fe-efficiency in roots of Vitis spp. in response to iron deficiency stress

BRANCADORO L; RABOTTI G; SCIENZA A; ZOCCHI G

Univ. Milan, ist. coltivazioni arboree, 20133 Milano, Italy

Journal: Plant and soil, 1995, 171 (2) 229-234

Language: English

Iron chlorosis induced by Fe-deficiency is a widespread nutritional disorder in many woody plants and in particular in grapevine. This phenomenon results from different environmental, nutritional and varietal factors. Strategy I plants respond to Fe-deficiency by inducing physiological and biochemical modifications in order to increase Fe uptake. Among these, acidification of the rhizosphere, membrane redox activities and synthesis of organic acids are greatly enhanced during Fe-deficiency. Grapevine is a strategy I plant but the knowledge on the physiological and biochemical responses to this iron stress deficiency in this plant is still very poor. In this work four different genotypes of grapevine were assayed for these parameters. It was found that there is a good correlation between genotypes which are known to be chlorosis-resistant and increase in both rhizosphere acidification and Fe SUP I SUP I SUP I reductase activity. In particular, when grown in the absence of iron, Vitis berlandieri and Vitis vinifera cv Cabernet sauvignon and cv Pinot blanc show a higher capacity to acidify the culture medium (pH was decreased by 2 units), a higher concentration of organic acids, a higher resting transmembrane electrical potential and a greater capacity to reduce Fe SUP I SUP I SUP I -chelates. On the contrary, Vitis riparia, well known for its susceptibility to iron chlorosis, fails to decrease the pH of the medium and shows a lower concentration in organic acids, lower capacity to reduce Fe SUP I SUP I SUP I

I and no difference in the resting transmembrane electrical potential.

6/3,AB/147 (Item 8 from file: 144)
DIALOG(R)File 144:Pascal
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11950531 PASCAL No.: 95-0130079
Effects of heavy metals on both induction and function of root Fe(III)
reductase in Fe-deficient cucumber (*Cucumis sativus* L.) plants
ALCANTARA E; ROMERA F J; CANETE M; DE LA GUARDIA M D
Univ. Cordoba, escuela T.S. ing. agronomos Montes, Cordoba 14080, Spain
Journal: Journal of experimental botany, 1994, 45 (281) 1893-1898
Language: English
Heavy metals are known to induce Fe chlorosis in different plant species.
Heavy-metal-induced chlorosis is generally correlated with low plant Fe
contents, suggesting effects of heavy metals on Fe mobilization and uptake.
Under Fe-deficient conditions, dicotyledonous plants enhance root Fe(III)
reductase activity, thus increasing the capacity to reduce Fe(III) to
Fe(II), the form in which roots absorb Fe. We studied the effect of several
heavy metals (Mn, Pb, Zn, Mo, Ni, Cu, and Cd) on the induction of enhanced
root Fe(III) reductase by 11 -d-old Fe-deficient cucumber (*Cucumis sativus*
L. cv. Ashley). The effect of these heavy metals on the function of the
induced Fe(III) reductase was also investigated. Results showed that some
heavy metals can inhibit both the induction and function of root Fe(III)
reductase. Ni, at 20 μ M, and Cu and Cd, at 5 μ M concentration or
higher, severely inhibited the induction of root Fe(III) reductase while
Mn, Pb, Zn, and Mo had little effect, even at concentrations higher than 20
 μ M. Function of the induced root Fe(III) reductase only was negatively
affected by Cu and Ni

6/3,AB/148 (Item 9 from file: 144)
DIALOG(R)File 144:Pascal
(c) 2002 INIST/CNRS. All rts. reserv.

11019851 PASCAL No.: 93-0529357
Reduction of ferric ion by *Listeria monocytogenes* and other species of
Listeria
DENEER H G; BOYCHUK I
Univ. Saskatchewan, dep. microbiology, Saskatoon SK S7N 0W0, Canada
Journal: Canadian journal of microbiology, 1993, 39 (5) 480-485
Language: English Summary Language: French

6/3,AB/149 (Item 10 from file: 144)
DIALOG(R)File 144:Pascal
(c) 2002 INIST/CNRS. All rts. reserv.

07198111 PASCAL No.: 86-0086863
Regulated redox processes at the plasmalemma of plant root cells and
their function in iron uptake
BIENFAIT H F
Univ. Amsterdam, plant physiology dep., Amsterdam SM 1098, Netherlands
Journal: Journal of bioenergetics and biomembranes, 1985, 17 (2)
73-83
Language: ENGLISH

6/3,AB/150 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res
(c) 2002 Thomson Derwent & ISI. All rts. reserv.

0171771 DBA Accession No.: 94-14322

Isolation, purification, and further characterization of an
L-phenylalanine-oxidase from *Morganella morganii* - L-amino-acid-oxidase
isolation and properties

AUTHOR: Bouvrette P; +Luong J H T

CORPORATE AFFILIATE: Biotechnol.Res.Inst.Montreal Nat.Res.Counc.Canada

CORPORATE SOURCE: Biotechnology Research Institute, National Research
Council Canada, Montreal, Quebec, Canada H4P 2R2.

JOURNAL: Appl.Biochem.Biotechnol. (48, 2, 61-74) 1994

CODEN: ABIBDL

LANGUAGE: English

ABSTRACT: The production of an L-amino-acid-oxidase (EC-1.4.3.2) by
Morganella morganii 53187 (formerly *Proteus morganii*) was
growth-associated and decreased sharply as the culture reached the
stationary phase. Based on this finding, the preparation of
spheroplasts by lysozyme (EC-3.2.1.17)-EDTA disruption was performed
using cells harvested during the exponential growth phase. CHAPS, at
the surfactant to protein ratio of 2.5, was very effective in
solubilizing most of the enzyme attached to the membranes while
preserving the activity of the solubilized enzyme. The resulting enzyme
was purified by hydrophobic interaction chromatography on
Phenyl-Sepharose CL-4B, ionexchange chromatography on DEAE-Sephacel and
gel filtration on Sephacryl S-200 HR. The enzyme was purified 19-fold
in a yield of 12% (specific activity 252.2 U/mg protein). The
selectivity of the purified enzyme toward L-amino acids was
pH-dependent. At pH 6.35, the enzyme was very specific to L-leucine,
but selectivity for L-phenylalanine was improved at pH 7.4. The optimum
temp. was 35-43 deg. 1,1'-**Dimethylferricinium-reductase**
activity was detected in the presence of L-Phe. (24 ref)

6/3,AB/151 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res
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0156116 DBA Accession No.: 93-14168

Effects of O₂ on metal-reductase activity and cytochrome content in a
facultative Fe(III)-reducing bacterium - **ferric-reductase**
activity and effect on iron, uranium or cobalt heavy metal recovery
from e.g. waste-water (conference abstract)

AUTHOR: Gorby Y A; Bolton Jr H

CORPORATE SOURCE: Pacific Northwest Laboratory, P.O. Box 999, Richland, WA
99352, USA.

JOURNAL: Abstr.Gen.Meet.Am.Soc.Microbiol. (93 Meet., 368) 1993

CODEN: 0005P

LANGUAGE: English

ABSTRACT: With the onset of anoxic conditions, Fe(III) is the most abundant
electron acceptor available for microbial growth in many sediment
environments. The Fe(III)-reducing facultatively anaerobic bacterium
BrY was analyzed for **ferric-reductase** activity and
cytochrome content over a range of dissolved oxygen tension (DOT)
values. Cells grown in continuous culture at saturated DOT expressed no
ferric-reductase activity in anaerobic assays, nor did they
produce detectable levels of cytochrome-c. Additionally, these cells
were unable to reduce uranium (VI) and cobalt (III)-EDTA. **Ferric-**
reductase activity and cytochrome-c production were induced in
cells cultured with DOT at levels below that of air saturation. The
cells cultured with depressed DOT also reduced U(VI) and Co(III)-EDTA.
Results showed that enzymes involved in dissimilatory Fe(III) and metal
reduction, which may involve cytochrome-c, were induced by depressed O₂
concentrations. This information is vital for optimizing growth
conditions for metal-reducing bacteria for remediation of waste-water
contaminated with heavy metals and radionuclides. (0 ref)

6/3,AB/152 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res
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0001420 DBA Accession No.: 82-00420 PATENT
D-Fructose-dehydrogenase (D-fructose;**ferricytochrome
oxydoreductase**) a new enzyme - derived from Acetobacter spp.;
Gluconobacter cerinus Gluconobacter industirus and Acetobacter xylinus
PATENT ASSIGNEE: Minoru-Ameyama 1982
PATENT NUMBER: JP 57063085 PATENT DATE: 820416 WPI ACCESSION NO.:
82-46651E (4623)
PRIORITY APPLIC. NO.: JP 80139165 APPLIC. DATE: 801004
NATIONAL APPLIC. NO.: JP 80139165 APPLIC. DATE: 801004
LANGUAGE: Japanese
ABSTRACT: D-Fructose;**ferricytochrome oxydoreductase** derived
from Acetobacter spp. (for example Gluconobacter cerinus IFO-3268,
Acetobacter xylinus IFO-3288) belongs to the enzyme classification EC
1.1.2.-. Optimal conditions for the enzyme activity were pH 4.5 and
temperature 20-25 deg. The Km is 0.01 mol. Gluconobacter industrius was
cultivated at pH 6.0-6.5 and 30 deg in stirred culture for 20 hr under
aeration. The cells were centrifuged, disrupted in a french press and
suspended in McIlvaine buffer. The suspension was ultracentrifuged and
then applied to a DEAE-cellulose column equilibrated with McIlvaine's
buffer at pH6. The pH of the buffer applied was continuously decreased
to obtain active fractions (300 ml) at about pH 5.2. The enzyme
solution was concentrated with a membrane filter (Toyo UP-50) against
polyethylene glycol 6000. The solution was then applied to a
hydroxyapatite column, followed by dialysis and centrifugation.
D-fructose;**ferricytochrome oxydoreductase** with 172 U/mg
activity was obtained. (7 pp)

times the messenger RNA (mRNA) content of Tetrahymena was the result of a self-regulating equilibrium between synthesis and decay. The rates of transcription and of degradation of mRNA and ribosomal RNA (rRNA) were found to be controlled independently, but decay was dominant in establishing the growth-specific quantities per cell. In the stationary phase about 94% of all poly(A)-RNA molecules and about 50% of all mRNA molecules were kinetically silent. The remaining portions were transcribed with high rates, but also degraded immediately. During the culture growth cycle the rate of rRNA net growth responded positively to the cellular rRNA content suggesting an autocatalytic effect of rRNA on the rate of its accumulation.

3/3,AB/12 (Item 12 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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04098256 83091061 PMID: 6294661

Extensive intragenic sequence homology in two distinct rat lens gamma-crystallin cDNAs suggests duplications of a primordial gene.

Moormann R J; den Dunnen J T; Bloemendal H; Schoenmakers J G

Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Nov 1982, 79 (22) p6876-80, ISSN

0027-8424 Journal Code: 7505876

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The nucleotide sequences of two different rat lens gamma-crystallin cDNA clones, pRL gamma 2 and pRL gamma 3, have been determined. pRL gamma 3 contains the complete coding information for a gamma-crystallin of 173 amino acids whereas pRL gamma 2 is incomplete in that it lacks the codons for the first three amino acids of a separate but very homologous gamma-crystallin of identical length. Both rat gamma-crystallins are homologous to the known amino acid sequence of bovine gamma-crystallin II which is only a single amino acid longer. The length of the region downstream the coding sequence to the A-A-T-A-A-A polyadenylation signal sequence is 40 nucleotides in each clone. In pRL gamma 3 the poly(A) signal sequence is followed at 14 nucleotides by a remnant of the poly(A) tail which indicates that this clone contains a complete 3' noncoding region. pRL gamma 2 has only seven nucleotides following this signal sequence and no poly(A) tail, suggesting an incomplete 3' end. The cDNA clones show an overall nucleotide sequence homology of 85%. The mutual homology at the amino acid level is 73% whereas their amino acid homology with bovine gamma-crystallin II is about 70%. The nucleotide sequence of each clone also reveals a high intragenic homology and seems to be duplicated in itself. We suggest that the gamma-crystallin genes have arisen by multiple duplications of a primordial gene which consisted of about 120 nucleotides.

3/3,AB/13 (Item 13 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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03511831 81063243 PMID: 6776990

Template-independent poly(A) x poly(U) synthesizing activity of different forms of Bacillus subtilis RNA polymerase.

Dooley M M; Halling S M; Doi R H

Biochimica et biophysica acta (NETHERLANDS) Nov 14 1980, 610

(1) p158-66, ISSN 0006-3002 Journal Code: 0217513

Contract/Grant No.: GM 05209; GM; NIGMS; GM 19673; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Several, but not all, forms of bacillus subtilis RNA polymerase found in vegetative and sporulating cells can synthesize poly(A) x poly(U) in vitro. The vegetative delta-containing form of RNA polymerase (E delta) has little or **no poly(A) x poly(U)**-synthesizing activity, whereas RNA polymerase core (E) and sigma-containing core (E delta) both have significant activity. When purified vegetative delta factor was added to core, the core synthetic activity was reduced essentially to that of the vegetative enzyme E delta. When E sigma enzymes from vegetative and sporulating cells were compared for their salt sensitivity, it was found that the sporulation enzyme E sigma retained much more of its activity at 0.1 M KCl than the vegetative enzyme E sigma. Furthermore, when sporulation enzyme E delta 1 was compared with vegetative enzyme E sigma, it was found that the activity of the E sigma 1 form was much more resistant to high KCl concentrations than that of the vegetative E sigma form. These differences in enzyme activity, as affected by salt concentrations, suggest that the conformations of the sporulation E sigma and E delta 1 enzymes are different from that found in vegetative E sigma enzyme. These differences in conformation may be involved in selective **gene** expression during sporulation.

3/3,AB/14 (Item 14 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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03296961 80112883 PMID: 527589

HeLa cell cytoplasmic **mRNA** contains three classes of sequences: predominantly poly(A)-free, predominantly poly(A)-containing and bimorphic.

Milcarek C

European journal of biochemistry / FEBS (GERMANY, WEST) Dec 17 1979, 102 (2) p467-76, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The **mRNA** species which exist in the HeLa cell polyribisomes in a form devoid of A sequences longer than 8 nucleotides constitute the poly(A)-free class of **mRNA**. The rapidly labelled component of this **mRNA** class shares no measurable sequence homology with poly(A)-containing RNA. If poly(A)-free **mRNA** larger than 12 S labelled for 2 h in vivo is hybridized with total cellular DNA, it hybridizes primarily with single-copy DNA. When a large excess of steady poly(A)-containing RNA is added before hybridization of labelled poly(A)-free RNA, no inhibition of hybridization occurs. This indicates the existence of a class of poly(A)-free **mRNA** with **no poly(A)**-containing counterpart. Some **mRNA** species can exist solely as poly(A)-containing mRNAs. These mRNAs in HeLa cells are found almost exclusively in the **mRNA** species present only a few times per cell (scarce sequences). Some **mRNA** species can exist in two forms, poly(A)containing and lacking, as evidenced by the translation data in vitro of Kaufmann et al. [Proc. Natl Acad. Sci. U.S.A. 74, 4801--4805 (1977)]. In addition, if cDNA to total poly(A)-containing **mRNA** is fractionated into abundant and scarce classes, 47% of the scarce class cDNA can be readily hybridized with poly(A)-free **mRNA**. 10% of the abundant cDNA to poly(A)-containing **mRNA** will hybridize with poly(A)-free sequences very rapidly while the other 90% hybridize 160 times more slowly, indicating two very different frequency distributions. The cytoplasmic metabolism of these three distinct **mRNA** classes is discussed.

3/3,AB/15 (Item 15 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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02997851 79062391 PMID: 718932

The synthesis and degradation of presumptive messenger RNA in cultured mouse leukemia cells during the inhibition of protein synthesis.

Takenaka K; Endo H; Kuwano M

Biochimica et biophysica acta (NETHERLANDS) Nov 21 1978, 521

(1) p295-307, ISSN 0006-3002 Journal Code: 0217513

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

RNA synthesis in mouse leukemia L5178Y cells was inhibited depending upon the time of treatment by blasticidin S or by ricin, which inhibits specifically protein synthesis. When blasticidin S or ricin blocked protein synthesis by more than 90% of the control, marked accumulation of monosome was accompanied by the decrease of pulse-labeled RNA (20% of that in the control) in the polysomes and monosome fraction. The size distribution of pulse-labeled RNA among polysomal fractions including monosome obtained from the cells treated with either blasticidin S, ricin or L-asparaginase showed that the size of presumptive mRNA was shifted from 18 S to 9--10 S. Treatment of a blasticidin S-resistant (Bla-R) subline derived from L5178Y cells (Kuwano, M., Matsui, K., Takenaka, K., Akiyama, S. and Endo, H. (1977) Int. J. Cancer 20, 296--302) with L-asparaginase or ricin induced smaller size (9--10 S) RNA, but treatment of Bla-R cells with blasticidin S did not. Such shorter RNA fragments could not be observed even when cellular protein synthesis was inhibited by treatment for short time with blasticidin S (40--80% of the control activity). Smaller RNA fragments accumulated after drastic inhibition of protein synthesis were composed of 74% of polyadenylate sequence lacking poly(A)(-)RNA with peak of approx. 10 S and 26% of polyadenylate sequence containing poly(A)(+)RNA with a peak of 18 S, whereas cytoplasmic polysomal RNA of the control contained 46% poly(A)(+) with a peak of 18 S and 54% poly(A)(-)RNA with a 10--18 S peak. Cytoplasmic poly(A)(+)RNA degraded biphasically with half-lives of approx. 2 h and 8--10 h in exponentially growing mouse cells. However, in degradation of poly(A)(+)RNA molecules being formed in the cells pretreated with blasticidin S for 3 h, the rapid phase of decay with a half-life of approx. 2 h was interrupted by successively appearing poly(A)(+)RNA with a longer half-life of 8--10 h in cytoplasm. However, when the cells were pretreated with blasticidin S for 6 h, there appeared no poly(A)(+)RNA population with the rapid-decay in cytoplasm.

3/3,AB/16 (Item 16 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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02977341 79045342 PMID: 710438

Message sequences are not adjacent to poly(A) in heterogeneous nuclear RNA of Friend leukemic cells.

Mackedonski V V; McConkey E H

European journal of biochemistry / FEBS (GERMANY, WEST) Oct 1978,

90 (2) p397-404, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Hybridization of labeled RNA with excess amounts of unlabeled complementary DNA (cDNA) was used to investigate the location of cytoplasmic mRNA sequences in heterogeneous nuclear RNA (hnRNA) of noninduced Friend leukemic cells. A heterologous hybrid between hnRNA and cytoplasmic cDNA was formed. Two homologous hybrids were also formed, one between poly(A)-containing mRNA and cytoplasmic cDNA, and the other

between poly-(A)-containing hnRNA and nuclear cDNA. All hybrids were selected on hydroxyapatite columns after RNase treatment. The hybrids were further investigated for the presence of poly(A). **No poly(A)** was found in the heterologous hybrid, while both homologous hybrids contained poly(A). From these results we conclude that there exists a spacer nucleotide sequence between the poly(A) and the message sequences in hnRNA.

3/3,AB/17 (Item 17 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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02609647 77187706 PMID: 140861

Characterization and in vitro translation of polyadenylated messenger ribonucleic acid from *Neurospora crassa*.

Lucas M C; Jacobson J W; Giles N H

Journal of bacteriology (UNITED STATES) Jun 1977, 130 (3)
p1192-8, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Ribonucleic acid (RNA) extracted from *Neurospora crassa* has been fractionated by oligodeoxythymidylic acid [oligo(dT)]-cellulose chromatography into polyadenylated messenger RNA [poly(A) mRNA] and unbound RNA. The poly(A) mRNA, which comprises approximately 1.7% of the total cellular RNA, was further characterized by Sepharose 4B chromatography and polyacrylamide gel electrophoresis. Both techniques showed that the poly(A) mRNA was heterodisperse in size, with an average molecular weight similar to that of 17S ribosomal RNA (rRNA). The poly(A) segments isolated from the poly(A) mRNA were relatively short, with three major size classes of 30, 55, and 70 nucleotides. Gel electrophoresis of the non-poly(A) RNA indicated that it contained primarily rRNA and 4S RNA. The optimal conditions were determined for the translation of *Neurospora* mRNA in a cell-free wheat germ protein-synthesizing system. Poly(A) mRNA stimulated the incorporation of [14C]leucine into polypeptides ranging in size from 10,000 to 100,000 daltons. The RNA that did not bind to oligo(dT)-cellulose also stimulated the incorporation of [14C]leucine, indicating that this fraction contains a significant concentration of mRNA which has either **no poly(A)** or very short poly(A) segments. In addition, the translation of both poly(A) mRNA and unbound mRNA was inhibited by 7-methylguanosine-5'-monophosphate (m7G5'p). This is preliminary evidence for the existence of a 5'-RNA "cap" on *Neurospora* mRNA.

3/3,AB/18 (Item 18 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

02181531 76022384 PMID: 1236796

Thyroglobulin messenger RNA: translation of a 33-S mRNA into a peptide immunologically related to thyroglobulin.

Vassart G; Brocas H; Lecocq R; Dumont J E

European journal of biochemistry / FEBS (GERMANY, WEST) Jun 16 1975, 55 (1) p15-22, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Poly(UC)--Sepharose chromatography of the RNA extracted from a thyroid fraction sedimenting between 800 X g and 27000 X g allows the purification

of two RNA fractions amounting each to 1% of the applied material. The first one is loosely bound to the column from which it is eluted at 25 degrees C. It is mainly composed of 16-S and 12-S RNA comprising **no poly(A)** sequences. This could correspond to mitochondrial rRNA. The second one, which is eluted at 50 degrees C, is poly(A)-rich and represents 33-S and 17--18-S RNA species. The 33-S RNA resists heating at 80 degrees C, suggesting that it is composed of one polynucleotide chain. When injected into *Xenopus* oocytes, the 33-S RNA specifically promotes the synthesis of a peptide with an apparent molecular weight of 185000 and an apparent sedimentation coefficient of 10-S. This peptide is immunologically related to thyroglobulin and could represent its main precursor. Under the conditions tested it does not polymerize spontaneously into 19-S thyroglobulin, suggesting that assembly of the molecule could require specific, post-translational alterations of the precursor and/or the presence of additional lighter subunits.

3/3,AB/19 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11023401 BIOSIS NO.: 199799644546
Partial sequence analysis of randomly selected watermelon (*Citrullus lanatus* (Thunb.) Mansf.) cDNA clones.
AUTHOR: Ok Sung Han; Shin Jeong Sheop(a); Chung Young Soo; Kwon Hyok Ji
AUTHOR ADDRESS: (a)Div. Plant Technol., Graduate Sch. Biotechnol., Korea Univ., Seoul 136-701**South Korea
JOURNAL Journal of Plant Biology 40 (1):p1-7 1997
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: An expressed sequence tag (EST) is simply a segment of a sequence over 150 bp from a randomly selected cDNA. EST helps to quickly identify functions of expressed genes and to understand the complexity of **gene** expression with database comparison. Sequencing of random cDNA clones can be applicable to discovery of new genes, mapping of the genome, identification of coding regions in genomic sequences, and antisense method. To accomplish these goals, in this research, randomly selected cDNA sequencing was performed with watermelon plant. Among 30 clones picked up and analyzed, all clones had an insert length over 0.5 kb. The average size of insert was about 1.3 kb. The size range of most cDNA insert was 1.0-2.0 kb. For sequence comparison, data from the coding region at 5' end of selected cDNA should be much more informative than those from the untranslated 3' tail. Thirty clones were sequenced from one end (5' end). Of these 29 had no poly (A) tail in this direction, while only one was inverted. Thus, this library is over 96% unidirectional. Two clones had homologies to ribulose biphosphate carboxylase/oxygenase (Rubisco) small subunit precursor **gene**. Thirteen cDNAs had high degree of sequence similarity to genes from other organisms. The remaining cDNA clones seem to be new genes not only in watermelon but also in all organisms.

1997

3/3,AB/20 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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03955607 BIOSIS NO.: 000076041173
A POPULATION KINETIC APPROACH TO RNA FORMATION AND DEGRADATION IN GROWING AND RESTING CELLS
AUTHOR: JAUKE F; RINALDY A R
AUTHOR ADDRESS: INST. TIERPHYSIOL. JUSTUS LIEBIG-UNIV., D-6300 GIESSEN,

GERMANY.
JOURNAL: EXP CELL RES 143 (1). 1983. 163-174. 1983
FULL JOURNAL NAME: Experimental Cell Research
CODEN: ECREA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Labeled RNA was extracted from growing and stationary cultures of the ciliate Tetrahymena and was separated chromatographically into poly(A)- and **no poly(A)**-containing fractions. A new method was used to derive from the data (cpm/A260, and tD, doubling time of RNA) absolute values of 3 growth terms which fully describe the population kinetics of RNA molecules: the rates of transcription, decay and net growth. At all times the **mRNA** content of Tetrahymena was the result of a self-regulating equilibrium between synthesis and decay. The rates of transcription and of degradation of **mRNA** and rRNA were found to be controlled independently, but decay was dominant in establishing the growth-specific quantities per cell. In the stationary phase .apprx. 94% of all poly(A)-RNA molecules and .apprx. 50% of all **mRNA** molecules were kinetically silent. The remaining portions were transcribed with high rates, but also degraded immediately. During the culture growth cycle the rate of rRNA net growth responded positively to the cellular rRNA content suggesting an autocatalytic effect of rRNA on the rate of its accumulation.

1983

3/3,AB/21 (Item 3 from file: 5)
DIALOG(R) File 5:Biosis Previews(R)
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03870899 BIOSIS NO.: 000075048972
EXTENSIVE INTRA GENIC SEQUENCE HOMOLOGY IN 2 DISTINCT RAT LENS GAMMA
CRYSTALLIN COMPLEMENTARY DNA SUGGESTS DUPLICATIONS OF A PRIMORDIAL
GENE

AUTHOR: MOORMANN R J M; DEN DUNNEN J T; BLOEMENDAL H; SCHOENMAKERS J G G
AUTHOR ADDRESS: DEP. MOLECULAR BIOL., UNIV. NIJMEGEN, NIJMEGEN, 6525 ED,
NETHERLANDS.

JOURNAL: PROC NATL ACAD SCI U S A 79 (22). 1982. 6876-6880. 1982
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The nucleotide sequences of 2 different rat lens .gamma.-crystallin c[complementary]DNA clones, pRL.gamma.2 and pRL.gamma.3, were determined. pRL.gamma.3 contains the complete coding information for a .gamma.-crystallin of 173 amino acids whereas pRL.gamma.2 is incomplete in that it lacks the codons for the first 3 amino acids of a separate but very homologous .gamma.-crystallin of identical length. Both rat .gamma.-crystallins are homologous to the known amino acid sequence of bovine .gamma.-crystallin II which is only a single amino acid longer. The length of the region downstream the coding sequence to the A-A-T-A-A-A polyadenylation [poly(A)] signal sequence is 40 nucleotides in each clone. In pRL.gamma.3 the poly(A) signal sequence is followed at 14 nucleotides by a remnant of the poly(A) tail which indicates that this clone contains a complete 3' noncoding region. pRL.gamma.2 has only 7 nucleotides following this signal sequence and **no poly(A)** tail, suggesting an incomplete 3' end. The cDNA clones show an overall nucleotide sequence homology of 85%. The mutual homology at the amino acid level is 73% whereas their amino acid homology with bovine .gamma.-crystallin II is about 70%. The nucleotide

sequence of each clone also reveals a high intragenic homology and seems to be duplicated in itself. The .gamma.-crystallin genes may have arisen by multiple duplications of a primordial **gene** which consisted of about 120 nucleotides.

1982

3/3,AB/22 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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03255998 BIOSIS NO.: 000071069109
TEMPLATE INDEPENDENT POLY ADENYLIC-ACID POLY URIDYLIC-ACID SYNTHESIZING
ACTIVITY OF DIFFERENT FORMS OF BACILLUS-SUBTILIS RNA POLYMERASE
AUTHOR: DOOLEY M M; HALLING S M; DOI R H
AUTHOR ADDRESS: DEP. OF BIOCHEM. AND BIOPHYSICS, UNIV. OF CALIF., DAVIS, CA
95616, USA.
JOURNAL: BIOCHIM BIOPHYS ACTA 610 (1). 1980. 158-166. 1980
FULL JOURNAL NAME: Biochimica et Biophysica Acta
CODEN: BBACA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Several, but not all, forms of B. subtilis RNA polymerase found in vegetative and sporulating cells can synthesize poly(A) .cntdot. poly(U) in vitro. The vegetative .delta.-containing form of RNA polymerase (E.delta.) has little or **no poly(A)** .cntdot. poly(U)-synthesizing activity; RNA polymerase core (E) and .sigma.-containing core (E.sigma.) both have significant activity. When purified vegetative .delta. factor was added to core, the core synthetic activity was reduced essentially to that of the vegetative enzyme E.delta.. When E.sigma. enzymes from vegetative and sporulating cells were compared for their salt sensitivity, it was found that the sporulation enzyme E.sigma. retained more of its activity at 0.1 M KCl than the vegetative enzyme E.sigma.. When sporulation enzyme E.delta.1 was compared with vegetative enzyme E.sigma., the activity of the E.delta.1 form was more resistant to high KCl concentration than that of the vegetative E.sigma. form. These differences in enzyme activity, as affected by salt concentrations, suggest that the conformations of the sporulation E.sigma. and E.delta.1 enzymes are different from that found in vegetative E.sigma. enzyme. These differences in conformation may be involved in selective **gene** expression during sporulation.

1980

3/3,AB/23 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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03253338 BIOSIS NO.: 000071066449
RELATIVE DISTRIBUTION OF POST NUCLEAR POLY ADENYLIC-ACID CONTAINING RNA
ABUNDANCE GROUPS WITHIN THE NUCLEAR AND POST NUCLEAR POLY ADENYLATED AND
NONPOLYADENYLATED RNA POPULATIONS OF THE LACTATING GUINEA-PIG MAMMARY
GLAND
AUTHOR: BATHURST I C; CRAIG R K; HERRIES D G; CAMPBELL P N
AUTHOR ADDRESS: COURTAULD INST. BIOCHEM., MIDDX. HOSP. MED. SCH., LONDON
W1P 7PN, UK.
JOURNAL: BIOCHEM J 192 (2). 1980. 489-498. 1980
FULL JOURNAL NAME: Biochemical Journal
CODEN: BIJOA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: RNA isolated from the post-nuclear supernatant of the lactating guinea pig mammary gland was fractionated with oligo(dT)-cellulose into 3 populations; those that bound at low salt [long poly(A) tracts, 78-32 nucleotides]; those that bound at high salt [shorter poly(A) tracts, 48-21 nucleotides]; and those that did not bind [no poly(A) or short poly(A) tracts, < 20 nucleotides]. Nuclear RNA was fractionated into 2 populations, those that bound in low salt and those that did not bind. All the post-nuclear RNA fractions directed the synthesis of milk proteins in a Krebs II ascites cell-free system. 3H-labeled DNA complementary to the post-nuclear poly(A)-containing RNA population (low-salt fraction) was fractionated into abundant (milk-protein mRNA), moderately abundant and scarce sequences. This complementary DNA was then used to investigate the distribution of the mRNA sequences in the different RNA populations. This showed that all sequences were present in polyadenylated and non-polyadenylated fractions, but that major quantitative differences were apparent. The abundant milk protein mRNA sequences predominated in the low salt post-nuclear poly(A)-containing RNA fraction, whereas the moderately abundant sequences predominated in the non-polyadenylated post-nuclear RNA fraction. In total cellular RNA, those sequences deemed initially to be moderately abundant within the low-salt poly(A)-containing RNA population were present at a concentration very similar to those of the abundant milk protein mRNA (.apprx. 6 .times. 10⁵ copies of each sequence/cell). Similarly, analysis of the nuclear RNA populations showed that the abundant and so-called moderately abundant sequences were present in essentially identical concentrations (2 .times. 10³ copies of each sequence/cell). The majority of these (90-95%) were non-polyadenylated. The results are discussed in terms of the post-transcriptional mechanisms involved in the regulation of gene expression in the lactating guinea pig mammary gland.

1980

3/3,AB/24 (Item 6 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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02990555 BIOSIS NO.: 000070016173
 ISOLATION AND CHARACTERIZATION OF POLY ADENYLATED RNA SPECIES FROM
 SPORULATING CELLS OF BACILLUS-SUBTILIS
 AUTHOR: KERJAN P; SZULMAJSTER J
 AUTHOR ADDRESS: LAB. ENZYMOL., CNRS, 91190 GIF-SUR-YVETTE, FR.
 JOURNAL: BIOCHEM BIOPHYS RES COMMUN 93 (1). 1980. 201-208. 1980
 FULL JOURNAL NAME: Biochemical and Biophysical Research Communications
 CODEN: BBRCA
 RECORD TYPE: Abstract
 LANGUAGE: ENGLISH

ABSTRACT: The appearance of a population of polyadenylated RNA during sporulation of B. subtilis is reported. This poly(A) RNA was characterized by hybridization to [3H]poly(U), by its ability to bind oligo (dT)-cellulose and by its resistance to RNases A and T1. Most of the poly(A) sequences are located at the 3' terminus of the RNA chains and are of about 160-180 nucleotides length. Little or no poly(A) RNA was found in vegetative cells or in stationary stage cells of an asporogenic mutant blocked at zero stage of sporulation process. The polyadenylated RNA might play a role in the regulations of gene expression during sporulation.

1980

3/3,AB/25 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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02983647 BIOSIS NO.: 000070009265
HELA CELL CYTOPLASMIC MESSENGER RNA CONTAINS 3 CLASSES OF SEQUENCES
PREDOMINANTLY POLY ADENYLIC-ACID-FREE PREDOMINANTLY POLY ADENYLIC-ACID
CONTAINING AND BIMORPHIC
AUTHOR: MILCAREK C
AUTHOR ADDRESS: DEP. MICROBIOL., COLL. PHYSICIANS SURG., COLUMBIA UNIV.,
701 W. 168TH ST., NEW YORK, N.Y. 10032, USA.
JOURNAL: EUR J BIOCHEM 102 (2). 1979 (RECD. 1980). 467-476. 1979
FULL JOURNAL NAME: European Journal of Biochemistry
CODEN: EJBCA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The mRNA species which exist in the HeLa [human cervical carcinoma] cell polyribosomes in a form devoid of A [adenine] sequences longer than 8 nucleotides constitute the poly(A)-free class of mRNA. The rapidly labeled component of this mRNA class shares no measurable sequence homology with poly(A)-containing RNA. If poly(A)-free mRNA larger than 12 S labeled for 2 h in vivo is hybridized with total cellular DNA, it hybridizes primarily with single-copy DNA. When a large excess of steady poly(A)-containing RNA is added before hybridization of labeled poly(A)-free RNA, no inhibition of hybridization occurs. This indicates the existence of a class of poly(A)-free mRNA with no poly(A)-containing counterpart. Some mRNA species can exist solely as poly(A)-containing mRNA. These mRNA in HeLa cells are found almost exclusively in the mRNA species present only a few times per cell (scarce sequences). Some mRNA species can exist in 2 forms, poly(A)containing and lacking, as evidenced by the translation data in vitro of Kaufmann et al. (1977). If DNA complementary to total poly(A)-containing mRNA is fractionated into abundant and scarce classes, 47% of the scarce class cDNA can be readily hybridized with poly(A)-free mRNA. About 10% of the abundant cDNA to poly(A)-containing mRNA will hybridize with poly(A)-free sequences very rapidly while the other 90% hybridize 160 times more slowly, indicating 2 very different frequency distributions. The cytoplasmic metabolism of these 3 distinct mRNA classes is discussed.

1979

3/3,AB/26 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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02960569 BIOSIS NO.: 000069068687
VIRUS SPECIFIC RNA SYNTHESIS IN CELLS INFECTED BY INFECTIOUS PANCREATIC
NECROSIS VIRUS
AUTHOR: SOMOGYI P; DOBOS P
AUTHOR ADDRESS: DEP. MICROBIOL., COLL. BIOL. SCI., UNIV. GUELPH, GUELPH,
ONT. N1G 2W1, CAN.
JOURNAL: J VIROL 33 (1). 1980. 129-139. 1980
FULL JOURNAL NAME: Journal of Virology
CODEN: JOVIA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Pulse-labeling experiments with [3H]uridine revealed that the rate of infectious pancreatic necrosis virus-specific RNA synthesis was maximal at 8-10 h after infection [Chinook salmon embryo CHSE-214 cells]

and was completely diminished by 12-14 h. Three forms of RNA intermediates were detected: a putative transcription intermediate (TRI) which comigrated in acrylamide gels with virion double-stranded RNA (dsRNA) after RNase treatment; a 24S genome length mRNA which could be resolved into 2 bands by polyacrylamide gel electrophoresis; and a 14S dsRNA component indistinguishable from virion RNA by gradient centrifugation and gel electrophoresis. The TRI was LiCl precipitable; sedimented slightly faster and broader (14-16S) than the 14S virion dsRNA; had a lower electrophoretic mobility in acrylamide gels than dsRNA, barely entering acrylamide gels as a heterogenous component; yielded genome-sized pieces of dsRNA after RNase digestion; and was the most abundant RNA form early in the infectious cycle. The 24S single-stranded RNA was thought to be the viral mRNA since it became labeled during short pulses; was found in the polysomal fraction of infected cells; and hybridized to denatured viral RNA, forming 2 segments of RNase-resistant RNA that comigrated with virion dsRNA in gels. The 24S mRNA component was formed before the synthesis of dsRNA and radioactivity could be chased from 24S single-stranded RNA to dsRNA; 24S RNA may serve as template for the synthesis of complementary strands to form dsRNA. Similar to reovirus, infectious pancreatic necrosis viral 24S mRNA contained no poly(A) tracts.

1980

3/3,AB/27 (Item 9 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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02648133 BIOSIS NO.: 000067036197
 MESSAGE SEQUENCES ARE NOT ADJACENT TO POLY ADENYLIC-ACID IN HETEROGENEOUS
 NUCLEAR RNA OF FRIEND LEUKEMIC CELLS
 AUTHOR: MACKEDONSKI V V; MCCONKEY E H
 AUTHOR ADDRESS: INST. MOL. BIOL., BULG. AKAD. NAUK., BG-1113 SOFIA, BULG.
 JOURNAL: EUR J BIOCHEM 90 (2). 1978 397-404. 1978
 FULL JOURNAL NAME: European Journal of Biochemistry
 CODEN: EJBCA
 RECORD TYPE: Abstract
 LANGUAGE: ENGLISH

ABSTRACT: Hybridization of labeled RNA with excess amounts of unlabeled complementary DNA (cDNA) was used to investigate the location of cytoplasmic mRNA sequences in heterogeneous nuclear RNA (hnRNA) of noninduced mouse Friend leukemic cells. A heterologous hybrid between hnRNA and cytoplasmic cDNA was formed. Two homologous hybrids were also formed, one between poly(A)-containing mRNA and cytoplasmic cDNA and the other between poly(A)-containing hnRNA and nuclear cDNA. All hybrids were selected on hydroxylapatite columns after RNase treatment. The hybrids were further investigated for the presence of poly(A). No poly(A) was found in the heterologous hybrid while both homologous hybrids contained poly(A). There apparently exists a spacer nucleotide sequence between the poly(A) and the message sequences in hnRNA.

1978

3/3,AB/28 (Item 10 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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02644665 BIOSIS NO.: 000067032727
 CHARACTERISTICS AND POLY ADENYLATE CONTENT OF THE ACTIN MESSENGER RNA OF

MOUSE SARCOMA 180 ASCITES CELLS
AUTHOR: GEOGHEGAN T E; SONENSHEIN G E; BRAWERMAN G
AUTHOR ADDRESS: DEP. BIOCHEM. PHARMACOL., TUFTS UNIV. SCH. MED., BOSTON,
MASS. 02111, USA.
JOURNAL: BIOCHEMISTRY 17 (20). 1978 4200-4207. 1978
FULL JOURNAL NAME: Biochemistry
CODEN: BICHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Actin is a major protein component of mouse sarcoma-180 ascites cells. It is produced in large amounts in a wheat germ cell-free system supplemented with total polysomal RNA from these cells. Adsorption of the poly(A)+ RNA onto oligo(dT)-cellulose leads to the retention of the template activity for most polypeptides but leaves a substantial portion of the actin mRNA in the unadsorbed fraction. The actin mRNA that binds to oligo(dT)-cellulose contains a large proportion of chains unable to bind to Millipore filters. The other major poly(A)+ mRNA bind nearly as well to Millipore filters as to oligo(dT)-cellulose. This implies that the distribution of poly(A) sizes in the actin mRNA is atypical, with a large proportion of the chains having relatively short poly(A) segments and with many chains containing either very short segments or no poly(A) at all. The translation of actin mRNA is preferentially inhibited in the presence of excess poly(A)+ RNA. Both the poly(A)-deficient forms of actin mRNA exhibit this sensitivity to inhibition of translation. Inhibitors of polypeptide chain initiation such as poly(A) or poly(U) did not inhibit preferentially actin mRNA translation. The poly(A)- actin mRNA appears to be functional in the cell, since it is associated with polysomes in cytoplasmic extracts. A 26-fold enrichment in the poly(A)-deficient actin mRNA was achieved by first isolating a 50S ribonucleoprotein particle from (ethylenedinitrilo)tetraacetic acid treated polysomes and subjecting the deproteinized material to oligo(dT)-cellulose fractionation, followed by zone centrifugation.

1978

3/3,AB/29 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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02615646 BIOSIS NO.: 000067003704
SUPER INDUCTION OF HUMAN FIBROBLAST INTERFERON PRODUCTION FURTHER EVIDENCE
FOR INCREASED STABILITY OF INTERFERON MESSENGER RNA
AUTHOR: SEHGAL P B; LYLES D S; TAMM I
AUTHOR ADDRESS: ROCKEFELLER UNIV., NEW YORK, N.Y. 10021, USA.
JOURNAL: VIROLOGY 89 (1). 1978 186-198. 1978
FULL JOURNAL NAME: Virology
CODEN: VIRLA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Cytoplasmic polyadenylated interferon mRNA, synthesized in human diploid fibroblasts (FS-4 strain) largely within the first 3 h of exposure to poly(I).cntdot.poly(C), is approximately 850-900 nucleotides in size (12 S) as determined by sedimentation of dimethylsulfoxide denatured mRNA through a sucrose gradient and translation of RNA in each gradient fraction by microinjection into oocytes of Xenopus laevis. Newly synthesized cytoplasmic interferon mRNA has a poly(A) length > 100 nucleotides as determined by step elution from a poly(U)-Sephrose column with varying concentrations of formamide and subsequent translation of each eluted fraction. There is a pool of translatable nuclear polyadenylated interferon mRNA molecules which also

sediment at approximately 12 S. No poly(A)-lacking interferon mRNA is detectable. One hour after the beginning of poly(I).cntdot.poly(C) induction the concentration of translatable interferon mRNA in the nuclear pool is higher than that in the cytoplasmic pool. Interferon mRNA in the nuclear pool peaks at 2 h and is undetectable by 4-5 h, while in the cytoplasmic pool it peaks between 2 and 3 h and is barely detectable by 6 h. The rate of interferon secretion in a culture of FS-4 cells peaks between 2.5 and 3.5 h after the beginning of poly(I).cntdot.poly(C) induction and secretion is shut off by 6-8 h. The concentration of cytoplasmic, phenol-extractable, interferon mRNA declines with a half-life of 0.5-1.0 h during the shutoff phase, as does the rate of interferon secretion. The rapid shutoff of interferon production which occurs between 3 and 8 h after induction is prevented when FS-4 cultures are induced and maintained in 5,6-dichloro-1-.beta.-D-ribofuranosylbenzimidazole (DRB, 40 .mu.M), a selective and reversible inhibitor of hn[heterogeneous nuclear]RNA and mRNA synthesis. This leads to an approximately 10-fold increase in the cumulative interferon yield in the first 24 h of induction. In the presence of DRB, both the concentration of phenol-extractable, translatable interferon mRNA and the rate of interferon secretion in induced cultures decline with virtually identical half-lives of approximately 6-8 h. A theoretical analysis of the available data indicates that the increased functional stability of interferon mRNA is the major factor in interferon superinduction by DRB. The increased stability possibly results from an inhibition by DRB of the synthesis of a rapidly turning over repressor RNA involved in the inactivation or degradation of interferon mRNA. Since the poly(A) of interferon mRNA continues to shorten in the presence of DRB, it is unlikely that increased stability of interferon mRNA is the result of an inhibition of poly(A) metabolism.

1978

3/3,AB/30 (Item 12 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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02417421 BIOSIS NO.: 000065074464
 CHARACTERIZATION OF ADENOVIRUS RNA SYNTHESIZED IN THE PRESENCE OF AN
 ADENOSINE ANALOG FAILURE OF POLY ADENYLATE ADDITION
 AUTHOR: SWART C; HODGE L D
 AUTHOR ADDRESS: DEP. HUM. GENET., YALE UNIV. SCH. MED., NEW HAVEN, CONN.
 06510, USA.
 JOURNAL: VIROLOGY 84 (2). 1978 374-389. 1978
 FULL JOURNAL NAME: Virology
 CODEN: VIRLA
 RECORD TYPE: Abstract
 LANGUAGE: ENGLISH

ABSTRACT: Synthesis of adenovirus-specific RNA in the presence of toyocamycin, an adenosine analog, late in infection of [human cervical carcinoma] HeLa S3 cells was investigated. The effect of this analog on nuclear metabolism was examined because, under the appropriate conditions, there is an apparent accumulation of rapidly sedimenting nuclear viral RNA (HnRNA) and no new viral mRNA associates with polyribosomes. Under these conditions there was an approximate 10% substitution by toyocamycin for adenosine in viral HnRNA. A similar amount was incorporated into virus-associated RNA but there was little effect on the synthesis, the size or the appearance in the cytoplasm of this species of viral RNA. In the presence of the analog no poly(A)-rich segments could be detected in nuclear viral RNA. Two 5' termini containing the methylated components 7mG and m6Am were recovered and constituted proportionately the same amount in selected RNA

sequences whether or not synthesis had occurred in the presence of the adenosine analog. Relative to the recovery of 5' termini, selectively extracted RNA synthesized in the presence of toyocamycin yielded nearly 2-fold less m6Ap. Since rapid sedimentation of nuclear viral RNA implies incomplete processing of molecules, these results suggest that the incorporation of toyocamycin interferes with RNA metabolism because of its prevention of polyadenylation and/or reduction in methylation of internal adenosine residues. There is apparently a sequence of events in which the introduction of at least some 5' alterations and internal methylations can occur prior to and independent of poly(A) additions.

1978

3/3,AB/31 (Item 13 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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02214869 BIOSIS NO.: 000064057393
COMPLETE TURNOVER OF POLY ADENYLIC-ACID ON MATERNAL MESSENGER RNA OF
SEA-URCHIN EMBRYOS
AUTHOR: DOLECKI G J; DUNCAN R F; HUMPHREYS T
JOURNAL: CELL 11 (2). 1977 339-344. 1977
FULL JOURNAL NAME: Cell
CODEN: CELLB
RECORD TYPE: Abstract

ABSTRACT: Measurement of the incorporation of radioactive adenosine into precursor pools and into poly(A) of fertilized sea urchin [Colobocentrotus atratus] eggs showed that the amount of adenosine incorporated into poly(A) after a 2 h incubation approximated the total poly(A) content of the embryos. This was observed whether the incubation was begun at fertilization when the poly(A) content was tripling or at 2.5 h after fertilization when the poly(A) levels were not changing, and indicated that poly(A) turned over continually and completely. The turnover appeared to take place on polysomal mRNA, since after 10 or 120 min of incubation. Of the 3H-adenosine incorporated into poly(A), 75% was on polysomes. Poly(A) lengths before and after fertilization were not significantly different, indicating that the increase in poly(A) content reflected the addition of poly(A) sequences onto mRNA molecules which previously contained no poly(A) sequences or only short poly(A) sequences. New and preexisting poly(A) tracts must have turned over to produce the incorporation observed. The radioactive poly(A) tracts measured by alkaline release of adenosine began as short sequences and gradually extended their lengths until they reached a size consistent with the idea that the poly(A) sequences became fully radioactive. This labeling pattern showed that the poly(A) turned over from the 3' end terminal probably by a shortening and lengthening mechanism.

1977

3/3,AB/32 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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02196057 BIOSIS NO.: 000064038575
CHARACTERIZATION AND IN-VITRO TRANSLATION OF POLY ADENYLATED MESSENGER RNA
FROM NEUROSPORA-CRASSA
AUTHOR: LUCAS M C; JACOBSON J W; GILES N H
JOURNAL: J BACTERIOL 130 (3). 1977 1192-1198. 1977
FULL JOURNAL NAME: Journal of Bacteriology
CODEN: JOBAA

RECORD TYPE: Abstract

ABSTRACT: RNA extracted from *N. crassa* was fractionated by oligodeoxythymidylic acid [oligo(dT)]-cellulose chromatography into polyadenylated **mRNA** [poly(A) **mRNA**] and unbound RNA. The poly(A) **mRNA**, which comprises approximately 1.7% of the total cellular RNA, was further characterized by Sepharose 4B chromatography and polyacrylamide gel electrophoresis. Both techniques showed that the poly(A) **mRNA** was heterodisperse in size, with an average molecular weight similar to that of 17S ribosomal RNA (rRNA). The poly(A) segments isolated from the poly(A) **mRNA** were relatively short, with 3 major size classes of 30, 55 and 70 nucleotides. Gel electrophoresis of the non-poly(A) RNA indicated that it contained primarily rRNA and 4S RNA. The optimal conditions were determined for the translation of *Neurospora* **mRNA** in a cell-free wheat germ protein-synthesizing system. Poly(A) **mRNA** stimulated the incorporation of [14C]leucine into polypeptides ranging in size from 10,000-100,000 daltons. The RNA that did not bind to oligo(dT)-cellulose also stimulated into incorporation of [14C]leucine, indicating that this fraction contains a significant concentration of **mRNA** which has either **no poly(A)** or very short poly(A) segments. The translation of poly(A) **mRNA** and unbound **mRNA** was inhibited by 7-methylguanosine-5'-monophosphate (m7G5'p). This is preliminary evidence for the existence of a 5'-RNA cap on *Neurospora* **mRNA**.

1977

3/3,AB/33 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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02117365 BIOSIS NO.: 000063032359
INTRA CELLULAR DISTRIBUTION AND POLY ADENYLATE CONTENT OF ADENO ASSOCIATED
VIRUS RNA SEQUENCES
AUTHOR: CARTER B J
JOURNAL: VIROLOGY 73 (1). 1976 273-285. 1976
FULL JOURNAL NAME: Virology
CODEN: VIRLA
RECORD TYPE: Abstract

ABSTRACT: The synthesis of adeno-associated virus (AAV2) RNA in [human oral carcinoma] KB3 cells coinfecting with adenovirus type 2 as a helper was studied. Previous studies revealed a discrete 20 S AAV RNA species which was present in the nucleus and polysomes and a 2nd, heterogenous population of smaller AAV RNA molecules (4-18 S) present only in the nucleus and nonpolysomal regions of the cytoplasm. In this study, the AAV genome sequence representation and poly(A) sequences in AAV RNA were correlated with the size of the RNA and its cellular distribution. Most of the 20 S AAV RNA contained a poly(A) sequence 200 nucleotides long; the heterogenous 4-18 S AAV RNA contained little or **no poly(A)**. The poly(A) (+) and the poly(A) (-) RNA, and RNA isolated from the cell nucleus, cytoplasm or polysomes, contained the same set of AAV RNA sequences complementary to 70-75% of the AAV DNA minus strand. Apparently a single polyadenylated AAV **mRNA** species is synthesized and this represents most, if not all, of the entire portion of the AAV genome that is stably transcribed.

1976

3/3,AB/34 (Item 16 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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02114639 BIOSIS NO.: 000063029633
UTERO GLOBIN MESSENGER RNA TRANSLATION IN-VITRO
AUTHOR: BULLOCK D W; WOO S L C; O'MALLEY B W
JOURNAL: BIOL REPROD 15 (4). 1976 435-443. 1976
FULL JOURNAL NAME: Biology of Reproduction
CODEN: BIREB
RECORD TYPE: Abstract

ABSTRACT: The **mRNA** coding for the progesterone-induced protein uteroglobin was extracted from endometrial tissue of rabbits in early pregnancy and enriched by binding to oligo-dT-cellulose. After translation in a cell-free system derived from wheat germ, total **mRNA** activity was assessed by measuring the incorporation of 35S-methionine into TCA-precipitable peptides and specific **mRNA** activity by immunoprecipitation with specific uteroglobin antibodies purified by affinity chromatography. Approximately 85% of total **mRNA** activity was recovered after dT-cellulose chromatography, 10% in the bound fraction and 75% in the unbound RNA, suggesting that the majority of endometrial **mRNA** species lacked poly A sequences of longer than about 20 residues. No poly A could be detected by 3H-poly U hybridization in the unbound fraction. In contrast, 69% of total **mRNA** activity was present in dT-bound RNA from rabbit liver. The immunoprecipitable cell-free translation products of endometrial dT-RNA gave a single peak of radioactivity on electrophoresis in 15% polyacrylamide gels containing sodium dodecyl sulfate. The peak was completely displaced by the addition of an excess of authentic nonradioactive uteroglobin to the immunoprecipitation reaction and was absent from products of translation without added endometrial RNA. The cell-free product migrated more slowly than authentic uteroglobin, suggesting the synthesis of a precursor protein. So uteroglobin **mRNA** could be detected in dT-bound RNA from rabbit liver. The proportion of uteroglobin **mRNA** in endometrial dT-bound RNA reached a peak on day 4 of pregnancy and declined subsequently to nonpregnant levels on day 8, a pattern similar to that of uteroglobin secretion.

1976

3/3,AB/35 (Item 17 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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02111325 BIOSIS NO.: 000063026318
ISOLATION AND IDENTIFICATION OF THE MESSENGER RNA FOR A STRUCTURAL LIPO
PROTEIN OF THE ESCHERICHIA-COLI OUTER MEMBRANE
AUTHOR: TAKEISHI K; YASUMURA M; PIRTLE R; INOUE M
JOURNAL: J BIOL CHEM 251 (20). 1976 6259-6266. 1976
FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract

ABSTRACT: The cells of E. coli strain CP 78 were labeled with [32P]Pi and the total radioactive RNA was prepared from the cells. The **mRNA** that codes for a structural lipoprotein in the outer membrane was purified from the total RNA by 3 successive electrophoreses on polyacrylamide slab gels, twice at pH 8.3 and once at pH 3.5 in 7 M urea. Approximately 0.002% of the total radioactive phosphate used was incorporated into the fraction containing the most purified **mRNA**. The 2-dimensional fingerprint of the T1 ribonuclease digest of the 32P-labeled **mRNA** showed that the purity of the **mRNA** was as high as 90%. A preliminary sequence analysis was carried out on the T1 ribonuclease oligonucleotides which were separated by the fingerprinting procedure. By using the established amino acid sequence of the

lipoprotein and the genetic code, 3 relatively long oligonucleotides were assigned to code for 3 different parts of the lipoprotein. From these data, the present RNA fraction was identified as the lipoprotein mRNA. From the analysis of the T1 ribonuclease oligonucleotides, the mRNA was 360 \pm 10 nucleotides in length. Although the length of the mRNA was enough to code for 2 lipoprotein molecules, T1 ribonuclease digestion of the mRNA yielded only 1 mol/mol of mRNA of the individual oligonucleotides assigned to parts of the amino acid sequence of the lipoprotein. This suggests that the mRNA codes for only 1 molecule of the lipoprotein. The mRNA has no poly-A sequence at the 3' end.

mature 23S rRNA. The size distribution of poly(A) tails generated in vitro, averaging 50 nt in length, is comparable to that previously reported in vivo. PAP I activity is associated exclusively with the polysomes. Exogenously added PAP I does not restore mRNA decay to PAP I-polysomes, suggesting that, in vivo, PAP I may be part of a multiprotein complex. The potential of this in vitro system for analyzing mRNA decay in E. coli is discussed.

3/3,AB/2 (Item 2 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

08763056 96120862 PMID: 8590479

The organization structure and regulatory elements of Chlamydomonas histone genes reveal features linking plant and animal genes.

Fabry S; Muller K; Lindauer A; Park P B; Cornelius T; Schmitt R
Lehrstuhl, fur Genetik, Universitat Regensburg, Germany.

Current genetics (UNITED STATES) Sep 1995, 28 (4) p333-45,
ISSN 0172-8083 Journal Code: 8004904

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed



The genome of the green alga Chlamydomonas reinhardtii contains approximately 15 gene clusters of the nucleosomal (or core) histone H2A, H2B, H3 and H4 genes and at least one histone H1 gene. Seven non-allelic histone gene loci were isolated from a genomic library, physically mapped, and the nucleotide sequences of three isotypes of each core histone gene species and one linked H1 gene determined.

The core histone genes are organized in clusters of H2A-H2B and H3-H4 pairs, in which each gene pair shows outwardly divergent transcription from a short (< 300 bp) intercistronic region. These intercistronic regions contain typically conserved promoter elements, namely a TATA-box and the three motifs TGGCCAG-G(G/C)-CGAG, CGTTGACC and CGGTTG. Different from the genes of higher plants, but like those of

animals and the related alga volvox, the 3' untranslated regions contain no poly A signal, but a palindromic sequence (3'

palindrome) essential for mRNA processing is present. One single H1 gene was found in close linkage to a H2A-H2B pair. The H1 upstream region contains the octameric promoter element GGTGACC (also found upstream of the core histone genes) and two specific sequence motifs that are shared only with the Volvox H1 promoters. This suggests differential transcription of the H1 and the core histone genes. The H1 gene is interrupted by two introns. Unlike Volvox H3 genes, the three sequenced H3 isoforms are intron-free. Primer-directed PCR of genomic DNA demonstrated, however, that at least 8 of the about 15 H3 genes do contain one intron at a conserved position. In synchronized C. reinhardtii cells, H4 mRNA levels (representative of all core histone mRNAs) peak during cell division, suggesting strict replication-dependent gene control. The derived peptide sequences place C. reinhardtii core histones closer to plants than to animals, except that the H2A histones are more animal-like. The peptide sequence of histone H1 is closely related to the V. carteri VH1-II (66% identity). Organization of the core histone gene in pairs, and non-polyadenylation of mRNAs are features shared with animals, whereas peptide sequences and enhancer elements are shared with higher plants, assigning the volvocalean histone genes a position intermediate between animals and plants.

3/3,AB/3 (Item 3 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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b 155, 5
05feb03 15:40:50 User242957 Session D592.2
\$0.00 0.072 DialUnits File410
\$0.00 Estimated cost File410
\$0.00 Estimated cost this search
\$0.00 Estimated total session cost 0.220 DialUnits

SYSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1966-2003/Jan W4

(c) format only 2003 The Dialog Corp.

File 5:Biosis Previews(R) 1969-2003/Jan W4

(c) 2003 BIOSIS

*File 5: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

Set Items Description

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? s (gene or mrna) (p) ("no" (w) poly (w) "a")

>>>Invalid syntax

? s (gene or mrna) and ("no" (w) poly (w) "a")

Processing

1366382 GENE

352554 MRNA

2753045 NO

180364 POLY

13834064 A

70 NO(W) POLY(W) A

S1 50 (GENE OR MRNA) AND ("NO" (W) POLY (W) "A")

? rd

...examined 50 records (50)

...completed examining records

S2 38 RD (unique items)

? s s2 and py<1998

Processing

38 S2

20949924 PY<1998

S3 35 S2 AND PY<1998

? t s3/3,ab/all

3/3,AB/1 (Item 1 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.

09172033 97075094 PMID: 8975250

Development of an in vitro **mRNA** decay system for Escherichia coli:
poly(A) polymerase I is necessary to trigger degradation.

Ingle C A; Kushner S R

Department of Genetics, University of Georgia, Athens 30602-7223, USA.

Proceedings of the National Academy of Sciences of the United States of
America (UNITED STATES) Nov 12 1996, 93 (23) p12926-31, ISSN

0027-8424 Journal Code: 7505876

Contract/Grant No.: GM28760; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Using a novel Escherichia coli in vitro decay system in which polysomes are the source of both enzymes and **mRNA**, we demonstrate a requirement for poly(A) polymerase I (PAP I) in **mRNA** turnover. The in vitro decay of two different mRNAs (trxA and lpp) is triggered by the addition of ATP only when polysomes are prepared from s strain carrying the wild-type **gene** for PAP I (pcnB+). The relative decay rates of these two messages are similar in vitro and in vivo. Poly(A) tails are formed on both mRNAs, but no **poly(A)** are detected on the 3' end of

(galactokinase or galK) that can be readily assayed in mammalian cells. Our results demonstrate that the presence of a poly(A) region is important for efficient **gene** expression and that the use of the poly(A) region of bovine growth hormone (bGH) reproducibly results in three times higher expression than that of SV40 early or human collagen poly(A) regions. We further demonstrate that changing the promoter region on these chimeric transcription units does not change the effect of the poly(A) region. Neither does changing the assay **gene**, since comparison of the same poly(A) regions behind another marker **gene** (xanthine-guanine phosphoribosyl transferase or xgprt) leads to identical differences in expression. When we examine the levels of poly(A)+ RNA that result from each transcription unit, we find that they correlate precisely with the **gene** expression levels. Apparently the 3' end of an RNA is a determinant of steady-state mRNA levels and, in turn, the subsequent production of the protein product.

3/3,AB/10 (Item 10 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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05032699 86084943 PMID: 3000978
Flaviviridae.
Westaway E G; Brinton M A; Gaidamovich SYa; Horzinek M C; Igarashi A;
Kaariainen L; Lvov D K; Porterfield J S; Russell P K; Trent D W
Intervirology (SWITZERLAND) 1985, 24 (4) p183-92, ISSN
0300-5526 Journal Code: 0364265
Document type: Journal Article; Review
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The family Flaviviridae comprises the genus Flavivirus, which contains 65 related species and two possible members. They are small, enveloped RNA viruses (diameter 45 nm) with peplomers comprising a single glycoprotein E. Other structural proteins are designated C (core) and M (membrane-like). The single strand of RNA is infectious and has a molecular weight of about 4 X 10⁶ and an m7G 'cap' at the 5' end but no poly(A) tract at the 3' end; it functions as the sole messenger. The **gene** sequence commences 5'-C-M-E.... The replication strategy and the mode of morphogenesis are distinct from those of the Togaviridae which are slightly larger and morphologically similar in some respects. Flaviviruses infect a wide range of vertebrates, and many are transmitted by arthropods.

3/3,AB/11 (Item 11 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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04152534 83131916 PMID: 6186505
A population-kinetical approach to RNA formation and degradation in growing and in resting cells.
Jauker F; Rinaldy A R
Experimental cell research (UNITED STATES) Jan 1983, 143 (1)
p163-74, ISSN 0014-4827 Journal Code: 0373226
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Labelled RNA was extracted from growing and stationary cultures of the ciliate Tetrahymena and was separated chromatographically into poly(A)- and no poly(A)-containing fractions. A new method was used to derive from the data (cpm/A260, and tD, doubling time of RNA) absolute values of three growth terms which fully describe the population kinetics of RNA molecules: the rates of transcription, decay, and net growth. At all

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06394836 90094420 PMID: 2403559

The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antigen and proteoglycan core/link proteins.

Wolffe E J; Gause W C; Pelfrey C M; Holland S M; Steinberg A D; August J T

Department of Pharmacology and Molecular Sciences, Johns Hopkins University School of Medicine, Baltimore, Maryland 21205.

Journal of biological chemistry (UNITED STATES) Jan 5 1990, 265

(1) p341-7, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: 5 T32 GM 07626; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We describe the isolation and sequencing of a cDNA encoding mouse Pgp-1. An oligonucleotide probe corresponding to the NH2-terminal sequence of the purified protein was synthesized by the polymerase chain reaction and used to screen a mouse macrophage lambda gt11 library. A cDNA clone with an insert of 1.2 kilobases was selected and sequenced. In Northern blot analysis, only cells expressing Pgp-1 contained mRNA species that hybridized with this Pgp-1 cDNA. The nucleotide sequence of the cDNA has a single open reading frame that yields a protein-coding sequence of 1076 base pairs followed by a 132-base pair 3'-untranslated sequence that includes a putative polyadenylation signal but no poly(A) tail. The translated sequence comprises a 13-amino acid signal peptide followed by a polypeptide core of 345 residues corresponding to an Mr of 37,800. Portions of the deduced amino acid sequence were identical to those obtained by amino acid sequence analysis from the purified glycoprotein, confirming that the cDNA encodes Pgp-1. The predicted structure of Pgp-1 includes an NH2-terminal extracellular domain (residues 14-265), a transmembrane domain (residues 266-286), and a cytoplasmic tail (residues 287-358). Portions of the mouse Pgp-1 sequence are highly similar to that of the human CD44 cell surface glycoprotein implicated in cell adhesion. The protein also shows sequence similarity to the proteoglycan tandem repeat sequences found in cartilage link protein and cartilage proteoglycan core protein which are thought to be involved in binding to hyaluronic acid.

3/3,AB/9 (Item 9 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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05147171 86219707 PMID: 2872023

Differential effects of polyadenylation regions on gene expression in mammalian cells.

Pfarr D S; Rieser L A; Woychik R P; Rottman F M; Rosenberg M; Reff M E

DNA (Mary Ann Liebert, Inc.) (UNITED STATES) Apr 1986, 5 (2)

p115-22, ISSN 0198-0238 Journal Code: 8302432

Contract/Grant No.: AM32770; AM; NIADDK

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The steady-state level attained for any protein in mammalian cells is in part determined by its steady-state level of mRNA. Sequence information in and around the 3' end of an RNA which is involved in specifying and regulating polyadenylation [poly(A)] may have important consequences on mRNA levels, and ultimately on expression of the protein product. In this report we compare the effects on gene expression which result from placing several different poly(A) regions, or no poly(A) region, downstream from a marker gene

poly(A)+ RNA were detected in spermatogonia, elongated spermatids, Sertoli cells, myoid cells, fibroblasts, macrophages, and Leydig cells. No poly(A)+ RNA was detected in residual bodies of elongated spermatids. At stages IX-XI of the seminiferous cycle, the nuclei and cytoplasm of pachytene spermatocytes contained approximately equal amounts of poly(A)+ RNA, suggesting nuclear RNA storage and/or a reduced processing rate of mRNA precursors at this stage of germ cell differentiation. To examine the distribution of poly(A)+ RNAs in subcellular components of testicular cells, electron microscope radioautography was used. In germ cells and Sertoli cells, poly(A)+ RNA was often seen free in the cytoplasm or associated with the endoplasmic reticulum and was only occasionally found associated with mitochondria, lysosomes, lipid inclusions, and axonemes. As previously reported for the mRNAs of transition protein 1 and protamine 1 [Morales et al., J Cell Sci 1991; 100:119-131], no compartmentalization of poly(A)+ RNAs was detected in the cytoplasm of round and elongated spermatids. No poly(A)+ RNA was detected in association with the radial body and in most sections, the chromatoid body did not contain any significant amounts of poly(A)+ RNA.

3/3,AB/5 (Item 5 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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07783913 93309467 PMID: 8321235
Evidence that the SKI antiviral system of Saccharomyces cerevisiae acts by blocking expression of viral mRNA.
Widner W R; Wickner R B
Section on Genetics of Simple Eukaryotes, National Institute of Diabetes and Digestive and Kidney Diseases, Bethesda, Maryland 20892.
Molecular and cellular biology (UNITED STATES) Jul 1993, 13 (7)
p4331-41, ISSN 0270-7306 Journal Code: 8109087
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The SKI2 gene is part of a host system that represses the copy number of the L-A double-stranded RNA (dsRNA) virus and its satellites M and X dsRNA, of the L-BC dsRNA virus, and of the single-stranded replicon 20S RNA. We show that SKI2 encodes a 145-kDa protein with motifs characteristic of helicases and nucleolar proteins and is essential only in cells carrying M dsRNA. Unexpectedly, Ski2p does not repress M1 dsRNA copy number when M1 is supported by an L-A cDNA clone; nonetheless, it did lower the levels of M1 dsRNA-encoded toxin produced. Since toxin secretion from cDNA clones of M1 is unaffected by Ski2p, these data suggest that Ski2p acts by specifically blocking translation of viral mRNAs, perhaps recognizing the absence of cap or poly(A). In support of this idea, we find that Ski2p represses production of beta-galactosidase from RNA polymerase I [no cap and no poly(A)] transcripts but not from RNA polymerase II (capped) transcripts.

3/3,AB/6 (Item 6 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

07485625 93013058 PMID: 1398149
A rabbit AldA pseudogene derived from a partially spliced primary aldolase A transcript.
Amsden A B; Penhoet E E; Tolan D R
Biology Department, Boston University, MA 02215.
Gene (NETHERLANDS) Oct 21 1992, 120 (2) p323-4, ISSN 0378-1119 Journal Code: 7706761
Contract/Grant No.: DK38821; DK; NIDDK; GM32344; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The entire AldA processed pseudogene of rabbit was isolated and characterized. The pseudogene encodes the C-terminal portion of the protein from amino acids (aa) 126-363. There are deletions, insertions and nucleotide (nt) substitutions distributed throughout the 931 bp of identity shared with the 1.4-kb mRNA. There are 21 replacement codon substitutions, including a clearly deleterious change in the stop codon. This processed pseudogene has several uncommon features: (i) it has a 5'-boundary coincident with an intron/exon junction and does not encode the entire mRNA, (ii) there is a broken direct repeat that overlaps the region of shared identity with the mRNA rather than flanking it, and (iii) there is no poly(A) sequence. This processed pseudogene probably arose by integration of a DNA copy of a partially spliced primary transcript. The structure of this gene has added implications for the timing of posttranscriptional processing events.

3/3,AB/7 (Item 7 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.

06395381 90097865 PMID: 2152967

cDNA genes formed after infection with retroviral vector particles lack the hallmarks of natural processed pseudogenes.

Dornburg R; Temin H M

McArdle Laboratory for Cancer Research, University of Wisconsin, Madison 53706.

Molecular and cellular biology (UNITED STATES) Jan 1990, 10 (1)

p68-74, ISSN 0270-7306 Journal Code: 8109087

Contract/Grant No.: CA-07175; CA; NCI; CA-22443; CA; NCI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Retroviral proteins can encapsidate RNAs without retroviral cis-acting sequences. Such RNAs are reverse transcribed and inserted into the genomes of infected target cells to form cDNA genes. Previous investigations by Southern blot analysis of such cDNA genes suggested that they were truncated at the 3' and the 5' ends (R. Dornburg and H. M. Temin, Mol. Cell. Biol. 8:2328-2334, 1988). To analyze such cDNA genes further, we cloned three cDNA genes (derived from a hygromycin B phosphotransferase gene) in lambda vectors and analyzed them by DNA sequencing. We found that they did not correspond to the full-length mRNA: they were truncated at both the 3' and the 5' ends, did not contain a poly(A) tract, and were not flanked by direct repeats. The 3'-end junctions to chromosomal DNA of five more cDNA genes were amplified by polymerase chain reaction, cloned in pUC vectors, and sequenced. All of these cDNA genes had 3'-end truncations, and no poly(A) tracts were found. Further

polymerase chain reaction experiments were performed to detect hygromycin B phosphotransferase cDNA genes with a poly(A) tract in DNA extracted from a pool of about 500 colonies of cells containing cDNA genes. No hygromycin B phosphotransferase cDNA gene with a poly(A) tract was found.

Investigation of two preintegration sites by Southern analysis revealed that deletions were present in chromosomal DNA at the site of the integration of the cDNA genes. Naturally occurring processed pseudogenes correspond to the full-length mRNA, contain a poly(A) sequence, and are flanked by direct repeats. (ABSTRACT TRUNCATED AT 250 WORDS)

3/3,AB/8 (Item 8 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

3/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

02447603 77028870 PMID: 824286

Isolation and identification of the messenger ribonucleic acid for a structural lipoprotein of the Escherichia coli outer membrane.

Takeishi K; Yasumura M; Pirtle R; Inouye M

Journal of biological chemistry (UNITED STATES) Oct 25 1976, 251

(20) p6259-66, ISSN 0021-9258 Journal Code: 2985121R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The cells of Escherichia coli strain CP 78 were labeled with [32P]orthophosphate and the total radioactive RNA was prepared from the cells. The mRNA that codes for a structural lipoprotein in the outer membrane was purified from the total RNA by three successive electrophoreses on polyacrylamide slab gels, twice at pH 8.3 and once at pH 3.5 in 7 M urea. Approximately 0.002% of the total radioactive phosphate used was incorporated into the fraction containing the most purified mRNA. The two-dimensional fingerprint of the T1 ribonuclease digest of the 32P-labeled mRNA showed that the purity of the mRNA was as high as 90%. A preliminary sequence analysis was carried out on the T1 ribonuclease oligonucleotides which had been separated by the fingerprinting procedure. By using the established amino acid sequence of the lipoprotein and the genetic code, three relatively long oligonucleotides were assigned to code for three different parts of the lipoprotein. From these data, the present RNA fraction was identified as the lipoprotein mRNA. From the analysis of the T1 ribonuclease oligonucleotides, the mRNA was estimated to be 360 +/- 10 nucleotides in length. Although the length of the mRNA was enough to code for 2 lipoprotein molecules, T1 ribonuclease digestion of the mRNA yielded only 1 mol/mol of mRNA of the individual oligonucleotides assigned to parts of the amino acid sequence of the lipoprotein. This suggests that the mRNA codes for only 1 molecule of the lipoprotein. It was also found that the mRNA has **no polyadenylate sequence** at the 3' end.

3/3,AB/7 (Item 1 from file: 50)
DIALOG(R)File 50:CAB Abstracts
(c) 2003 CAB International. All rts. reserv.

02762655 CAB Accession Number: 931643423

Nucleotide sequence of an Arabidopsis thaliana turgor-responsive TMP-B cDNA clone encoding transmembrane protein with a major intrinsic protein motif.

Shagan, T.; Meraro, D.; Bar-Zvi, D.

Department of Life Sciences, Ben-Gurion University of the Negev, PO Box 653, Beer-Sheva 84105, Israel.

Plant Physiology vol. 102 (2): p.689-690

Publication Year: 1993

ISSN: 0032-0889 --

Language: English

Document Type: Journal article

Nucleotide and deduced amino acid sequences are reported for the 1057 nucleotide-long cDNA T4 (EMBL accession number X69294). It consists of 13 nucleotides in the 5'-untranslated region, 858 nucleotides in the ORF and 186 nucleotides in the 3'-untranslated region. It has **no polyadenylation signal** nor a poly(A) tail at the 3'-end. The protein contains 286 amino acids, has an Mr of 30,612 Da, and the major intrinsic protein motif is located at amino acid residues 109-118. Six

putative transmembrane sequences are located at amino acid residues 53-75, 89-111, 132-150, 175-198, 204-227 and 263-280. Overall amino acid identity of TMP-B with TMP-A and the pea turgor-responsive cDNA 7a is 93 and 84%, respectively, and similarities are 96.5 and 91%, respectively. In the coding sequence, identity with that of TMP-A and 7a is 82 and 74%, respectively; 80% of the changes are in the 3rd codon position. Of the 286 codons, 137 are altered between TMP-B and TMP-A. In 118 of the altered codons, the nucleotide change does not result in a change of the amino acid encoded by it, causing the 2 polypeptides to differ only in 17 amino acid residues. 10 ref.

3/3,AB/8 (Item 2 from file: 50)
DIALOG(R)File 50:CAB Abstracts
(c) 2003 CAB International. All rts. reserv.

02746788 CAB Accession Number: 931640949

Nucleotide sequence of an Arabidopsis thaliana turgor-responsive cDNA clone encoding TMP-A, a transmembrane protein containing the major intrinsic protein motif.

Shagan, T.; Bar-Zvi, D.

Department of Life Sciences, Ben-Gurion University of the Negev, PO Box 653, Beer-Sheva 84105, Israel.

Plant Physiology vol. 101 (4): p.1397-1398

Publication Year: 1993

ISSN: 0032-0889 --

Language: English

Document Type: Journal article

Nucleotide and deduced amino acid sequences are reported for the 1105 nucleotide-long cDNA clone T8 (EMBL accession number X68293), consisting of 54 nucleotides in the 5'-untranslated region, 859 nucleotides in the ORF and 192 nucleotides in the 3'-untranslated region. **No polyadenylated signal** or tail was observed at the 3'-end of the cDNA. The deduced 286 amino acid protein (Mr 30 578 Da) has 6 putative transmembrane sequences at amino acid residues 53-75, 89-111, 132-150, 175-198, 204-227 and 263-280. The major intrinsic protein motif is located at amino acid residues 109-118. TMP-A shows high homology to protein encoded by the turgor-responsive 7a cDNA from pea with an overall amino acid identity of 84%, a similarity of 91% and a nucleotide sequence identity of 74%. 10 ref.

3/3,AB/9 (Item 3 from file: 50)
DIALOG(R)File 50:CAB Abstracts
(c) 2003 CAB International. All rts. reserv.

01184244 CAB Accession Number: 821383310

Evidence that potato leafroll virus RNA is positive-stranded, is linked to a small protein and does not contain polyadenylate.

Mayo, M. A.; Barker, H.; Robinson, D. J.; Tamada, T.; Harrison, B. D.

Scottish Crop Res. Inst., Invergowrie, Dundee, UK.

Journal of General Virology vol. 59 (1): p.163-167

Publication Year: 1982

ISSN: 0022-1317 --

Language: English

Document Type: Journal article

RNA from particles of PLRV infected tobacco mesophyll protoplasts. Treating the RNA with proteinase K did not abolish its infectivity. In messenger-dependent rabbit reticulocyte lysate, PLRV RNA induced the synthesis of specific polypeptides: a major product of mol. wt. 71 000 but no product the size of coat protein. PLRV RNA is therefore positive-stranded. A genome-linked protein (apparent mol wt. 7000) was detected in preparations of PLRV RNA but **no polyadenylate sequence** was found. These features may prove to be characteristic of

luteoviruses. 20 ref.

3/3,AB/10 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal
(c) 2003 INIST/CNRS. All rts. reserv.

11362411 PASCAL No.: 94-0185587

The gamma -tubulin-encoding gene from the basidiomycete fungus, *Ustilago violacea*, has a long 5'-untranslated region

HONG LUO; PERLIN M H

Univ. Louisville, dep. biology, Louisville KY 40292, USA

Journal: Gene, 1993, 137 (2) 187-194

Language: English

The gene (gamma -tub) encoding gamma -tubulin (gamma -Tub) was isolated from a cosmid library constructed for *Ustilago violacea* by using a PCR-amplified DNA fragment as a probe. About 2.8 kb of DNA sequence was analyzed and found to encode a protein of 469 amino acids highly homologous to the gamma -Tub from other organisms. There were eight introns interrupting the coding sequence. A TATA-like sequence was found 389 bp upstream from the initial Met codon. **No polyadenylation signal** was found in the 3' non-coding region. Southern blot analyses indicated that gamma -tub is a single-copy gene. Northern blot analyses indicated that a 1.81-kb RNA species was transcribed. Primer extension experiments determined that the transcription start point (tsp) is at 58 bp downstream from the putative TATA box, with another possible tsp at 95 bp downstream

```

? s (gene or mrna) (p) ("no" (w) poly (w) "a")
>>>Invalid syntax
? s (gene or mrna) and ("no" (w) poly (w) "a")
Processing
      1366382  GENE
      352554  MRNA
      2753045  NO
      180364  POLY
      13834064  A
          70  NO(W) POLY(W) A
S1      50  (GENE OR MRNA) AND ("NO" (W) POLY (W) "A")
? rd
...examined 50 records (50)
...completed examining records
      S2      38  RD (unique items)
? s s2 and py<1998
Processing
          38  S2
      20949924  PY<1998
      S3      35  S2 AND PY<1998
? t s3/3,ab/all

```

active site of the enzyme. The expressed sequence tag was expressed as a fusion protein in *Escherichia coli*, with a carboxyl terminal deletion removing one region of high identity between the two proteins. The protein product of this construct was found to have inositol 1,3,4-trisphosphate 5/6-kinase activity. The *Arabidopsis* enzyme produced both inositol 1,3,4,6-tetrakisphosphate and inositol 1,3,4,5-tetrakisphosphate as products in a ratio of 1:3, in contrast with the human enzyme which gives a product ratio of 3:1.

3/3,AB/2 (Item 2 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

07990872 94131282 PMID: 8299946

The gamma-tubulin-encoding gene from the basidiomycete fungus, *Ustilago violacea*, has a long 5'-untranslated region.

Luo H; Perlin M H
Department of Biology, University of Louisville, KY 40292.
Gene (NETHERLANDS) Dec 31 1993, 137 (2) p187-94, ISSN
0378-1119 Journal Code: 7706761

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The gene (gamma-tub) encoding gamma-tubulin (gamma-Tub) was isolated from a cosmid library constructed for *Ustilago violacea* by using a PCR-amplified DNA fragment as a probe. About 2.8 kb of DNA sequence was analyzed and found to encode a protein of 469 amino acids highly homologous to the gamma-Tub from other organisms. There were eight introns interrupting the coding sequence. A 'TATA'-like sequence was found 389 bp upstream from the initial Met codon. **No polyadenylation signal** was found in the 3' non-coding region. Southern blot analyses indicated that gamma-tub is a single-copy gene. Northern blot analyses indicated that a 1.81-kb RNA species was transcribed. Primer extension experiments determined that the transcription start point (tsp) is at 58 bp downstream from the putative TATA box, with another possible tsp at 95 bp downstream. The long 5' non-coding sequence of the RNA contained several small open reading frames; their possible roles in the regulation of gamma-tub translation are discussed.

3/3,AB/3 (Item 3 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

07474139 92412147 PMID: 1530649

Cloning and sequencing of a gene encoding yeast thioltransferase.
Gan Z R
Department of Biological Chemistry, Merck Research Laboratory, West Point, PA 19486.

Biochemical and biophysical research communications (UNITED STATES) Sep 16 1992, 187 (2) p949-55, ISSN 0006-291X Journal Code: 0372516

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

A 69 bp yeast genomic DNA fragment encoding yeast thioltransferase was amplified by PCR technique. A yeast genomic DNA library was screened by a specific probe obtained from the PCR product. A 718 bp DNA fragment was found to encode yeast thioltransferase and its flanking sequence. The deduced amino acid sequence of the gene, designated TTR, agrees with that derived from conventional amino acid sequence analysis except two extra amino acids on the C-terminus. In contrast to yeast thioredoxin, Southern

blot analysis of total yeast genomic DNA indicated that there was only one copy of gene encoding yeast thiotransferase. A putative TATA box was found at 109 bp from the starting codon. However, **no polyadenylation signal** sequence was identified on the DNA sequence downstream the 3' end of the gene.

3/3,AB/4 (Item 4 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.

06562187 90262645 PMID: 2344393

Human spermidine synthase: cloning and primary structure.

Wahlfors J; Alhonen L; Kauppinen L; Hyvonen T; Janne J; Eloranta T

Department of Biochemistry, University of Kuopio, Finland.

DNA and cell biology (UNITED STATES) Mar 1990, 9 (2) p103-10,

ISSN 1044-5498 Journal Code: 9004522

Erratum in DNA Cell Biol 1990 Sep;9(7):543

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Using a synthetic deoxyoligonucleotide mixture constructed for a tryptic peptide of the bovine enzyme as a probe, cDNA coding for the full-length subunit of spermidine synthase was isolated from a human decidua cDNA library constructed on phage lambda gt11. After subcloning into the Eco RI site of pBR322 and propagation, both strands of the insert were sequenced using a shotgun strategy. Starting from the first start codon, which was immediately preceded by a GC-rich region including four overlapping CCGCC consensus sequences, an open reading frame for a 302-amino-acid polypeptide was resolved. This peptide had an Mr of 33,827, started with methionine, and ended with serine. The identity of the isolated cDNA was confirmed by comparison of the deduced amino acid sequence with resolved sequences of the tryptic peptides of bovine spermidine synthase. The coding strand of the cDNA revealed no special regulatory or ribosome-binding signals within 82 nucleotides preceding the start codon and **no polyadenylation**

signal within 247 nucleotides following the stop codon. The coding region, containing a 13-nucleotide repeat close to the 5' end, was longer than, and very different from, that of the bacterial counterpart. This region seems to be of retroviral origin and shows marked homology with sequences found in a variety of human, mammalian, avian, and viral genes and mRNAs. By computer analysis, the first 200 nucleotides of the 5' end of the coding strand appear able to form a very stable secondary structure with a free energy change of -157.6 kcal/mole. (ABSTRACT TRUNCATED AT 250 WORDS)

3/3,AB/5 (Item 5 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.

02750989 78066354 PMID: 618834

Pea enation mosaic virus genome RNA contains **no polyadenylate** sequences and cannot be aminoacylated.

German T L; De Zoeten G A; Hall T C

Intervirology (SWITZERLAND) 1978, 9 (4) p226-30, ISSN

0300-5526 Journal Code: 0364265

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

An active synthetase enzyme preparation from peas (*Pisum sativum* L.) did not catalyze the aminoacylation of pea enation mosaic virus RNA. The viral RNA was shown not to contain polyadenylic acid sequences.

ds

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Set      Items  Description
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S3       10     RD (unique items)
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Processed 10 of 18 files ...
Processing
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>>> or undefined in one or more files.
Processing
Completed processing all files
      65085893 PY<1998
      6800419 NO
      1108 AATAAA
      0 NO(W)AATAAA
S4      0 PY<1998 AND (NO (W) "AATAAA")
? s "AATAAA"
S5      1108 "AATAAA"
? s s5 and py<1998
Processing
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>>> started at PY=A stopped at PY=196U
Processing
Processed 10 of 18 files ...
Processing
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>>> or undefined in one or more files.
Completed processing all files
      1108 S5
      65085893 PY<1998
S6      876 S5 AND PY<1998
? s s6 and (no (w) signal)
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      6800419 NO
      1303390 SIGNAL
      3365 NO(W) SIGNAL
S7      0 S6 AND (NO (W) SIGNAL)
? s s6 and (no (w) polyadenyl?)
      876 S6
      6800419 NO
      30113 POLYADENYL?
      61 NO(W) POLYADENYL?
S8      2 S6 AND (NO (W) POLYADENYL?)
? rd
>>>Duplicate detection is not supported for File 235.
>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.
...completed examining records
S9      2 RD (unique items)
? t s9/3,ab/all
>>>No matching display code(s) found in file(s): 65, 235, 306

9/3,AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

04231015 83218919 PMID: 6304500
```

Preparation of a "functional library" of African green monkey DNA fragments which substitute for the processing/polyadenylation signal in the herpes simplex virus type 1 thymidine kinase gene.

Santangelo G M; Cole C N

Molecular and cellular biology (UNITED STATES) Apr 1983, 3 (4)
p643-53, ISSN 0270-7306 Journal Code: 8109087

Contract/Grant No.: CA-16038; CA; NCI; RR 0538; RR; NCRR

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Fragments of African green monkey (*Cercopithecus aethiops*) DNA (3.5 to 18.0 kilobases) were inserted downstream from the thymidine kinase (TK, tk) coding region in pTK206/SV010, a gene construct which lacks both copies of the hexanucleotide 5'-**AATAAA**-3' and contains a simian virus 40 origin of replication, allowing it to replicate in Cos-1 cells. **No polyadenylated** tk mRNA was detected in Cos-1 cells transfected by pTK206/SV010. The ability of simian DNA fragments to restore tk gene expression was examined by measuring the incorporation of [125I]iododeoxycytidine into DNA in Cos-1 cells transfected by pTK206/SV010 insertion derivatives. tk gene expression was restored by the insertion in 56 of the 67 plasmids analyzed, and the level of expression equaled or exceeded that obtained with the wild-type tk gene in 30 of these. In all plasmids examined that showed restoration of tk gene expression, polyadenylated tk mRNA of discrete size was detected. The sizes of these tk mRNAs were consistent with the existence of processing and polyadenylation signals within the inserted DNA fragments. The frequency with which inserted fragments restored tk gene expression suggests that the minimal signal for processing and polyadenylation is a hexanucleotide (AAUAAA or a similar sequence). LTK- cells were biochemically transformed to TK+ with representative insertion constructs. pTK206/SV010 transformed LTK- cells at a very low frequency; the frequency of transformation with insertion derivatives was 40 to 12,000 times higher.

9/3,AB/2 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

04192761 BIOSIS NO.: 000077018805

PREPARATION OF A FUNCTIONAL LIBRARY OF AFRICAN GREEN MONKEY

CERCOPITHECUS-AETHIOPS DNA FRAGMENTS WHICH SUBSTITUTE FOR THE PROCESSING
POLY ADENYLATION SIGNAL IN THE HERPES SIMPLEX VIRUS TYPE 1 THYMIDINE
KINASE GENE

AUTHOR: SANTANGELO G M; COLE C N

AUTHOR ADDRESS: DEP. OF HUMAN GENETICS, YALE UNIV. SCH. OF MED., NEW HAVEN,
CONN. 06510.

JOURNAL: MOL CELL BIOL 3 (4). 1983. 643-653. 1983

FULL JOURNAL NAME: Molecular and Cellular Biology

CODEN: MCEBD

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Fragments of African green monkey (*Cercopithecus aethiops*) DNA (3.5-18.0 kilobases) were inserted downstream from the thymidine kinase (TK, tk) coding region in pTK206/SV010, a gene construct which lacks both copies of the hexanucleotide 5'-**AATAAA**-3' and contains a SV40 origin of replication, allowing it to replicate in Cos-1 cells. **No polyadenylated** tk mRNA was detected in Cos-1 cells transfected by pTK206/SV010. The ability of simian DNA fragments to restore tk gene expression was examined by measuring the incorporation of [125I]iododeoxycytidine into DNA in Cos-1 cells transfected by pTK206/SV010 insertion derivatives, tk gene expression was restored by the insertion in 56 of the 67 plasmids analyzed, and the level of

expression equaled or exceeded that obtained with the wild-type tk gene in 30 of these. In all plasmids examined that showed restoration of tk gene expression, polyadenylated tk mRNA of discrete size was detected. The sizes of these tk mRNA were consistent with the existence of processing and polyadenylation signals within the inserted DNA fragments. The frequency with which inserted fragments restored tk gene expression suggests that the minimal signal for processing and polyadenylation is a hexanucleotide (AAUAAA or a similar sequence). Mouse LTK- cells were biochemically transformed to TK+ with representative insertion constructs. pTK206/SV010 transformed LTK- cells at a very low frequency; the frequency of transformation with insertion derivatives was 40-12,000 times higher.

1983

b 155, 5, agri
03feb03 18:10:47 User242957 Session D588.2
\$0.00 0.071 DialUnits File410
\$0.00 Estimated cost File410
\$0.01 TELNET
\$0.01 Estimated cost this search
\$0.01 Estimated total session cost 0.223 DialUnits

SYSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1966-2003/Jan W4
File 5:Biosis Previews(R) 1969-2003/Jan W4
(c) 2003 BIOSIS
*File 5: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.
File 6:NTIS 1964-2003/Feb W1
(c) 2003 NTIS, Intl Cpyrght All Rights Res
*File 6: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.
File 10:AGRICOLA 70-2003/Jan
(c) format only 2003 The Dialog Corporation
File 34:SciSearch(R) Cited Ref Sci 1990-2003/Jan W4
(c) 2003 Inst for Sci Info
*File 34: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.
File 50:CAB Abstracts 1972-2002/Dec
(c) 2003 CAB International
*File 50: Truncating CC codes is recommended for full retrieval. See Help News50 for details.
File 65:Inside Conferences 1993-2003/Feb W1
(c) 2003 BLDSC all rts. reserv.
File 94:JICST-EPlus 1985-2003/Nov W3
(c) 2003 Japan Science and Tech Corp(JST)
File 98:General Sci Abs/Full-Text 1984-2003/Dec
(c) 2003 The HW Wilson Co.
File 99:Wilson Appl. Sci & Tech Abs 1983-2003/Dec
(c) 2003 The HW Wilson Co.
File 143:Biol. & Agric. Index 1983-2003/Dec
(c) 2003 The HW Wilson Co
File 144:Pascal 1973-2003/Jan W4
(c) 2003 INIST/CNRS
File 203:AGRIS 1974-2002/Nov
Dist by NAL, Intl Copr. All rights reserved
File 235:AGROProjects 1990-2003/Q1
(c) 2003 PJB Publications,Ltd.
File 266:FEDRIP 2003/Dec
Comp & dist by NTIS, Intl Copyright All Rights Res
File 306:Pesticide Fact File 1998/Jun
(c) 1998 BCPC
File 357:Derwent Biotech Res. 1982-2003/Feb W1
(c) 2003 Thomson Derwent & ISI
*File 357: File is now current. See HELP NEWS 357.
Alert feature enhanced for multiple files, etc. See HELP ALERT.
File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
(c) 1998 Inst for Sci Info

Set	Items	Description
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? s poly(w) "a"

Processing

Processing

Processing

Processed 10 of 18 files ...

Processing

Completed processing all files


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539838 POLY
40986530 A
S1 45237 POLY(W) "A"
? s s1 and py<1999
Processing
>>>File 10 processing for PY= : PY=1999
>>> started at PY=A stopped at PY=196U
Processing
Processing
Processed 10 of 18 files ...
Processing
>>>One or more prefixes are unsupported
>>> or undefined in one or more files.
Completed processing all files
45237 S1
68900547 PY<1999
S2 37041 S1 AND PY<1999
? s s2 and "gt"
37041 S2
88682 GT
S3 310 S2 AND "GT"
? s s3 and transform?
310 S3
1688696 TRANSFORM?
S4 16 S3 AND TRANSFORM?
? rd
>>>Duplicate detection is not supported for File 235.
>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.
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S5 14 RD (unique items)
? t s5/3,ab/all
>>>No matching display code(s) found in file(s): 65, 235, 306

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5/3,AB/1 (Item 1 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

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09165085 97060453 PMID: 8903488

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The somatic mutation frequency of the **transforming** growth factor beta receptor type II gene varies widely among different cancers with microsatellite instability.

Abe T; Ouyang H; Migita T; Kato Y; Kimura M; Shiiba K; Sunamura M; Matsuno S; Horii A

Department of Molecular Pathology, Tohoku University School of Medicine, Sendai, Japan.

European journal of surgical oncology : the journal of the European Society of Surgical Oncology and the British Association of Surgical Oncology (ENGLAND) Oct 1996, 22 (5) p474-7, ISSN 0748-7983

Journal Code: 8504356

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Disruption of the DNA mismatch repair system, characterized by microsatellite instability (MSI), plays an important role in the course of human carcinogenesis. Frequent somatic mutations in a polyadenine (poly(A)) tract and two GT repeats within the coding region of the **transforming** growth factor beta (TGFbeta) receptor II (RII) gene were reported in colorectal cancers with MSI. We examined mutations of RII in cancers of various organs with MSI and found deletions at the **poly(A)** tract in eight of nine (89%) gastric cancers and four of five (80%) colorectal cancers. In contrast, no mutations were found in cancers of the pancreas, endometrium, or lungs. These results suggest

that TGFbeta-mediated growth control plays a very important role in the stomach and colorectum.

5/3,AB/2 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

08884945 BIOSIS NO.: 199396036446
A bone marrow stromal cell line is a source and target for platelet-derived growth factor.
AUTHOR: Abboud Sherry L
AUTHOR ADDRESS: Dep. Med., Univ. Texas Health Science Cent., 7703 Floyd Curl Drive, San Antonio, TX 78284**USA
JOURNAL: Blood 81 (10):p2547-2553 1993
ISSN: 0006-4971
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Platelet-derived growth factor (PDGF) stimulates multi-potent and erythroid progenitors as well as stromal fibroblasts. Any of the three dimeric forms of PDGF (AA, AB, or BB) could potentially interact with these cells; however, the precise cellular origin of PDGF production in the bone marrow microenvironment is not known. In the present study, we found that medium conditioned by MBA-2, murine bone marrow-derived endothelial cells, contains PDGF activity that competes for (125I)PDGF binding to human foreskin fibroblasts and is mitogenic for these fibroblasts. Northern analysis of poly(A)+ RNA from MBA-2 shows the expression of both PDGF A-chain and B-chain mRNAs. Because cytokines such as transforming growth factor-beta (TGF-beta) regulate hematopoiesis and stimulate PDGF in certain mesenchymal cells, we determined whether TGF-beta influences PDGF secretion and gene expression in MBA-2. TGF-beta induced PDGF A-chain and B-chain mRNAs and the release of PDGF activity. Each of the three PDGF isoforms also stimulated DNA synthesis in MBA-2, but with different potency (BB gt AB gt AA). Ligand binding studies showed specific binding of labeled PDGF BB and, to a lesser extent, PDGF AA isoform, consistent with predominant expression of the PDGF-beta receptor in MBA-2. These data show that murine endothelial stromal cells release PDGF activity and respond to PDGF. Local production of PDGF in the marrow microenvironment may play an important role in regulating hematopoietic and stromal cell proliferation.

1993

5/3,AB/3 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

04289653 BIOSIS NO.: 000078019195
CLONING OF COMPLEMENTARY DNA SEQUENCES OF HUMAN ADENOSINE DEAMINASE
EC-3.5.4.4
AUTHOR: WIGINTON D A; ADRIAN G S; FRIEDMAN R L; SUTTLE D P; HUTTON J J
AUTHOR ADDRESS: DEPARTMENT OF MEDICINE, UNIVERSITY OF TEXAS HEALTH SCIENCE CENTER, SAN ANTONIO, TEXAS 78284.
JOURNAL: PROC NATL ACAD SCI U S A 80 (24). 1983 (RECD. 1984). 7481-7485.
1983
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Cloned c[complementary]DNA sequences of human adenosine deaminase (ADA; adenosine aminohydrolase, EC 3.5.4.4) were isolated from a cDNA library constructed in bacteriophage .lambda.gt 10. The cDNA for the library was prepared from poly(A)+ RNA isolated from a human T-lymphoblast cell line, CCRF-CEM. The library was initially screened by differential plaque hybridization to labeled cDNA prepared from human T- and B-lymphoblast cell lines with a 21-fold difference in levels of translatable ADA mRNA. Two recombinants containing cloned cDNA sequences for ADA were identified by hybridization-selected translation. Both recombinants contained approximately 1600 base pairs of inserted human DNA. Restriction maps of the two inserts were not identical. One contained approximately 40 base pairs of additional DNA toward the center of the cDNA. The cloned cDNA specifically hybridized to 5 fragments generated by HindIII digestion of human genomic DNA. It also hybridized to human lymphoblast RNA species 1.6 and 5.8 kilobases in length. The cDNA was used as a probe to estimate ADA mRNA levels in human lymphoblast cell lines. ADA mRNA levels correlate closely with levels of ADA catalytic activity and ADA protein in cell lines containing structurally normal ADA. A leukemic T-lymphoblast line produced 6-9 times as much ADA protein and ADA mRNA as **transformed** B-lymphoblast lines. Two mutant B-lymphoblast lines from patients with hereditary ADA deficiency contained unstable ADA protein but had 3-4 times the normal level of ADA mRNA.

1983

5/3,AB/4 (Item 1 from file: 34)
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci
(c) 2003 Inst for Sci Info. All rts. reserv.

06025200 Genuine Article#: XP995 Number of References: 18
Title: Intronic polyadenylation in the human glycylamide ribonucleotide formyltransferase gene (ABSTRACT AVAILABLE)
Author(s): Kan JLC; Moran RG (REPRINT)
Corporate Source: VIRGINIA COMMONWEALTH UNIV,MED COLL VIRGINIA, MASSEY CANC CTR, MCV BOX 980230/RICHMOND//VA/23298 (REPRINT); VIRGINIA COMMONWEALTH UNIV,MED COLL VIRGINIA, MASSEY CANC CTR/RICHMOND//VA/23298; VIRGINIA COMMONWEALTH UNIV,MED COLL VIRGINIA, DEPT PHARMACOL & TOXICOL/RICHMOND//VA/23298

Journal: NUCLEIC ACIDS RESEARCH, 1997, V25, N15 (AUG 1), P3118-3123
ISSN: 0305-1048 Publication date: 19970801
Publisher: OXFORD UNIV PRESS, GREAT CLARENDON ST, OXFORD, ENGLAND OX2 6DP
Language: English Document Type: ARTICLE

Abstract: The mouse glycylamide ribonucleotide formyltransferase (CART) locus is known to produce two functional proteins, one by recognition and use of an intronic polyadenylation site and the other by downstream splicing. We now report a similar intronic polyadenylation mechanism for the human CART locus. The human CART gene has two potential polyadenylation signals within the identically located intron as that involved in intronic polyadenylation in the mouse gene. Each of the potential polyadenylation signals in the human gene was followed by an extensive polyT rich tract, but only the downstream signal was preceded by a GT tract. Only the downstream signal was utilized. The poIyT rich tract which followed the functional polyadenylation site in the human GART gene was virtually identical in sequence to a similarly placed region in the mouse gene. An exact inverted complement to the poIyT rich stretch following the active polyadenylation signal was found in the upstream intron of the human gene, suggesting that a hairpin loop may be involved in this intronic polyadenylation.

5/3,AB/5 (Item 2 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2003 Inst for Sci Info. All rts. reserv.

05947146 Genuine Article#: XJ585 Number of References: 24
Title: The **GT**-rich sequence in the U5 region of rous sarcoma virus
long terminal repeat is required for transcription termination and 3'
processing (ABSTRACT AVAILABLE)
Author(s): Cleavinger PJ; Kandala JC; Guntaka RV (REPRINT)
Corporate Source: UNIV MISSOURI,SCH MED, DEPT MOL MICROBIOL &
IMMUNOL/COLUMBIA//MO/65212 (REPRINT); UNIV MISSOURI,SCH MED, DEPT MOL
MICROBIOL & IMMUNOL/COLUMBIA//MO/65212; MAYO CLIN,DEPT INTERNAL
MED/ROCHESTER//MN/
Journal: FOLIA BIOLOGICA, 1997, V43, N4, P153-160
ISSN: 0015-5500 Publication date: 19970000
Publisher: INST MOLECULAR GENETICS, FOLIA BIOLOGICA(PRAHA) FLEMINGOVO N.2,
PRAGUE 6, CZECH REPUBLIC 166 37
Language: English Document Type: ARTICLE
Abstract: The sequences in the LTR of Rous sarcoma virus that are required
for transcription termination and polyadenylation have been determined.
A vector containing LTR-neo-LTR has been constructed and deletions in
the U5 region of the downstream LTR have been made. The DNAs from
wild-type and deletion mutant recombinant plasmids were introduced into
QT6 cells and G418-resistant **transformants** were selected. Those
transformants with neo sequences in the arrangement, LTR-neo-LTR,
were analyzed for transcription termination and polyadenylation by
Northern blot analysis and by S1 protection experiments. The results
indicate that the polyadenylation signal, AATAAA, located in the U3
region alone, is not sufficient for 3' end processing and that the
sequence between +20 and +44 in the U5 region is absolutely required
for transcription termination or endonucleolytic cleavage and
polyadenylation.

5/3,AB/6 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2003 Inst for Sci Info. All rts. reserv.

00830384 Genuine Article#: EZ838 Number of References: 30
Title: 3' PROCESSING IN DICTYOSTELIUM - UNUSUAL SEQUENCE REQUIREMENTS AND
INTERACTION WITH A DOWNSTREAM PROMOTER (Abstract Available)
Author(s): MANIAK M; NELLEN W
Corporate Source: MAX PLANCK INST BIOCHEM,ZELLBIOL ABT/D-8033
MARTINSRIED//FED REP GER/; MAX PLANCK INST BIOCHEM,ZELLBIOL ABT/D-8033
MARTINSRIED//FED REP GER/
Journal: MOLECULAR MICROBIOLOGY, 1991, V5, N2, P245-251
Language: ENGLISH Document Type: ARTICLE
Abstract: We have determined the sequence requirements for 3'-processing in
Dictyostelium and find that a single AATAAA site, embedded in an
A/T-rich environment is sufficient. A synthetic oligonucleotide
containing the additional **GT**/T-rich element, which is necessary
for 3'-processing in higher eukaryotes, is not used in Dictyostelium.
On the basis of reports suggesting termination signals (upstream
terminators) in Dictyostelium promoters, we investigated possible
interactions between processing signals and regulatory elements. Our
data suggest that upstream termination enhances transcription from a
downstream promoter.

5/3,AB/7 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
(c) 2003 The HW Wilson Co. All rts. reserv.

04004113 H.W. WILSON RECORD NUMBER: BGSA99004113
Nonsegmented negative-strand RNA viruses: genetics and manipulation of

viral genomes.
Conzelmann, Karl-Klaus
Annual Review of Genetics v. 32 (1998) p. 123-62
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 19760

ABSTRACT: The genetics and manipulation of nonsegmented negative-strand RNA viruses (NSVs) are discussed. Protocols that have been developed to recover NSVs entirely from cDNA have opened up this group of viruses to detailed molecular genetic and virus biology analyses. The gene-expression strategy of nonsegmented NSVs involves the replication of ribonucleoprotein complexes and sequential synthesis of free mRNA. This strategy permits the use of NSVs to express heterologous sequences and has definite advantages in terms of easy manipulation of constructs, high capacity for foreign sequences, genetically stable expression, and the possibility of controlling the levels of expression. Furthermore, chimeric virus vectors carrying novel envelope protein genes and targeted to defined host cells offer interesting prospects for biomedical applications and transient gene therapy.

5/3,AB/8 (Item 2 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
(c) 2003 The HW Wilson Co. All rts. reserv.

03546744 H.W. WILSON RECORD NUMBER: BGS197046744
Basic mechanisms of transcript elongation and its regulation.
Uptain, S. M
Kane, C. M; Chamberlin, M. J
Annual Review of Biochemistry (Annu Rev Biochem) v. 66 ('97) p. 117-72
SPECIAL FEATURES: bibl il ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 27298

ABSTRACT: Ternary complexes of DNA-dependent RNA polymerase with its DNA template and nascent transcript are central intermediates in transcription. In recent years, several unusual biochemical reactions have been discovered that affect the progression of RNA polymerase in ternary complexes through various transcription units. These reactions can be signaled intrinsically, by nucleic acid sequences and the RNA polymerase, or extrinsically, by protein or other regulatory factors. These factors can affect any of these processes, including promoter proximal and promoter distal pausing in both prokaryotes and eukaryotes, and therefore play a central role in regulation of gene expression. In eukaryotic systems, at least two of these factors appear to be related to cellular **transformation** and human cancers. New models for the structure of ternary complexes, and for the mechanism by which they move along DNA, provide plausible explanations for novel biochemical reactions that have been observed. These models predict that RNA polymerase moves along DNA without the constant possibility of dissociation and consequent termination. A further prediction of these models is that the polymerase can move in a discontinuous or inchworm-like manner. Many direct predictions of these models have been confirmed. However, one feature of RNA chain elongation not predicted by the model is that the DNA sequence can determine whether the enzyme moves discontinuously or monotonically. In at least two cases, the encounter between the RNA polymerase and a DNA block to elongation appears to specifically induce a discontinuous mode of synthesis. These findings provide important new insights into the RNA chain elongation process and offer the prospect of understanding many significant biological regulatory systems at the molecular level. With permission, from the Annual Review of Biochemistry Volume 66, 1997, by Annual Reviews Inc.

(<http://www.annurev.org>).

5/3,AB/9 (Item 3 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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03546285 H.W. WILSON RECORD NUMBER: BGSI97046285
Transcription of protein-coding genes in trypanosomes by RNA polymerase I.
Lee, Mary Gwo-Shu
Van der Ploeg, Lex H. T
Annual Review of Microbiology (Annu Rev Microbiol) v. 51 ('97) p. 463-89
SPECIAL FEATURES: bibl il ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 13724

ABSTRACT: In eukaryotes, RNA polymerase (pol) II transcribes the protein-coding genes, whereas RNA pol I transcribes the genes that encode the three RNA species of the ribosome {the ribosomal RNAs (rRNAs)} at the nucleolus. Protozoan parasites of the order Kinetoplastida may represent an exception, because pol I can mediate the expression of exogenously introduced protein-coding genes in these single-cell organisms. A unique molecular mechanism, which leads to pre-mRNA maturation by trans-splicing, facilitates pol I-mediated protein-coding gene expression in trypanosomes. Trans-splicing adds a capped 39-nucleotide mini-exon, or spliced leader transcript, to the 5' end of the main coding exon posttranscriptionally. In other eukaryotes, the addition of a 5' cap, which is essential for mRNA function, occurs exclusively as a result of RNA pol II-mediated transcription. Given the assumption that cap addition represents the limiting factor, trans-splicing may have uncoupled the requirement for RNA pol II-mediated mRNA production. A comparison of the α -amanitin sensitivity of transcription in naturally occurring trypanosome protein-coding genes reveals that a unique sub set of protein-coding genes--the variant surface glycoprotein (VSG) expression sites and the procyclin or the procyclic acidic repetitive protein (PARP) genes--are transcribed by an RNA polymerase that is resistant to the mushroom toxin α -amanitin, a characteristic of transcription by RNA pol I. Promoter analysis and a pharmacological characterization of the RNA polymerase that transcribes these genes have strengthened the proposal that the VSG expression sites and the PARP genes represent naturally occurring protein-coding genes that are transcribed by RNA pol I. Reprinted by permission of the publisher.

5/3,AB/10 (Item 4 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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03051106 H.W. WILSON RECORD NUMBER: BGSI95051106
Microbiology to 10,500 meters in the deep sea.
Yayanos, A. Aristides
Annual Review of Microbiology (Annu Rev Microbiol) v. 49 ('95) p. 777-805
SPECIAL FEATURES: bibl il ISSN: 0066-4227
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 14157

ABSTRACT: Microorganisms in the deep sea live at high pressures, low and high temperatures, and in darkness. These parameters and their food supply govern their lives. The study of these creatures gives us an opportunity to see how life processes work at some of the highest temperatures and pressures of the biosphere. Cultured bacterial isolates can grow to over 100 MPa at 2{degree}C and to over 40 MPa at over 100{degree}C. These

cultures comprise the foundation for the study of the molecular biology and biotechnology of these isolates. The PTK diagram shows how temperature and pressure affect the growth rate of a bacterium and helps in the search for relationships among bacteria from habitats differing in temperature and pressure. Reprinted by permission of the publisher.

5/3,AB/11 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2003 Thomson Derwent & ISI. All rts. reserv.

0091291 DBR Accession No.: 89-09282 PATENT
Fungal catalase DNA - Candida tropicalis recombinant catalase production in Escherichia coli
PATENT ASSIGNEE: Mitsubishi-Chem. 1989
PATENT NUMBER: JP 1086879 PATENT DATE: 890331 WPI ACCESSION NO.: 89-141723 (8919)
PRIORITY APPLIC. NO.: JP 87246950 APPLIC. DATE: 870930
NATIONAL APPLIC. NO.: JP 87246950 APPLIC. DATE: 870930
LANGUAGE: Japanese
ABSTRACT: DNA encoding fungal, e.g. Candida sp., catalase (EC-1.11.1.6) is new. Also new is a method for producing recombinant catalase without growth retardation by ethanol byproducts. Poly(A)-RNA extracted with phenol and ethanol, from Candida Tropicalis, grown in the presence of n-alkane, is purified by oligo-dt-cellulose chromatography and used to construct a cDNA gene bank in phage lambda-gt -11. cDNA was prepared from the mRNA by reverse-transcriptase (EC-2.7.7.49) in the presence of a 12-18 b oligo-dt primer. The gene bank is screened using a specific antibody. Recombinant phages containing the catalase gene fused to the beta-galactosidase (EC-3.2.1.23) gene under the control of the lactose operon promoter are used to transform Escherichia coli. Transformants are induced to produce the fusion protein by addition of isopropyl-beta-D-galactopyranoside to the culture medium. (16pp)

5/3,AB/12 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2003 Thomson Derwent & ISI. All rts. reserv.

0076611 DBR Accession No.: 88-07460 PATENT
Human Factor-VIII-C analog free of other proteins - produced from recombinant DNA and used in the treatment of coagulation disorders
PATENT ASSIGNEE: Rorer 1988
PATENT NUMBER: EP 265778 PATENT DATE: 880504 WPI ACCESSION NO.: 88-120930 (8818)
PRIORITY APPLIC. NO.: US 919153 APPLIC. DATE: 861015
NATIONAL APPLIC. NO.: EP 87115043 APPLIC. DATE: 871014
LANGUAGE: English
ABSTRACT: Human Factor-VIII-C analog free of other human proteins is new together with a cDNA clone encoding the complete Factor-VIII-C sequence. Genetically engineered analogs to Factor-VIII-C provide a dependable, readily available therapeutic agent for use in hemophilia and coagulation disorder treatment in humans or animals. mRNA is extracted from a tissue sample of cultured cells, enriched by poly(A) mRNA-containing material and used to synthesize a single-strand cDNA using reverse-transcriptase (EC-2.7.7.49). Double-stranded cDNA is synthesized using DNA-polymerase (EC-2.7.7.7) and inserted into an expression vector, which is used to transform a host cell. Factor-VIII-C analog cDNA containing clones are detected by specific antibodies against part or all of the analog protein. In an example, total RNA was extracted from human umbilical vein endothelial cells and used to prepare poly(A)-containing RNA. Double-stranded cDNA was prepared and made

blunt-ended, treated with EcoRI-methylase and DNA-polymerase-I, ligated with phosphorylated EcoRI linkers and inserted into phage lambda-gt -11 to form a library. The gene was expressed in mouse C127 cell cultures. (42pp)

5/3,AB/13 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2003 Thomson Derwent & ISI. All rts. reserv.

0075714 DBR Accession No.: 88-06563 PATENT
Gene encoding batroxobin - cloning and expression; hemostatic enzyme
PATENT ASSIGNEE: Yamashina I 1988
PATENT NUMBER: JP 63049084 (Kokai) PATENT DATE: 880301
WPI ACCESSION NO.: 88-096821 (8814)
PRIORITY APPLIC. NO.: JP 86193058 APPLIC. DATE: 860819
NATIONAL APPLIC. NO.: JP 86193058 APPLIC. DATE: 860819
LANGUAGE: Japanese
ABSTRACT: A gene encodes a polypeptide having the batroxobin (EC-3.4.21.29) amino acid sequence. The gene is hybridized with an oligonucleotide of sequence CCI CCI CTI CTT ACA CTA TAI TTI CII GT, in which the 12th T may be substituted by C, the 15th A by G, and the 18th A by G. For preparation of the gene, RNA is isolated from a poison gland of Bothrops atrox moojeni (from South America). Poly-A mRNA is then isolated and used in the construction of double-stranded cDNA. The cDNA is inserted into a vector and used to transform a host for the production of batroxobin. The method ensures a stable supply of the protein. Batroxobin is a thrombin-like enzyme which specifically disconnects fibrinogen A to produce soluble fibrin. (11pp)

5/3,AB/14 (Item 4 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2003 Thomson Derwent & ISI. All rts. reserv.

0068557 DBR Accession No.: 87-12905 PATENT
New DNA sequence coding for Factor-XIIIIa - and expressed proteins, useful as diagnostic and for producing antibodies
PATENT ASSIGNEE: Behringwerke 1987
PATENT NUMBER: EP 236978 PATENT DATE: 870916 WPI ACCESSION NO.: 87-258275 (8737)
PRIORITY APPLIC. NO.: DE 3621371 APPLIC. DATE: 860626
NATIONAL APPLIC. NO.: EP 87103322 APPLIC. DATE: 870306
LANGUAGE: German
ABSTRACT: A DNA sequence (I) coding for Factor-XIIIIa expresses proteins useful as diagnostic agents for detecting genetic diseases associated with Factor-XIIIIa deficiency. Total RNA is isolated from mature, human placental tissue and the poly-A fraction is used to form double-stranded cDNA, which is used to construct a gene bank in phage lambda-gt10. The gene bank was screened using oligonucleotide probes to isolate clones containing overlapping portions of the Factor-VIIIIa coding sequences. Clone gt-12 was incubated with EcoRI to isolate a 17046 bp fragment and this was cloned in pIC19H to give pIC19H-12.1. Similarly, clone gt 10-11 was used to construct pIC19H11.1. Vector 12.1 was cut with ClaI and 11.1 with BamHI, and the fragments were hybridized and transformed into Escherichia coli to yield plasmid pFXIIII-13 containing the whole coding region. This plasmid contained 2693 bp of Factor-XIIIIa DNA and expressed a hybrid protein of 732 amino acids of natural XIIIIa plus 44 N-terminal acids. pFXIIII-13 can be modified to make it suitable for use with yeast or animal cells. (30 ref)


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(30 ref)
? ds

Set      Items  Description
S1       45237  POLY(W)"A"
S2       37041  S1 AND PY<1999
S3        310   S2 AND "GT"
S4        16   S3 AND TRANSFORM?
S5        14   RD (unique items)
? s s3 not s4
          310   S3
          16   S4
        S6    294  S3 NOT S4
? rd
>>>Duplicate detection is not supported for File 235.
>>>Duplicate detection is not supported for File 306.

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>>>Records from unsupported files will be retained in the RD set.
...examined 50 records (50)
...examined 50 records (100)
...examined 50 records (150)
...examined 50 records (200)
...examined 50 records (250)
...completed examining records
      S7      212  RD (unique items)
? s s7 and (yeast or plant)
          212  S7
          508177 YEAST
          4387292 PLANT
      S8      13  S7 AND (YEAST OR PLANT)
? t s8/3,ab/all
>>>No matching display code(s) found in file(s): 65, 235, 306

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8/3,AB/1      (Item 1 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

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09391315  97283747  PMID: 9137825
Characterization and expression analysis of a banana gene encoding
1-aminocyclopropane-1-carboxylate oxidase.
Huang P L; Do Y Y; Huang F C; Thay T S; Chang T W
Department of Horticulture, National Taiwan University, Taipei, ROC.
pungling@cc.ntu.edu.tw
Biochemistry and molecular biology international (AUSTRALIA) Apr
1997, 41 (5) p941-50, ISSN 1039-9712 Journal Code: 9306673
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
A cDNA encoding the banana 1-aminocyclopropane-1-carboxylate (ACC)
oxidase has previously been isolated from a cDNA library that was
constructed by extracting poly(A)+ RNA from peels of ripening
banana. This cDNA, designated as pMAO2, has 1,199 bp and contains an open
reading frame of 318 amino acids. In order to identify ripening-related
promoters of the banana ACC oxidase gene, pMAO2 was used as a probe to
screen a banana genomic library constructed in the lambda EMBL3 vector. The
banana ACC oxidase MAO2 gene has four exons and three introns, with all of
the boundaries between these introns and exons sharing a consensus
dinucleotide sequence of GT-AG. The expression of MAO2 gene in banana
begins after the onset of ripening (stage 2) and continuous into later
stages of the ripening process. The accumulation of MAO2 mRNA can be
induced by 1 microliter/l exogenous ethylene, and it reached steady state
level when 100 microliters/l exogenous ethylene was present.

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8/3,AB/2 (Item 2 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09228628 97134958 PMID: 8980518

Organization and characterization of the ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit epsilon N-methyltransferase gene in tobacco.

Ying Z; Janney N; Houtz R L
Department of Horticulture and Landscape Architecture, University of Kentucky, Lexington 40546, USA.

Plant molecular biology (NETHERLANDS) Nov 1996, 32 (4) p663-71
, ISSN 0167-4412 Journal Code: 9106343

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) large subunit (LS) epsilon N-methyltransferase (Rubisco LSMT) catalyzes the posttranslational methylation of the epsilon-amino group of Lys-14 in the LS of Rubisco in many higher plant species including tobacco. The tobacco Rubisco LSMT gene (rbcMT-T) and its cDNA were isolated, sequenced, and characterized. The gene contains 6 exons and spans about 6 kb. Primer extension analysis indicated one transcription start site located 93 nt upstream of the translation initiation site. Sequence analysis of the 5'-flanking region suggests several potential binding sites for transcription factors, including 7 GT -1 elements and an HSP-70.5 element. Gene dosage analysis by Southern hybridization demonstrated that the tobacco rbcMT-T gene is present as a single copy in the tobacco haploid genome. The full-length cDNA for tobacco rbcMT-T is 1974 nt in length excluding the 3' poly(A)15 tail, and encodes a 491 amino acid polypeptide with a molecular mass of ca. 56kDa. The deduced amino acid sequence of tobacco Rubisco LSMT has 64.5% identity and 75.3% similarity with the sequence of pea Rubisco LSMT, and both proteins contain several copies of a conserved imperfect leucine-rich repeat motif.

8/3,AB/3 (Item 3 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09110600 97008246 PMID: 8855401

Northern blot analysis of simple repetitive sequence transcription in plants.

Gortner G; Pfenninger M; Kahl G; Weising K

Department of Biology, University of Frankfurt am Main, Germany.

Electrophoresis (GERMANY) Jul 1996, 17 (7) p1183-9, ISSN

0173-0835 Journal Code: 8204476

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The presence of simple repetitive sequence motifs in RNA from various plant species was probed by Northern blot analysis. Hybridization of total, poly(A)(+)- and poly(A)(-)-RNA with microsatellite-complementary oligonucleotide probes revealed distinct bands with most but not all probe/species combinations, demonstrating the presence of di-, tri- and tetranucleotide repeat motifs in plant transcripts. Only trinucleotide repeat-derived hybridization signals were found to be enriched in the poly(A)(+)-fraction. The quality of Northern blot signals proved to be highly dependent on hybridization stringency. Thus, under the stringency conditions usually applied for oligonucleotide hybridization, some probes [(GT)8, (CAC)5, (TCC)5, and (CCTA)4] cross-hybridized to bands corresponding in size to 18S and/or 26S rRNA. Cross-hybridization to rRNA was significantly reduced at higher stringencies. These results stress the importance of carefully adjusting

the hybridization conditions in Northern blot analysis of simple sequence transcripts.

8/3,AB/4 (Item 4 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07380030 92304405 PMID: 1351729

Characterization of plastid 5-aminolevulinate dehydratase (ALAD; EC 4.2.1.24) from spinach (*Spinacia oleracea* L.) by sequencing and comparison with non-**plant** ALAD enzymes.

Schaumburg A; Schneider-Poetsch H A; Eckerskorn C
Botanisches Institut, Universitat zu Koln.

Zeitschrift fur Naturforschung. C, Journal of biosciences (GERMANY)
Jan-Feb 1992, 47 (1-2) p77-84, ISSN 0341-0382 Journal Code:
8912155

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We have sequenced 5-aminolevulinate dehydratase (ALAD; EC 2.4.1.24) of a **plant**. A full-length cDNA clone (1727 bp) encoding this enzyme has been identified by immunoscreening a lambda **gt** 11 cDNA library of spinach. ALAD is not a **plant**-specific enzyme; however, the **plant** enzyme differs from the well known ALAD enzymes of bacteria, **yeast** and animals in structural and biochemical properties and in that it is located in the plastid. Differences and homologies can be traced back to the molecular level. The mature ALAD subunit, whose N-terminus was determined by automatic Edman degradation, is a protein of 367 amino acid residues and has a Mr of 40,132. This figure is in the range of molecular weights of non-**plant** ALADs. The active centre is highly conserved and the same is true for the ion-binding domain, except that 4 cysteines of the non-**plant** enzymes (binding Zn²⁺) have disappeared and a total of 6 aspartic acids meets the demands of Mg(2+)-binding. However, there are more distinct differences. Apart from a transit sequence of 56 amino acids targeting the plastid, the N-terminal part of the mature **plant** enzyme differs considerably from non-**plant** ALAD enzymes. It is rich in prolines and hydroxylated amino acids. The apparent Mr on SDS-PAGE is 45,000 or higher, but up to now posttranslational modifications have not been found.

8/3,AB/5 (Item 5 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06938891 91246173 PMID: 2038317

Different classes of polyadenylation sites in the **yeast** *Saccharomyces cerevisiae*.

Irniger S; Egli C M; Braus G H

Institute of Microbiology, Swiss Federal Institute of Technology (ETH), Zurich.

Molecular and cellular biology (UNITED STATES) Jun 1991, 11 (6)
p3060-9, ISSN 0270-7306 Journal Code: 8109087

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

This report provides an analysis of the function of polyadenylation sites from six different genes of the **yeast** *Saccharomyces cerevisiae*. These sites were tested for their ability to turn off read-through transcription into the URA3 gene in vivo when inserted into an ACT-URA3 fusion gene. The 3' ends of all polyadenylation sites inserted into the test system in their natural configuration are identical to the 3' ends of the chromosomal genes. We identified two classes of polyadenylation sites: (i) efficient

9/3,AB/181 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2003 Inst for Sci Info. All rts. reserv.

05077971 Genuine Article#: TN858 Number of References: 45
Title: THE ORGANIZATION OF THE GENE (EPB72) ENCODING THE HUMAN ERYTHROCYTE
BAND-7 INTEGRAL MEMBRANE-PROTEIN (PROTEIN-7.2B) (Abstract Available)
Author(s): UNFRIED I; ENTLER B; PROHASKA R
Corporate Source: UNIV VIENNA, INST BIOCHEM, VIENNA BIOCTR, DR BOHR GASSE
9-3/A-1030 VIENNA//AUSTRIA/; UNIV VIENNA, INST BIOCHEM, VIENNA
BIOCTR/A-1030 VIENNA//AUSTRIA/
Journal: GENOMICS, 1995, V30, N3 (DEC 10), P521-528
ISSN: 0888-7543

Language: ENGLISH Document Type: ARTICLE

Abstract: The human gene EPB72 coding for the band 7 integral membrane protein, a major protein of the erythrocyte membrane, was isolated from a genomic DNA library and characterized. Spanning similar to 30 kb, the human EPB72 gene comprises seven exons ranging from 73 to 2331 bp; intron sizes range from 970 to similar to 11,200 bp. The first exon contains the 5'-untranslated region (61 nucleotides) and the coding sequence for the N-terminal domain; the second exon encodes the hydrophobic domain, including flanking cysteine and lysine residues. Exon 7 contains the C-terminal portion and a 2-kb 3'-untranslated region. The potential promoter region contains several consensus sequences for ubiquitous transcription factors (Sp1, AP1, AP2, CP1/2, NF kappa B, CREB, Ets-1, and CACC/GT-BF) and two imperfect sequences for erythroid factors (EKLF and GATA-1), in accordance with the ubiquitous distribution of the EPB72 mRNA in different cell types. No TATA box was apparent. An inverted Alu repeat element, flanked by nonamer direct repeats, was identified within the region -913/-620, relative to the cap site. Six additional Alu repeat elements, including one monomer and one trimer, were identified within the introns and the 3'-untranslated region. Two polyadenylation signals in the 3'-noncoding region of exon 7 enable the production of two mRNA species. (C) 1995 Academic Press, Inc.

9/3,AB/182 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2003 Inst for Sci Info. All rts. reserv.

01452468 Genuine Article#: HA344 Number of References: 40
Title: SALT-INDUCIBLE BETAIN ALDEHYDE DEHYDROGENASE FROM SUGAR-BEET - CDNA
CLONING AND EXPRESSION (Abstract Available)
Author(s): MCCUE KF; HANSON AD
Corporate Source: MICHIGAN STATE UNIV, US DOE, PLANT RES LAB/E
LANSING//MI/48824; CTR RECH BIOL VEGETALE/MONTREAL H1X
2B2/QUEBEC/CANADA/

Journal: PLANT MOLECULAR BIOLOGY, 1992, V18, N1 (JAN), P1-11

Language: ENGLISH Document Type: ARTICLE

Abstract: Members of the Chenopodiaceae, such as sugar beet and spinach, accumulate glycine betaine in response to salinity or drought stress. The last enzyme in the glycine betaine biosynthetic pathway is betaine aldehyde dehydrogenase (BADH). In sugar beet the activity of BADH was found to increase two- to four-fold in both leaves and roots as the NaCl level in the irrigation solution was raised from 0 to 500 mM. This increase in BADH activity was paralleled by an increase in level of translatable BADH mRNA. Several cDNAs encoding BADH were cloned from a lambda-gt 10 library representing poly(A)+ RNA from salinized leaves of sugar beet plants, by hybridization with a spinach BADH cDNA. Three nearly full-length cDNA clones were confirmed

sites (originating from the genes GCN4 and PHO5) that were functional in a strict orientation-dependent manner and (iii) bidirectional sites (derived from ARO4, TRP1, and TRP4) that had a distinctly reduced efficiency. The ADH1 polyadenylation site was efficient and bidirectional and was shown to be a combination of two polyadenylation sites of two convergently transcribed genes. Sequence comparison revealed that all efficient unidirectional polyadenylation sites contain the sequence TTTTAT, whereas all bidirectional sites have the tripartite sequence TAG...TA (T)GT...TTT. Both sequence elements have previously been proposed to be involved in 3' end formation. Site-directed point mutagenesis of the TTTTAT sequence had no effect, whereas mutations within the tripartite sequence caused a reduced efficiency for 3' end formation. The tripartite sequence alone, however, is not sufficient for 3' end formation, but it might be part of a signal sequence in the bidirectional class of **yeast** polyadenylation sites. Our findings support the assumption that there are at least two different mechanisms with different sequence elements directing 3' end formation in **yeast**.

8/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06342815 90037024 PMID: 2808405

The structure of the gene encoding chain c of the hemoglobin of the earthworm, *Lumbricus terrestris*.

Jhiang S M; Riggs A F

Department of Zoology, University of Texas, Austin 78712.

Journal of biological chemistry (UNITED STATES) Nov 15 1989, 264

(32) p19003-8, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: GM35847; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The complete nucleotide sequence of the gene for chain c of hemoglobin of the earthworm *Lumbricus terrestris* has been determined. The sequence of 4037 base pairs (bp) includes about 310 bp of 5'-flanking sequence and 110 bp 3' to the **poly(A)** site. Comparison of cDNA and genomic sequences shows four silent differences in codons that suggest the presence of at least two genes. The coding sequence is split by two introns of 1344 and 1169 bp at highly conserved positions (Jhiang, S. M., Garey, J. R., and Riggs, A. F. (1988) *Science* 240, 334-336). The first intron possesses the unusual 5' splice junction sequence GC instead of **GT**. Many tandem triplet repeats based on (GAT) and (CCT) are present in the first intron. The second intron has nine tandem repeats based on the consensus sequence AAGGAAGGAGGTC. Each intron has several exact inverted repeats of 9-10 bp that might result in loops of 78-140 nucleotides in the RNA prior to splicing. The sequences in the second intron, at positions 2423-2644 are about 65% identical with parts of several genes found in **yeast** mitochondria and in DNA from several other organisms.

8/3,AB/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06338955 90032633 PMID: 2806235

Isolation of a cDNA encoding the rat liver S-adenosylmethionine synthetase.

Horikawa S; Ishikawa M; Ozasa H; Tsukada K

Department of Pathological Biochemistry, Tokyo Medical and Dental University, Japan.

European journal of biochemistry / FEBS (GERMANY, WEST) Oct 1 1989, 184 (3) p497-501, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

We have isolated cDNA clones encoding the rat liver S-adenosylmethionine synthetase by means of immunological screening from a phage lambda **gt** 11 expression library containing cDNA synthesized from adult rat liver **poly(A)**-RNA. The amino acid sequence deduced from the cDNA indicates that the rat liver enzyme for this protein contains 397 amino acid residues and has a molecular mass of 43697 Da. The deduced amino acid sequence of rat liver S-adenosylmethionine synthetase was 68% similar to those of **yeast** S-adenosylmethionine synthetases encoded by two unlinked genes SAM1 and SAM2. The rat liver S-adenosylmethionine synthetase also shows 52% similarity with the deduced amino acid sequence of the MetK gene encoding the S-adenosylmethionine synthetase in Escherichia coli.

8/3,AB/8 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09536861 BIOSIS NO.: 199497545231
Sequence and spatial requirements for the tissue- and species-independent 3'-end processing mechanism of **plant** mRNA.
AUTHOR: Wu Lin; Ueda Takashi; Messing Joachim(a)
AUTHOR ADDRESS: (a)Waksman Inst., Rutgers University, PO Box 759, Piscataway, NJ 08855-0759**USA
JOURNAL: Molecular and Cellular Biology 14 (10):p6829-6838 1994
ISSN: 0270-7306
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Two cis-regulatory regions are required for efficient mRNA 3'-end processing of the maize 27-kDa zein mRNA: a region containing a duplicated AAUGAA **poly(A)** signal and a region that is present upstream from it. Strict spatial positioning of these two regions is required for efficient mRNA 3'-end processing. Insertion of a stuffer sequence as short as 17 or 18 bp either between the upstream region and the two AAUGAA motifs or between the two AAUGAA motifs drastically reduced the efficiency of 3'-end processing. Mutational analyses of the nucleotide preference at the fourth position of the AAUGAA motif revealed the preference order G **gt** A mchgt C or U, suggesting that AAUAAA is neither a defective nor an optimal **poly(A)** signal for the 27-kDa zein mRNA. As for the 3' control region of the cauliflower mosaic virus (CaMV) transcription unit, the mRNA 3'-end processing mechanism mediated by the 27-kDa zein 3' control sequence is neither tissue nor species specific. The 3' upstream sequence of the 27-kDa zein gene can functionally replace that of the CaMV transcription unit. Conversely, the CaMV upstream sequence can mediate mRNA polyadenylation in the presence of a duplicated 27-kDa zein **poly(A)** signal. However, instead of the proximal **poly(A)** signal normally used in the 27-kDa zein mRNA, the distal signal is utilized. These results suggest that a general mechanism controls the 3'-end processing of **plant** mRNAs and that the cis-regulatory functions mediated by their upstream regions are interchangeable.

1994

8/3,AB/9 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08768243 BIOSIS NO.: 199395057594

Nucleotide sequence of the 3'-terminal region of potato virus T RNA.
AUTHOR: Ochi Motoyasu; Kashiwazaki Satoshi; Hiratsuka Kazuyuki; Namba
Shigetou(a); Tsuchizaki Tsuneo
AUTHOR ADDRESS: (a)Lab. Plant Pathology, Faculty Agriculture, Univ. Tokyo,
Bunkyo-ku, Tokyo 113**Japan
JOURNAL: Annals of the Phytopathological Society of Japan 58 (3):p416-425
1992
ISSN: 0031-9473
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English; Japanese

ABSTRACT: The partial sequence of the capillovirus potato virus T (PVT) RNA containing the 3'-terminal 2392 nucleotides, excluding the **poly(A)** tail, was determined from cloned cDNA. The sequence contains three open reading frames (ORFs) which encode putative proteins (in the 5' fwdarw 3' direction) of M-r **gt** 29,000 (**gt** 29K; ORF 1), M-r 40,451 (40K; ORF 2) and M-r 23,596 (24K; ORF 3), followed by an untranslated region of 188 nucleotides upstream of the 3' **poly(A)** tail. The 5'-proximal ORF 1 encodes a product with significant homologies to the C-terminal portions of the putative polymerase proteins of "alpha-like" supergroup of **plant** RNA viruses, including apple chlorotic leaf spot virus (ACLSV; closterovirus subgroup A), carlavirus, potexvirus and tymovirus. The PVT 24K protein shared several blocks of conserved amino acids with the coat proteins of filamentous viruses, i.e. ACLSV, beet yellows virus (BYV; closterovirus subgroup B), citrus tristeza virus (CTV; closterovirus subgroup C), potexvirus and carlavirus. The PVT 40K protein had homologies with putative movement proteins encoded by several **plant** viruses (e.g. ACLSV 50K protein). PVT and ACLSV showed a similar arrangement of three ORFs in the 3'-terminal region of their genomes. However, this arrangement differs significantly from that of BYV. The sequence represented here is the first report on the group capillovirus which was established recently. These results support a close relationship of PVT with ACLSV which is currently classified in the closterovirus subgroup A.

1992

8/3,AB/10 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2003 Inst for Sci Info. All rts. reserv.

05433791 Genuine Article#: VY664 Number of References: 37
Title: ORGANIZATION AND CHARACTERIZATION OF THE RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT N-EPSILON-METHYLTRANSFERASE GENE IN TOBACCO (Abstract Available)
Author(s): YING ZT; JANNEY N; HOUTZ RL
Corporate Source: UNIV KENTUCKY,DEPT HORT & LANDSCAPE ARCHITECTURE,PLANT PHYSIOL BIOCHEM MOL BIOL PROGRAM/LEXINGTON//KY/40546; UNIV KENTUCKY,DEPT HORT & LANDSCAPE ARCHITECTURE,PLANT PHYSIOL BIOCHEM MOL BIOL PROGRAM/LEXINGTON//KY/40546
Journal: PLANT MOLECULAR BIOLOGY, 1996, V32, N4 (NOV), P663-671
ISSN: 0167-4412
Language: ENGLISH Document Type: ARTICLE
Abstract: Ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) large subunit (LS) N-epsilon-methyltransferase (Rubisco LSMT) catalyzes the posttranslational methylation of the epsilon-amino group of Lys-14 in the LS of Rubisco in many higher **plant** species including tobacco. The tobacco Rubisco LSMT gene (rbcMT-T) and its cDNA were isolated, sequenced, and characterized. The gene contains 6 exons and spans about 6 kb. Primer extension analysis indicated one transcription start site located 93 nt upstream of the translation initiation site. Sequence

analysis of the 5'-flanking region suggests several potential binding sites for transcription factors, including 7 GT-1 elements and an HSP-70.5 element. Gene dosage analysis by Southern hybridization demonstrated that the tobacco rbcMT-T gene is present as a single copy in the tobacco haploid genome. The full-length cDNA for tobacco rbcMT-T is 1974 nt in length excluding the 3' poly(A)(15) tail, and encodes a 491 amino acid polypeptide with a molecular mass of ca. 56 kDa. The deduced amino acid sequence of tobacco Rubisco LSMT has 64.5% identity and 75.3% similarity with the sequence of pea Rubisco LSMT, and both proteins contain several copies of a conserved imperfect leucine-rich repeat motif.

8/3,AB/11 (Item 1 from file: 50)
DIALOG(R)File 50:CAB Abstracts
(c) 2003 CAB International. All rts. reserv.

03351082 CAB Accession Number: 971002208

Molecular cloning of the cDNA encoding an antifungal protein in *Gastrodia elata* Bl.

Shu QunFang; Xu JinTang; Sun YoungRu

Institute of Genetics, Academia Sinica, Beijing 100101, China.

Acta Botanica Sinica vol. 37 (9): p.685-690

Publication Year: 1995

ISSN: 0577-7496 --

Language: Chinese Summary Language: english

Document Type: Journal article

Antifungal protein (GAFP), the main inhibitor of fungal infection in the secondary corm of *G. elata* Bl, was isolated and purified from plants. Its molecular weight was c. 14 kD. Polyclonal antibodies against GAFP were produced. In in vitro tests, GAFP inhibited the growth of some fungi, including *Gibberella zeae*, in crops. cDNA was synthesized from poly(A) mRNA purified from *G. elata*. The cDNA was ligated into phage vector lambda gt 11 DNA and packaged in vitro and the phages were propagated on *E. coli* Y 1090. A lambda gt 11 expression library was constructed. A cDNA clone encoding antifungal protein was obtained by immunoscreening the library using the protein as a probe. The lambda DNA containing the insert was digested by *ECO RI*. After isolation and purification of the recombinant lambda DNA, the insert was obtained. The cDNA was 300 bp in length. The cDNA clone encoding antifungal protein had been isolated from *G. elata*. 20 ref.

8/3,AB/12 (Item 1 from file: 94)
DIALOG(R)File 94:JICST-EPlus
(c)2003 Japan Science and Tech Corp(JST). All rts. reserv.

02066107 JICST ACCESSION NUMBER: 94A0533893 FILE SEGMENT: JICST-E

Amplification of .BETA.-Tubulin cDNA from *Camellia sinensis* by PCR.

TAKEUCHI ATSUKO (1); MATSUMOTO SATORU (1); HAYATSU MASAHIITO (1)

(1) Minist. of Agric., For. and Fish., Natl. Res. Inst. of Veg. and Ornam. Plants and Tea.

Yasai, Chagyo Shikenjo Kenkyu Hokoku. B. Chagyo(Bulletin of the National Research Institute of Vegetables, Ornamental Plants and Tea. Series B Tea), 1994, NO.7, PAGE.13-20, FIG.5, REF.13

JOURNAL NUMBER: F0562CAI ISSN NO: 0916-6858 CODEN: KHYCE

UNIVERSAL DECIMAL CLASSIFICATION: 633.7 575.113.089

LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan

DOCUMENT TYPE: Journal

ARTICLE TYPE: Original paper

MEDIA TYPE: Printed Publication

ABSTRACT: Total RNAs were extracted from the leaves of *Camellia sinensis* cv. 'Yabukita' by the application of modified guanidinium and SDS-phenol procedures. The concentration of 2-mercaptoethanol in the

extraction media increased to 15%. Poly(A)+RNAs were isolated from the total RNAs and showed an efficient translation activity in vitro. A cDNA library was constructed from the poly(A)+RNA using .LAMBDA.gt 11 as vector. The library consisted of 2.9*10⁶ independent clones. A fragment was amplified from the recombinant phage DNA with .BETA.-tubulin specific primers. The sequence was 505bp in length and no antisense primer sequence was detected. The deduced amino acid sequence showed that the amplified fragment covered about one third of the .BETA.-tubulin coding region, and also showed an extensive homology to the .BETA.-tubulin sequences from other species of higher plants. This first report of a .BETA.-tubulin sequence from woody plants suggests that the amino acid sequences of .BETA.-tubulin are conserved in both herbaceous and woody plants. (author abst.)

8/3,AB/13 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
(c) 2003 The HW Wilson Co. All rts. reserv.

03751712 H.W. WILSON RECORD NUMBER: BGS198001712
Yeast genetics to dissect the nuclear pore complex and
nucleocytoplasmic trafficking.
Fabre, Emmanuelle
Hurt, Ed
Annual Review of Genetics (Annu Rev Genet) v. 31 (1997) p. 277-313
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 16676

ABSTRACT: Current knowledge of nuclear pore proteins (nucleoporins) and the mechanism of nucleocytoplasmic transport in **yeast** is examined. DNA replication and RNA production take place within the nucleus, whereas protein synthesis occurs in the cytoplasm. The nuclear pore complex is responsible for bidirectional trafficking between these 2 compartments, and nucleocytoplasmic transport is signal mediated, energy dependent, and needs nucleoporins as well as several soluble transport factors. The details of **yeast** nuclear pore

ds

Set	Items	Description
S1	45237	POLY(W) "A"
S2	37041	S1 AND PY<1999
S3	310	S2 AND "GT"
S4	16	S3 AND TRANSFORM?
S5	14	RD (unique items)
S6	294	S3 NOT S4
S7	212	RD (unique items)
S8	13	S7 AND (YEAST OR PLANT)

? s s7 not s8

212 S7

13 S8

S9 199 S7 NOT S8

? t s9/3,ab/all

>>>No matching display code(s) found in file(s): 65, 235, 306

9/3,AB/1 (Item 1 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

10017948 98440370 PMID: 9767118

cDNA cloning of two splice variants of a human copper-containing monoamine oxidase pseudogene containing a dimeric Alu repeat sequence.

Cronin C N; Zhang X; Thompson D A; McIntire W S

Molecular Biology Division, Department of Veterans Affairs Medical Center, 4150 Clement St., San Francisco, CA 94121, USA.

Gene (NETHERLANDS) Oct 5 1998, 220 (1-2) p71-6, ISSN

0378-1119 Journal Code: 7706761

Contract/Grant No.: HL-16251; HL; NHLBI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Two alternatively spliced transcripts, psiHLAO1 and psiHLAO2, of a copper-containing monoamine oxidase pseudogene have been isolated from a human-liver cDNA library. The larger psiHLAO1 cDNA (2073bp) contains a 5'-flanking segment of 134bp, followed by an apparent open reading frame (ORF) of 1725bp. The deduced amino acid sequence of this ORF (574 residues) shares 81.0% similarity with the 763-residue monoamine oxidase from human placenta (HPAO) (the N-terminal 533 residues of psiHLAO1 share 86.7% similarity with HPAO). The psiHLAO1 ORF is interrupted by an in-frame stop codon corresponding to amino acid 225 and terminates within a type S(a) dimeric Alu repeat sequence. psiHLAO2 appears to be an alternatively spliced variant of psiHLAO1 that has 413 bases of psiHLAO1 excised according to the 'GT -AG' rule. The slightly longer 3' end of the psiHLAO2 transcript shows that the Alu repeat is followed by an 11-bp poly(A) tract that, in turn, is followed by an AT-rich (81%) sequence of 105bp. A reverse transcriptase-polymerase chain reaction (RT-PCR) protocol was used to confirm that both psiHLAO1 and psiHLAO2 are transcribed in human liver and placenta. A search of the expressed sequence tag (EST) database indicates that, like HPAO, psiHLAO derives also from the region 17q21 of the human genome.

9/3,AB/2 (Item 2 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

09913556 98351569 PMID: 9688283

Cloning and characterization of the gene encoding human osteoprotegerin/osteoclastogenesis-inhibitory factor.

Morinaga T; Nakagawa N; Yasuda H; Tsuda E; Higashio K

Research Institute of Life Sciences, Snow Brand Milk Products, Co. Ltd, Tochigi, Japan.

European journal of biochemistry / FEBS (GERMANY) Jun 15 1998,
254 (3) p685-91, ISSN 0014-2956 Journal Code: 0107600
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The human osteoprotegerin (OPG)-osteoclastogenesis-inhibitory factor (OCIF) gene has been cloned and characterized. The OPG-OCIF gene is a single-copy gene consisting of five exons, and spans 29 kb of the human genome. All the exon/intron boundaries comply with the GT/AG rule. The translation-termination codon is present in exon 5 and a typical poly(A)-addition signal resides 173-nucleotides downstream of the translation-termination codon. A major transcription-initiation site is present 67-nucleotides upstream of the initiation ATG codon. Two minor sites are present further upstream. The 4.2-kb and 6.5-kb transcripts detected in IMR-90 cells were found to contain the 3'-half of intron 2 and the entire intron 2, respectively. In the OPG-OCIF gene, a single intron divides the stretch that encode four Cys-rich motifs, implying diversity from the other members of the tumor necrosis factor receptor (TNFR) family. Two death domain homologous regions (DDHs) present in tandem in OPG-OCIF are encoded separately by exons 4 and 5. The conservation of amino-acid sequences suggests that exon 4 is produced by a duplication of a portion of exon 5.

9/3,AB/3 (Item 3 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09898834 98324897 PMID: 9657976

Human mitochondrial phosphoenolpyruvate carboxykinase 2 gene. Structure, chromosomal localization and tissue-specific expression.

Modaressi S; Brechtel K; Christ B; Jungermann K
Institut fur Biochemie und Molekulare Zellbiologie,
Georg-August-Universitat, Humboldtallee 23, D-37073 Gottingen, Germany.
Biochemical journal (ENGLAND) Jul 15 1998, 333 (Pt 2) p359-66,
ISSN 0264-6021 Journal Code: 2984726R

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The mitochondrial (mt) phosphoenolpyruvate carboxykinase 2 (PCK2) gene was isolated by screening a human genomic library with a rat cytosolic (cy) PCK1 cDNA probe comprising sequences from exons 2-9 and by PCR amplification of human genomic DNA spanning consecutive exons with known primer pairs from mtPCK2 cDNA containing sequences from two putative neighbouring exons. The mtPCK2 gene spans approx. 10 kb and consists of ten exons and nine introns. All exon-intron junction sequences match the classical GT/AG rule. Northern blot analysis of poly(A)+ and total RNA from various tissues revealed one mRNA species of approx. 2.4 kb. The gene is expressed in a variety of human tissues, mainly in liver, kidney, pancreas, intestine and fibroblasts. In contrast with the cytosolic isoenzyme, the mitochondrial form might not have a purely gluconeogenic function. The mtPCK2 gene maps to chromosome 14q11.2-q12, in contrast with the cyPCK1 gene located on 20q13.2-q13.31.

9/3,AB/4 (Item 4 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09720480 98137791 PMID: 9469932

Cloning and molecular analysis of a cDNA and the Cs-mnp1 gene encoding a manganese peroxidase isoenzyme from the lignin-degrading basidiomycete Ceriporiopsis subvermisporea.

Lobos S; Larrondo L; Salas L; Karahanian E; Vicuna R

Departamento de Bioquímica y Biología Molecular, Facultad de Ciencias Químicas y Farmacéuticas, Universidad de Chile, Santiago, Chile.

Gene (NETHERLANDS) Jan 12 1998, 206 (2) p185-93, ISSN 0378-1119 Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

A cDNA (MnP13-1) and the Cs-mnp1 gene encoding for an isoenzyme of manganese peroxidase (MnP) from *C. subvermispora* were isolated separately and sequenced. The cDNA, identified in a library constructed in the vector Lambda ZIPLOX, contains 1285 nucleotides, excluding the poly(A) tail, and has a 63% G+C content. The deduced protein sequence shows a high degree of identity with MnPs from other fungi. The mature protein contains 364 amino acids, which are preceded by a 24-amino-acid leader sequence. Consistent with the peroxidase mechanism of MnP, the proximal histidine, the distal histidine and the distal arginine are conserved, although the aromatic binding site (L/V/I-P-X-P) is less hydrophilic than those of other peroxidases. A gene coding for the same protein (Cs-mnp1) was isolated from a genomic library constructed in Lambda GEM-11 vector using the cDNA MnP13-1 as a probe. A subcloned SacI fragment of 2.5kb contained the complete sequence of the Cs-mnp1 gene, including 162bp and 770bp of the upstream and downstream regions, respectively. The Cs-mnp1 gene possesses seven short intervening sequences. The intron splice junction sequences as well as the putative internal lariat formation sites adhere to the GT-AG and CTRAY rules, respectively. To examine the structure of the regulatory region of the Cs-mnp1 gene further, a fragment of 1.9kb was amplified using inverse PCR. A putative TATAA element was identified 5' of the translational start codon. Also, an inverted CCAAT element, SP-1 and AP-2 sites and several putative heat-shock and metal response elements were identified.

9/3,AB/5 (Item 5 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09694257 98125524 PMID: 9464248

Characterization of the mevalonate kinase 5'-untranslated region provides evidence for coordinate regulation of cholesterol biosynthesis.

Bishop R W; Chambliss K L; Hoffmann G F; Tanaka R D; Gibson K M

Geron Corporation, Menlo Park, California 94025, USA.

Biochemical and biophysical research communications (UNITED STATES) Jan 26 1998, 242 (3) p518-24, ISSN 0006-291X Journal Code: 0372516

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Using a probe derived from the 5'-untranslated region of the human mevalonate kinase (MK) cDNA, we screened a lambda gt 11 genomic library and obtained a single clone containing the 5' untranslated region of the gene. Nucleotide sequencing identified several putative regulatory elements, including two Sp1 (GC box) elements and a CCAAT box. A canonical TATA box was not detected. Directly adjacent to one Sp1 element was a sterol regulatory element (SRE), 5'-CACCCCAG-3', which was a 7/8 base pair match to the consensus sequences identified in the genes encoding 3-hydroxy-3-methyl-glutaryl-coenzyme A synthase and reductase, and the LDL receptor. There was no Sp1 element upstream of the SRE. Northern blot analysis in human CRL1508T cells revealed that quantities of MK poly A + RNA increased for cells grown in the presence of lipid-deficient calf serum, and further increased upon addition of 1 micromolar lovastatin. Primer extension analysis with human poly A+ RNA suggested at least 4 transcription initiation sites downstream from the CCAAT box. To assess sterol responsiveness of transcription initiation, a 1.4 kb genomic fragment upstream of the translational start site was fused to the pSV2cat

vector for transient expression in COS-7 cells, with chloramphenicol acetyltransferase (CAT) as the reporter gene. This construct demonstrated modest levels of CAT expression which was induced > 2-fold when cells were grown in lipoprotein-deficient calf serum. Our data provide further evidence for coordinate regulation of cholesterol biosynthesis in response to sterol.

9/3,AB/6 (Item 6 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09487412 97370044 PMID: 9224613

Intronic polyadenylation in the human glycylamide ribonucleotide formyltransferase gene.

Kan J L; Moran R G

Department of Pharmacology and Toxicology and the Massey Cancer Center, Medical College of Virginia, Virginia Commonwealth University, Richmond, VA 23298-0230, USA.

Nucleic acids research (ENGLAND) Aug 1 1997, 25 (15) p3118-23,
ISSN 0305-1048 Journal Code: 0411011

Contract/Grant No.: CA-27605; CA; NCI; T32-CA-09564; CA; NCI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The mouse glycylamide ribonucleotide formyltransferase (GART) locus is known to produce two functional proteins, one by recognition and use of an intronic polyadenylation site and the other by downstream splicing. We now report a similar intronic polyadenylation mechanism for the human GART locus. The human GART gene has two potential polyadenylation signals within the identically located intron as that involved in intronic polyadenylation in the mouse gene. Each of the potential polyadenylation signals in the human gene was followed by an extensive polyT rich tract, but only the downstream signal was preceded by a GT tract. Only the downstream signal was utilized. The polyT rich tract which followed the functional polyadenylation site in the human GART gene was virtually identical in sequence to a similarly placed region in the mouse gene. An exact inverted complement to the polyT rich stretch following the active polyadenylation signal was found in the upstream intron of the human gene, suggesting that a hairpin loop may be involved in this intronic polyadenylation.

9/3,AB/7 (Item 7 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09341398 97252969 PMID: 9098427

A wild-type mu s C-terminal gene is expressed in Bloom's syndrome cells.

Ozawa T; Kondo N; Kato Y; Motoyoshi F; Suzuki Y; Shimozaawa N; Kasahara K; Orii T

Department of Pediatrics, Gifu University School of Medicine, Japan.

European journal of immunogenetics : official journal of the British Society for Histocompatibility and Immunogenetics (ENGLAND) Apr 1994, 21 (2) p133-9, ISSN 0960-7420 Journal Code: 9106962

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Selective IgM deficiency is found commonly in patients with Bloom's syndrome (BS). Serum IgM concentrations were low though serum IgG and IgA concentrations were normal in both patients with BS included in the study. In a previous study the authors showed that selective IgM deficiency in BS is due to an abnormality in the maturation of surface IgM-bearing cells into IgM-secreting cells and a failure of secreted mu (mu s) mRNA synthesis. The membrane-bound mu (mu m) and mu s mRNA are produced from

transcripts of a single immunoglobulin mu gene by alternative RNA processing pathways. The control of mu s mRNA synthesis depends on the addition of **poly(A)** to mu s C-terminal segment. The study described here demonstrated that there was no mutation or deletion in the sequence including mu s C-terminal coding sequence, the RNA splice site (GG/TAAAC) at the 5' end of mu s C-terminal segment, and the AATAAA **poly(A)** signal sequence, and second **GT**-rich element immediately down-stream of the cleavage site in both patients.

9/3,AB/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09338318 97224488 PMID: 9070922

Human fatty aldehyde dehydrogenase gene (ALDH10): organization and tissue-dependent expression.

Chang C; Yoshida A

Department of Biochemical Genetics, Beckman Research Institute of the City of Hope, Duarte, California 91010, USA.

Genomics (UNITED STATES) Feb 15 1997, 40 (1) p80-5, ISSN 0888-7543 Journal Code: 8800135

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Mutations in the fatty aldehyde dehydrogenase gene (ALDH10) are responsible for Sjogren-Larsson syndrome (De Laurenzi et al., 1996). In this study, the expression and the genomic organization of the ALDH10 gene are reported. The gene spans approximately 31 kb and consists of 10 exons and 9 introns. All exon-intron junction sequences match the classical **GT** /**AG** rule. Both S1 nuclease protection assay and primer extension study suggest that the transcription initiation site is located 195 nucleotides upstream from the ATG codon. No canonical TATA box can be found in the 5'-flanking sequence of the gene, but a CCAAT-like box was found 58 bp upstream of the putative transcription start site. Sequence analysis of the 5'-flanking region revealed numerous potential binding sites for transcription factors Sp1 and AP-2 and one putative HIP-1 binding site. Northern blot analysis of **poly(A)**+ RNA from various tissues revealed two mRNA species, with sizes around 4.0 and 2.0 kb, that are derived from the differential use of two polyadenylation sites. Although this gene is expressed in a variety of human tissues, the expression level of ALDH10 in the liver and skeletal muscle appears to be higher than that in other tissues examined.

9/3,AB/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09165325 97080531 PMID: 8921876

Structural comparison of a portion of the rat and mouse growth hormone receptor/binding protein genes.

Zhou Y; He L; Kopchick J J

Edison Biotechnology Institute, Ohio University, Athens 45701, USA.

Gene (NETHERLANDS) Oct 24 1996, 177 (1-2) p257-9, ISSN 0378-1119 Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

A portion of the rat growth hormone receptor (GHR) gene was cloned by PCR. Restriction enzyme digestion and DNA sequence analyses revealed that an exon, exon 8A, encoding the carboxy terminus of the rat serum growth hormone binding protein (GHBP) was located between exons 7 and 8 of the rat GHR gene. Two tandem poly-adenylation (**poly A**) signals for the .

GHBP mRNA were found in the 3'-untranslated region of this exon. In addition, a GT repeat tract was found adjacent to the 5'-splice donor site of intron 7/8A. The similarity of the nucleotide sequences of the rat and mouse GHR/GP gene suggests that the poly A signals and GT repeat may be involved in the regulation of GHR and GHBP expression.

9/3,AB/10 (Item 10 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08985100 96353162 PMID: 8748121

Effect of perinatal hypothyroidism on expression of cytochrome c oxidase subunit I gene, which is cloned by differential plaque screening from the cerebellum of newborn rat.

Koibuchi N; Matsuzaki S; Ichimura K; Ohtake H; Yamaoka S
Department of Physiology, Dokkyo University School of Medicine, Tochigi, Japan.

Journal of neuroendocrinology (ENGLAND) Nov 1995, 7 (11)
p847-53, ISSN 0953-8194 Journal Code: 8913461

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Early development of the central nervous system is influenced by several hormones including thyroid hormone. This study was designed to clone the gene whose expression is changed in association with perinatal hypothyroidism in the rat cerebellum. Rats were sacrificed at 15 day-old postnatal age (P15) and their cerebella were removed. Poly (A)+ RNA was extracted to construct a cDNA library using lambda gt 10 cloning vector. Differential plaque screening was then performed using 32P-labeled antisense cDNA synthesized from poly (A)+ RNA of the methimazole-treated (hypothyroid) P15 rat cerebellum (hypothyroid probe), and of the euthyroid P15 rat cerebellum (euthyroid probe). The clones, which hybridized strongly to the euthyroid probe and weakly or not at all to the hypothyroid probe, were isolated. Sequence analysis of these clones revealed that all isolated clones encode cytochrome c oxidase subunit I (COX I), which is located in the mitochondrial DNA. The decrease in COX I gene expression was not seen in the animals, which received methimazole treatment and daily replacement of thyroid hormone. In situ hybridization detection showed not only overall decrease in COX I gene expression but also change in distribution of hybridization signal in the cerebellar cortex of hypothyroid rat. Such change was not observed in the T4-replaced animals. Based on the evidence that thyroid hormone greatly influences brain development, the results of the present study indicate that the terminal enzyme of mitochondrial respiratory chain, COX I is one of the important target molecules regulated by thyroid hormone in the newborn rat cerebellum.

9/3,AB/11 (Item 11 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08949254 96301407 PMID: 8660979

Structure and organization of the human neuronatin gene.

Dou D; Joseph R
Department of Neurology, Henry Ford Hospital & Health Sciences Center, Detroit, Michigan 48202, USA.

Genomics (UNITED STATES) Apr 15 1996, 33 (2) p292-7, ISSN 0888-7543 Journal Code: 8800135

Contract/Grant No.: NS01521; NS; NINDS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Neuronatin is a brain-specific human gene that we recently isolated and observed to be selectively expressed during brain development. In this report, the genomic structure and organization of human neuronatin is described. The human gene spans 3973 bases and contains three exons and two introns. Based on primer extension analysis, a single cap site is located 124 bases upstream from the methionine (ATG) initiation codon, in good context, GAACCATGG. The promoter contains a modified TATA box, CATAAA (-27), and a modified CAAT box, GGCGAAT (-59). The 5'-flanking region contains putative transcription factor binding sites for SP-1, AP-2 (two sites), delta-subunit, SRE-2, NF-A1, and ETS. In addition, a 21-base sequence highly homologous to the neural restrictive silence element that governs neuron-specific gene expression is observed at -421. Furthermore, SP-1 and AP-3 binding sites are present in intron 1. All splice donor and acceptor sites conformed to the GT/AG rule. Exon 1 encodes 24 amino acids, exon 2 encodes 27 amino acids, and exon 3 encodes 30 amino acids. At the 3'-end of the gene, the poly(A) signal, AATAAA, poly(A) site, and GT cluster are observed. The neuronatin gene is expressed as two mRNA species, alpha and beta, generated by alternative splicing. The alpha-form contains all three exons, whereas in the beta-form, the middle exon has been spliced out. The third nucleotide of all frequently used codons, except threonine, of neuronatin is either G or C, consistent with codon usage expected for Homo sapiens. This information about the structure of the human neuronatin gene will help in understanding the significance of this gene in brain development and human disease.

9/3,AB/12 (Item 12 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08374467 95134094 PMID: 7832644

Unusual splice sites in the E1A-E1B cotranscripts synthesized in adenovirus type 40-infected A549 cells.

Ishida S; Fujinaga Y; Fujinaga K; Sakamoto N; Hashimoto S

Cancer Research Institute, Sapporo Medical College, Japan.

Archives of virology (AUSTRIA) 1994, 139 (3-4) p389-402,

ISSN 0304-8608 Journal Code: 7506870

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The adenovirus E1 DNA region consists of two transcription units, E1A and E1B. In this paper we report that the E1A-E1B cotranscripts containing sequences of both the E1A and E1B regions are synthesized during adenovirus type 40 (Ad40) infection of A549 cells. Cytoplasmic RNA was isolated from Ad40-infected A549 cells at 24, 72, and 100 h post infection (p.i.). The complementary (c) DNA was synthesized by reverse transcription using an oligo-dT primer and then amplified by the polymerase chain reaction (PCR) using primers derived from the E1A and E1B regions. The cDNAs thus amplified were sequenced either directly or after cloning into bacteriophage M13 vectors. Analysis of cDNA indicated that the E1A-E1B cotranscripts are synthesized at 72 h p.i., but not at 24 or 100 h p.i. Nucleotide sequences of three cDNAs of the E1A-E1B cotranscripts indicated that the cotranscripts originate from the E1A promoter and lack sequences for both the E1A poly(A) site and E1B cap site. The splices create open reading frames for E1A-E1B fused polypeptides around the E1A-E1B junctions in these mRNAs. Most interestingly, the sequence analysis showed that the 5' and 3' splice junctions in the two E1A-E1B cotranscripts do not conform to the splice consensus GT-AG rule. Our results thus suggest that factor(s) which lead to unusual splicing in the E1 mRNAs are present in Ad40-infected A549 cells.

9/3,AB/13 (Item 13 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

08344914 95102624 PMID: 7804242

Cloning of a partial length cDNA encoding the C-terminal portion of the 75-77-kDa antigen of *Trypanosoma cruzi*.

Yang S; Bergman L W; Scholl D R; Rowland E C

Department of Biological Sciences, Ohio University, Athens 45701.

Journal of eukaryotic microbiology (UNITED STATES) Sep-Oct 1994,

41 (5) p435-41, ISSN 1066-5234 Journal Code: 9306405

Contract/Grant No.: AI23704; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

It has been suggested that several *Trypanosoma cruzi* antigens have possible protective epitopes which may be suitable vaccine candidates. We found previously that animals resistant to *T. cruzi* infection produced antibodies against the 75-77-kDa parasite antigen. To test the ability of the recombinant form of this antigen to protect animals from *T. cruzi* infection, the cDNA which encodes a portion of the 75-77-kDa antigen was cloned using a cDNA library constructed in an orientation-specific bacteriophage expression vector (lambda gt 11) from poly (A)+ RNA of Brazil strain epimastigotes. One clone, named SFS-40, was selected by screening the library using affinity purified antibodies specific for the 75-77-kDa parasite antigen as probe. The cDNA corresponding to the 1.7-kilobase insert of SFS-40 was subcloned into plasmid vectors and characterized. The cDNA sequence encodes a polypeptide of about 40 kDa. The putative product of the cDNA was homologous to members of the 70-kDa stress protein family. When epimastigotes were shifted from 29 degrees C to 37 degrees C, there was no change in the level of SFS-40 mRNA. In contrast, the 70-kDa heat shock protein mRNA of the parasite was increased about four fold by this treatment.

9/3,AB/14 (Item 14 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

08219635 94335554 PMID: 8057779

Identification of two promoter regions in the rat B-50/GAP-43 gene.

Eggen B J; Nielander H B; Rensen-de Leeuw M G; Schotman P; Gispen W H; Schrama L H

Laboratory for Physiological Chemistry, University of Utrecht, The Netherlands.

Brain research. Molecular brain research (NETHERLANDS) May 1994,

23 (3) p221-34, ISSN 0169-328X Journal Code: 8908640

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

To determine cis-acting elements controlling the rat B-50/GAP-43 gene expression, the genomic DNA encoding exon 1 and the 5' flanking sequence was isolated. Sequence analysis of 1 kb 5' untranslated region (UTR) revealed the presence of a (GA)-repeat and a (GT)-repeat. The size of the (GA)-repeat varied due to both an instability of phage lambda lambda DNA in *E. coli* and genomic variation between rats. Transcription initiation sites were mapped in 8-day-old rat brain poly(A)+ mRNA. Primer extension indicated multiple transcription start sites at -159 and -339/-342 nt upstream of the translation start site; reverse transcriptase coupled PCR showed that the most 5' transcription start site is located between -465 and -440. Northern blotting demonstrated that approximately 90% of the B-50 mRNAs initiates at approximately -50. Promoter analysis by transient transfection assays in undifferentiated and retinoic acid-differentiated P19-EC cells revealed that the rat B-50 gene contains two promoters. P1 (located between -750 and -407) contains commonly

observed promoter elements such as a TATA box and CCAAT boxes. P2 (located between -233 and -1) neither contains TATA boxes, CCAAT boxes nor consensus sequences of house-keeping gene promoters like GC-boxes. The activity of P1 is inhibited at neuroectodermal differentiation of P19-EC cells whereas the activity of P2 is stimulated. In 8 day old rat brain the majority of the B-50 mRNA transcripts are derived from P2. It is concluded that at this developmental stage P2 is the most important promoter.

9/3,AB/15 (Item 15 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08120441 94253112 PMID: 7515057

A splice variant of arrestin. Molecular cloning and localization in bovine retina.

Smith W C; Milam A H; Dugger D; Arendt A; Hargrave P A; Palczewski K
Department of Ophthalmology, University of Florida, Gainesville 32610.
Journal of biological chemistry (UNITED STATES) Jun 3 1994, 269

(22) p15407-10, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: EY01311; EY; NEI; EY06225; EY; NEI; EY09339; EY; NEI;

+

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Inactivation of photolyzed rhodopsin requires phosphorylation of the receptor and binding of the 48-kDa regulatory protein arrestin. We recently isolated a novel form of arrestin, termed p44, that is truncated at the COOH terminus (Palczewski, K., Buczylo, J., Ohguro, H., Annan, R. S., Carr, S. A., Crabb, J. W., Kaplan, M. W., Johnson, R. S., and Walsh, K. A. (1994) Protein Sci. 3, 319-329) and strongly inhibits Gt activation by non-phosphorylated rhodopsin. p44 is identical to arrestin except at the COOH terminus, where the 35 amino acids of arrestin are replaced by a single alanine residue. p44 is identified as a splice variant of arrestin based on the identical cDNA sequence of p44 with arrestin (except the 3' non-coding regions), the presence of an exon/intron junction at the Ser369 codon, and identical Southern hybridization patterns generated by the 3' non-coding portion of arrestin and p44. Immunocytochemistry reveals that p44 is localized in the photoreceptor outer segment, whereas arrestin is present throughout the cell. This specificity of localization to the outer segment is consistent with a role of p44 in the phototransduction cascade.

9/3,AB/16 (Item 16 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08118472 94245195 PMID: 8188256

The human gene (CSNK2A1) coding for the casein kinase II subunit alpha is located on chromosome 20 and contains tandemly arranged Alu repeats.

Wirkner U; Voss H; Lichter P; Ansorge W; Pyerin W
German Cancer Research Center, Heidelberg, Germany.

Genomics (UNITED STATES) Jan 15 1994, 19 (2) p257-65, ISSN

0888-7543 Journal Code: 8800135

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We have isolated and characterized a 18.9-kb genomic clone representing a central portion of the human casein kinase II (CKII) subunit alpha gene (CSNK2A1). Using the whole clone as a probe, the gene was localized on chromosome 20p13. The clone contains eight exons whose sequences comprise bases 102 to 824 of the coding region of the human CKII alpha. The exon/intron splice junctions conform to the gt/ag rule. Three of the nine introns are located at positions corresponding to those in the CKII

alpha gene of the nematode *Caenorhabditis elegans*. The introns contain eight complete and eight incomplete Alu repeats. Some of the Alu sequences are arranged in tandems of two or three, which seem to originate from insertions of younger Alu sequences into the poly(A) region of previously integrated Alu sequences, as indicated by flanking direct repeats.

9/3,AB/17 (Item 17 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08048439 94198434 PMID: 8148499

Gene organization of human protein C inhibitor, a member of SERPIN family proteins encoded in five exons.

Hayashi T; Suzuki K

Department of Molecular Biology of Genetic Disease, Mie University School of Medicine, Japan.

International journal of hematology (IRELAND) Oct 1993, 58 (3)
p213-24, ISSN 0925-5710 Journal Code: 9111627

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Protein C inhibitor (PCI), a plasma serine protease inhibitor, neutralizes activated protein C, which plays an important role in the regulation of blood coagulation. We determined the organization of the gene coding for this inhibitor. A human genomic phage DNA library was screened using the 32P-labeled protein C inhibitor cDNA as a probe and a phage genomic clone that contained the full length of the inhibitor gene, including the 5'- and 3'-flanking region, was isolated. The gene was characterized by restriction enzyme mapping, Southern blotting and sequencing all the coding parts as well as the 5'- and 3'-flanking regions. The protein C inhibitor gene spanned about 13 kilobase pairs and consisted of 5 exons and 4 introns as do the genes for human alpha 1-antitrypsin, alpha 1-antichymotrypsin, heparin cofactor II and rat angiotensinogen. All exon-intron boundaries agreed with the GT-AG rule. The 5'-flanking region contained no TATAA or CCAAT sequences, but contained the putative Sp-1 and AP-2 binding sites in the 5'-upstream region, which indicated promoter activity in human hepatoma cell line, HepG2, using the luciferase gene as a reporter gene and the polyadenylation site in the 3'-downstream region. A transcription initiation site was identified by primer extension analysis using template human liver poly(A)RNA. The length of the non-coding exon I of this inhibitor gene was similar to those of the other serine protease inhibitors as described above. These findings suggest that the protein C inhibitor gene evolved from a common ancestor gene of these serine protease inhibitors.

9/3,AB/18 (Item 18 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08036602 94171822 PMID: 8126009

CA/TG sequence at the 5' end of oligo(A)-tracts strongly modulates DNA curvature.

Nagaich A K; Bhattacharyya D; Brahmachari S K; Bansal M

Molecular Biophysics Unit, Indian Institute of Science, Bangalore.

Journal of biological chemistry (UNITED STATES) Mar 11 1994, 269

(10) p7824-33, ISSN 0021-9258 Journal Code: 2985121R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

An analysis of the base pair doublet geometries in available crystal structures indicates that the often reported intrinsic curvature of DNA

containing oligo-(d(A).d(T)) tracts may also depend on the nature of the flanking sequences. The presence of CA/TG doublet in particular at the 5' end of these tracts is expected to enhance their intrinsic bending property. To test this proposition, three oligonucleotides, d(GAAAAAC-CCCCC), d(CCCCCCAAAAAG), d(GAAAAATTTTTC), and their complementary sequences were synthesized to study the effect of various flanking sequences, at the 5' and 3' ends of the A-tracts, on the curvature of DNA in solution. An analysis of the polyacrylamide gel electrophoretic mobilities of these sequences under different conditions of salts and temperatures (below their melting points) clearly showed that the oligomer with CA/TG sequence in the center was always more retarded than the oligomer with AC/GT sequence, as well as the oligomer with AT/AT sequence. Hydroxyl radical probing of the sequences with AC/GT and CA/TG doublet junctions gives a similar cutting pattern in the A-tracts, which is quite different from that in the C-tracts, indicating that the oligo(A)-tracts have similar structures in the two oligomers. KMnO4 probing shows that the oligomer with a CA/TG doublet junction forms a kink that is responsible for its inherent curvature and unusual electrophoretic mobility. UV melting shows a reduced thermal stability of the duplex with CA/TG doublet junction, and circular dichroism (CD) studies indicate that a premelting transition occurs in the oligomer with CA/TG doublet step before global melting but not in the oligomer with AC/GT doublet step, which may correspond to thermally induced unbending of the oligomer. These observations indicate that the CA/TG doublet junction at the 5' end of the oligo(A)-tract has a crucial role in modulating the overall curvature in DNA.

9/3,AB/19 (Item 19 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08016782 94158897 PMID: 8114753

A functional polyadenylation signal is embedded in the coding region of chicken growth hormone receptor RNA.

Oldham E R; Bingham B; Baumbach W R

Agricultural Research Division, American Cyanamid Co. Princeton, New Jersey 08543.

Molecular endocrinology (Baltimore, Md.) (UNITED STATES) Nov 1993

, 7 (11) p1379-90, ISSN 0888-8809 Journal Code: 8801431

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

A study of chicken GH receptor (cGHR) expression has revealed that the two major liver and skeletal muscle transcripts of the cGHR are developmentally expressed. Expression of the larger (4.7 kilobases) transcript increases with age. The smaller transcript (0.7 kilobases) is a truncation product, resulting from alternative usage of a functional polyadenylation [poly(A)] signal embedded in the coding sequence. The extent to which alternative cleavage and polyadenylation occur displays some tissue and sex specificity. Cleavage and polyadenylation occur down-stream of the AATAAA portion of the poly(A) signal (cGHR positions 304-309) and up-stream of a GT-rich sequence. The truncated transcript appears to be translated, based on its association in vivo with polyribosomes, although the physiological role of the putative protein product of this truncated transcript is as yet unknown. Three other avian species (quail, turkey, and duck) also show a polyadenylated truncation of the GHR message due to a poly(A) signal at the same location in the coding sequence. In cell culture expression, mutation of AATAAA to AACAAAG prevents production of the truncated transcript. In a chimeric construct, the signal and neighboring sequence from the cGHR are sufficient to confer cleavage and polyadenylation upon the rat GHR, a gene that otherwise lacks the internal poly(A) signal. Alternative polyadenylation within the coding

region of a structural gene is discussed as a heretofore unknown means of post-transcriptional regulation of a gene product.

9/3,AB/20 (Item 20 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07899578 94035199 PMID: 8106087

3'-end processing of the maize 27 kDa zein mRNA.

Wu L; Ueda T; Messing J

Waksman Institute, Rutgers, State University of New Jersey, Piscataway 08855.

Plant journal : for cell and molecular biology (ENGLAND) Sep 1993

, 4 (3) p535-44, ISSN 0960-7412 Journal Code: 9207397

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Cis-regulatory elements involved in the mRNA 3'-end processing of the 27 kDa zein gene have been investigated by deletion and site-directed mutagenesis analyses. In the 3' flanking region of the 27 kDa zein gene, several AATAAA-like sequences and a sequence resembling the mammalian GT-rich sequence are present around the polyadenylation sites. Among the multiple AATAAA-like sequences, the duplicated AATGAA motifs, located 30-40 bp upstream from the polyadenylation sites, have been shown to play roles as polyadenylation signals. Although either of the two AATGAA motifs can function as a polyadenylation signal in chimeric gene constructs, the one proximal to the polyadenylation sites is likely to be the functional polyadenylation signal in the 27 kDa zein gene. Deletion of the downstream GT-rich sequence as well as alteration of the sequence surrounding the poly-adenylation sites has little effect on the mRNA 3'-end processing. However, the sequence elements located upstream from the polyadenylation signals are essential for the mRNA 3'-end processing. Mutations in the AATGAA motifs or the upstream sequences reduced the level of a reporter gene expression. A model depicting the mechanism involved in the 3'-end processing of the 27 kDa zein mRNA is presented.

9/3,AB/21 (Item 21 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07831940 93361468 PMID: 7689219

Human lung expresses unique gamma-glutamyl transpeptidase transcripts.

Wetmore L A; Gerard C; Drazen J M

Department of Medicine, Brigham and Women's Hospital, Boston, MA.

Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Aug 15 1993, 90 (16) p7461-5, ISSN

0027-8424 Journal Code: 7505876

Contract/Grant No.: HL19170; HL; NHLBI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

gamma-Glutamyl transpeptidase (EC 2.3.2.2, gamma GT) is a membrane-bound ectoenzyme that plays an important role in the metabolism of glutathione. It is composed of two subunits, both of which are encoded by a common mRNA. We examined the expression of gamma GT in human lung tissue by Northern blot analysis and screening a cDNA library made from human lung poly(A)+ RNA. Our results show that there are two gamma GT mRNA populations in human lung tissue. We define these as group I (2.4 kb) and group II (approximately 1.2 kb) transcripts. In the present communication, we characterize the unique lung transcript. Sequence analysis of representative clones shows that group I transcripts are virtually identical to those previously isolated from liver and placenta

but possess a unique 5' untranslated region. In marked contrast, group II transcripts appear to be human-lung-specific. Group II transcripts appear on Northern blots probed with full-length or 3'-biased gamma GT cDNA. Sequence analysis of group II clones shows them to be homologous with group I clones in the region that encodes the reading frame for the light chain; however, they possess a series of unique 5' untranslated regions, which suggests that they arise from lung-specific message processing. Additionally, approximately 50% of the isolated group II clones contain 34 nt substitutions compared with the "wild-type" gamma GT transcripts. These data indicate that human lung expresses unique gamma GT transcripts of unknown function as well as the classical form. The abundant group II transcripts may encode part of a heterodimer related to gamma GT or represent processed lung-specific pseudogenes.

9/3,AB/22 (Item 22 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07715930 93237110 PMID: 7682836

Genetic analysis of human placental aromatase deficiency.

Harada N

Division of Molecular Genetics, Fujita Health University, Aichi, Japan.

Journal of steroid biochemistry and molecular biology (ENGLAND) Mar
1993, 44 (4-6) p331-40, ISSN 0960-0760 Journal Code: 9015483

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Placental aromatase deficiency, which was characterized by maternal and fetal virilization and by a low level of estrogen excretion into urine during pregnancy, was studied by biochemical and molecular genetical techniques. Among enzymes participating in the electron transport system of the patient's placental microsomes, only aromatase activity was observed to be reduced (< 3% of normal levels). Northern and Western blotting analyses showed that the transcription of the aromatase gene and the translation of its mRNA seemed to proceed normally in the patient's tissue. However, the aromatase cDNA isolated from the patient was found to contain an extra DNA fragment of 87 base pairs (bp) which encoded 29 amino acids in frame but no termination codon. The insertion was located at the splicing point between exon 6 and intron 6 of the normal aromatase gene. The extra DNA fragment represented the first part of intron 6 except that its initial GT was altered to GC. These findings indicated that, in the patient's aromatase gene, the splicing between exon 6 and intron 6 did not occur at the normal position. This reflected the presence of one point mutation in its consensus sequence which caused the next cryptic consensus sequence 87 bp downstream, to be used according to the canonical GT/AG rule. The protein molecule thus translated contained an extra 29 amino acids. Furthermore, the patient's aromatase cDNA was observed to produce a protein molecule with a trace of activity in the transient expression system of COS-7 cells and in the high level expression system of baculovirus-insect cells. Direct DNA sequencing of aromatase genes from the patient and parents confirmed that this deficiency is a hereditary disease with an autosomal recessive inheritance pattern. The patient and parents are homozygote and heterozygotes, respectively, for this mutation.

9/3,AB/23 (Item 23 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07661262 93181229 PMID: 8382798

Structure and expression of the excision repair gene ERCC6, involved in the human disorder Cockayne's syndrome group B.

Troelstra C; Heslen W; Bootsma D; Hoeijmakers J H

Department of Cell Biology and Genetics, Erasmus University Rotterdam,

The Netherlands.

Nucleic acids research (ENGLAND) Feb 11 1993, 21 (3) p419-26,
ISSN 0305-1048 Journal Code: 0411011
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The human repair gene ERCC6--a presumed DNA (or RNA) helicase--has recently been found to function specifically in preferential nucleotide excision repair (NER). This NER subpathway is primarily directed towards repair of (the transcribed strand of) active genes. Mutations in the ERCC6 gene are responsible for the human hereditary repair disorder Cockayne's syndrome complementation group B, the most common form of the disease. In this report, the genomic organization and expression of this gene are described. It consists of at least 21 exons, together with the promoter covering a region of 82-90 kb on the genome. Postulated functional domains deduced from the predicted amino acid sequence, including 7 distinct helicase signatures, are--with one exception--encoded on separate exons. Consensus splice donor and acceptor sequences are present at all exon borders with the exception of the unusual splice donor at the end of exon VII. The 'invariable' GT dinucleotide in the consensus (C,A)AG/GTPuAGT is replaced by the exceptional GC. Based on 42 GC splice donor sequences identified by an extensive literature search we found a statistically highly significant better 'overall' match of the surrounding nucleotides to the consensus sequence compared to normal GT-sites. This confirms and extends the observation made recently by Jackson (Nucl. Acids Res., 19, 3795-3798 (1991)) derived from analysis of 26 cases. Analysis of ERCC6 cDNA clones revealed the occurrence of alternative polyadenylation, resulting in the (differential) expression of two mRNA molecules (which are barely detectable on Northern blots) of 5 and 7 kb in length.

9/3,AB/24 (Item 24 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07554814 93081737 PMID: 1333296
cDNA cloning of a tetraubiquitin gene, and expression of ubiquitin-containing transcripts, in aleurone layers of Avena fatua.
Reynolds G J; Hooley R
Department of Agricultural Sciences, University of Bristol, UK.
Plant molecular biology (NETHERLANDS) Nov 1992, 20 (4) p753-8,
ISSN 0167-4412 Journal Code: 9106343
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

A lambda gt 11 cDNA library, constructed from poly(A)+ mRNA isolated from Avena fatua aleurone layers incubated with 1 micromM gibberellin A1 (GA1) for 4 days, was screened with an anti-idiotypic antiserum raised against the GA-specific monoclonal antibody MAC 182. One positive clone was isolated, sequenced and shown to encode a tetraubiquitin based on the deduced amino acid sequence. This polyubiquitin cDNA exhibited a high degree of homology to a cloned wheat hexaubiquitin in its 3'-non-coding region. Analysis of total RNA isolated from A. fatua aleurone layers, treated without or with a range of concentrations of GA1 from 10(-11) to 10(-6) M, by northern blotting using the cDNA probe revealed 8 different ubiquitin-containing transcript classes all of which are constitutively expressed in aleurone and are regulated by GA1.

9/3,AB/25 (Item 25 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07518217 93043838 PMID: 1384819

Murine beta 1,4-galactosyltransferase: round spermatid transcripts are characterized by an extended 5'-untranslated region.

Harduin-Lepers A; Shaper N L; Mahoney J A; Shaper J H

Cell Structure and Function Laboratory, Johns Hopkins University School of Medicine, Baltimore, MD 21287.

Glycobiology (ENGLAND) Aug 1992, 2 (4) p361-8, ISSN 0959-6658

Journal Code: 9104124

Contract/Grant No.: 5T32GM07626; GM; NIGMS; CA45799; CA; NCI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We have previously shown that the expression of the gene encoding murine beta 1,4-galactosyltransferase (beta 1,4-GT, UDP-galactose:N-acetyl-D-glucosaminyl-glycopeptide 4-beta-D galactosyltransferase, EC 2.4.1.38) is fundamentally different between somatic and male germ cells (Shaper et al., 1990b). In somatic cells, two transcripts of 3.9 kb and 4.1 kb are produced. In contrast, in spermatogonia only the 4.1 kb transcript is expressed. Maturation of spermatogonia to pachytene spermatocytes is accompanied by reduced expression of the 4.1 kb transcript to barely detectable levels. Continued differentiation to haploid round spermatids is coincident with renewed expression in which the 4.1 kb transcript is replaced by two truncated transcripts of 2.9 and 3.1 kb. In this study, we report the characterization of a full-length beta 1,4-GT cDNA clone from a murine round spermatid library that corresponds to the 2.9 kb transcript. This transcript encodes the same open reading frame as the 4.1 kb transcript, but utilizes alternative poly(A) signals embedded within the long 3'-untranslated region of the somatic transcript. Based on sequence analysis, together with primer extension and S1 nuclease protection experiments, both the 2.9 and the 3.1 kb round spermatid beta 1,4-GT transcripts are distinguished by the presence of an additional 5'-untranslated sequence of approximately 560 bp that is absent in premeiotic germ cells and somatic cells. (ABSTRACT TRUNCATED AT 250 WORDS)

9/3,AB/26 (Item 26 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

07415844 92348437 PMID: 1379236

Molecular cloning and expression of rat liver N-heparan sulfate sulfotransferase.

Hashimoto Y; Orellana A; Gil G; Hirschberg C B

Department of Biochemistry and Molecular Biology, University of Massachusetts Medical Center, Worcester 01655.

Journal of biological chemistry (UNITED STATES) Aug 5 1992, 267

(22) p15744-50, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: GM 34396; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

N-Heparan sulfate sulfotransferase catalyzes the transfer of sulfate from 3'-phosphoadenosine 5'-phosphosulfate to the nitrogen of glucosamine in heparan sulfate. The enzyme has been previously purified to apparent homogeneity from rat liver (Brandan, E., and Hirschberg, C. B. (1988) J. Biol. Chem. 263, 2417-2422). We have now cloned the rat liver enzyme using the following strategy: (a) the amino acid sequence was obtained from tryptic peptides of the purified protein, (b) mixed oligonucleotides were generated based on the sequence of the tryptic peptides, (c) a polymerase chain reaction fragment was obtained using mixed oligonucleotide interprimer amplification of cDNA, and (d) this fragment was used to screen rat liver lambda gt 10 and lambda ZAP libraries. Three clones were obtained, one of which seems to contain the complete coding sequence of the

N-heparan sulfate sulfotransferase (N-HSST). Evidence that the cDNA clone corresponds to the previously purified and characterized N-HSST was the following: (a) the predicted sequence of the N-HSST contains all of the 11 tryptic peptides obtained from the purified protein, (b) when a cDNA containing the sequence coding for the N-HSST was introduced in a eukaryotic expression vector and transfected in COS-1 cells, the enzyme activity was expressed 9-fold over controls, and (c) the characteristic of the predicted protein fits with the purified protein in terms of molecular weight, membrane localization, and its being an N-linked glycoprotein. The size of the longest cDNA isolated is 4.1 kilobases, which is in close agreement with the 4.2-kilobase size of one of the mRNA observed in Northern analyses. In addition, messages of 7.0 and 8.5 kilobases were also observed, suggesting that a large portion is untranslated. The latter messages were the major mRNA species detected.

9/3,AB/27 (Item 27 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07332010 92261615 PMID: 1374839

Estrogen sulfotransferase of the rat liver: complementary DNA cloning and age- and sex-specific regulation of messenger RNA.

Demyan W F; Song C S; Kim D S; Her S; Gallwitz W; Rao T R; Slomczynska M; Chatterjee B; Roy A K

Department of Cellular and Structural Biology, University of Texas Health Science Center, San Antonio 78284.

Molecular endocrinology (Baltimore, Md.) (UNITED STATES) Apr 1992
, 6 (4) p589-97, ISSN 0888-8809 Journal Code: 8801431

Contract/Grant No.: P01-AG-06872; AG; NIA; R01-AG-03527; AG; NIA; R37-DK-14744; DK; NIDDK

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Mammalian estrogen sulfotransferase (EST; EC 2.8.2.4) sulfurylates the hydroxyl group of estrogenic steroids by transferring the sulfate from a cosubstrate adenosine 3'-phosphate-5'-phosphosulfate. Sulfurylated steroids do not bind to the estrogen receptor with high affinity and, therefore, are hormonally inactive. We have purified rat liver EST and developed monoclonal antibody to this enzyme. By immunoscreening a lambda gt-11 expression library constructed from male rat liver cDNAs, the cDNA clone corresponding to EST was identified and isolated. A recombinant expression plasmid (pCMV5) containing this cDNA insert when transfected into COS-7 cells generated both immunologically and enzymatically active EST. With the help of this cDNA probe, we have explored the regulation of the EST mRNA in the liver and the possible role of this enzyme in sex hormone action. During the lifespan of male rats, only the young adult animals show hepatic androgen responsiveness. Also, estrogenic hormones strongly antagonize androgen action in the rat liver. Northern blot analysis of liver RNA derived from male rats of different ages shows that the androgen sensitivity of young adult animals is associated with a high expression of EST mRNA. During the same period, mRNA corresponding to dehydroepiandrosterone sulfotransferase is markedly (approximately 10-fold) down-regulated. Such a correlation is in concordance with the role of these enzymes in the maintenance of hepatic androgen sensitivity during young adult life by inactivating the estrogenic and sparing the androgenic steroids. Furthermore, the increase in the hepatic androgen sensitivity of androgen-treated female rats is also associated with the induction of EST. (ABSTRACT TRUNCATED AT 250 WORDS).

9/3,AB/28 (Item 28 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07309644 92241858 PMID: 1315304

Invariant exon skipping in the human alpha-galactosidase A pre-mRNA: Ag+1 to t substitution in a 5'-splice site causing Fabry disease.

Sakuraba H; Eng C M; Desnick R J; Bishop D F

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Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Fabry disease, an inborn error of glycosphingolipid catabolism, results from lesions in the X-linked gene encoding the human lysosomal hydrolase, alpha-galactosidase A (alpha-D-galactoside galactohydrolase; EC 3.2.1.22). To detect alpha-galactosidase A RNA processing or stability defects causing Fabry disease, Northern hybridization analyses were performed with **poly(A)+** RNA isolated from cultured lymphoblasts from unrelated Fabry hemizygotes. Using a riboprobe complimentary to the normal 1.45-kb alpha-galactosidase A mRNA, a single 1.25-kb transcript was identified in three classically affected brothers from a Japanese Fabry family. Densitometric analysis revealed that the 1.25-kb transcripts were present at 50 to 60% of normal amounts. RNase A analysis identified a deletion of about 200 bp that appeared to include the entire 198 bp of exon 6. Amplification and direct sequencing of a genomic region containing exon 6 from an affected hemizygote revealed a g+1 to t transversion in the invariant **gt** consensus 5'-splice site of intron 6, which resulted in the deletion of the entire exon 6 sequence. This novel splicing lesion causing Fabry disease is the first g+1 to t transversion of a mammalian 5'-splice site that consistently eliminates the preceding exon.

9/3,AB/29 (Item 29 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

07250815 92178238 PMID: 1542303

Sequence of the gamma 2b membrane 3' untranslated region: polyA site determination and comparison to the gamma 2a membrane 3' untranslated region.

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Cellular and Molecular Biophysics, Columbia University, New York, NY 10032.

Molecular immunology (ENGLAND) Feb 1992, 29 (2) p279-85,

ISSN 0161-5890 Journal Code: 7905289

Contract/Grant No.: CA 16858; CA; NCI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We present here the nucleotide sequence of the gamma 2b membrane 3' untranslated region as well as approximately 443 nucleotides of 3' flanking sequence. Although this region contains two potential polyadenylation hexanucleotides AATAAA (located 1328 and 1407 nucleotides downstream of the last membrane exon), it appears that only the first site directs polyadenylation of the mature mRNA. The first AATAAA is followed by several sequences which may influence its relative strength: the region downstream of this AATAAA is 44% T-rich and contains a pair of CAYTG sequences (4/5 match) which overlap two sequences which have a 6/8 match to the sequence YGTGTTY. These sequences have been found in proximity to a large number of 3' ends [Gil and Proudfoot, Cell 49, 399-406 (1987); McLauchlan et al., Nucl. Acids Res. 13, 1347-1368. (1985); Berget, Nature 309, 179-182 (1984)]. The AATAAA site at position 1407 is not flanked by a T- or

GT-rich sequence and is followed by a single CAYTG sequence (4/5 match) and a single YGTGTTY sequence (6/8 match). The region downstream of the second AATAAA site also contains a sequence which has an 8/12 match with a sequence found in all heavy chain secreted 3' untranslated regions [Kobrin et al., Molec. Cell. Biol. 6, 1687-1697 (1986)]. Consistent with sequence comparisons between other regions of these two genes, the gamma 2b sequence has striking homology with the gamma 2a 3' untranslated region. A notable difference between gamma 2b and gamma 2a is the absence of an extensive array of GAA, GA, GGAA, and GGA repeats from the gamma 2b sequence. The GA repeats are postulated to form a stem loop structure in the gamma 2a 3' untranslated region; gamma 2b then would be missing the 5' half of the stem. Interestingly, neither the gamma 2b nor the gamma 2a 3' untranslated regions show large homologies to the mu, delta, gamma 3, or the alpha membrane 3' untranslated regions.

9/3,AB/30 (Item 30 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07209820 92147127 PMID: 1783392

Characterization of the human gene for a newly discovered carbonic anhydrase, CA VII, and its localization to chromosome 16.

Montgomery J C; Venta P J; Eddy R L; Fukushima Y S; Shows T B; Tashian R E

Department of Human Genetics, University of Michigan Medical School, Ann Arbor 48109-0618.

Genomics (UNITED STATES) Dec 1991, 11 (4) p835-48, ISSN 0888-7543 Journal Code: 8800135

Contract/Grant No.: 5T32 GM07315; GM; NIGMS; GM-20454; GM; NIGMS; GM-24681; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Six carbonic anhydrase (CA) isozymes (CA I-VI) in mammals and other amniotes have been described. We have isolated an additional CA gene from a human genomic library and designated its putative product carbonic anhydrase VII (CA VII). The gene is approximately 10 kb long and contains seven exons and six introns found at positions identical to those determined for the previously described CA I, CA II, and CA III genes. The finding of a 17-bp GT-rich segment in a position 28 bp downstream of the poly(A)+ signal and the high correspondence of the 5' and 3' splice sites of the six introns with consensus junction sequences are consistent with the gene being functional. The 5' flanking regions of the CA VII gene do not contain the TATA and CAAT promoter elements usually found within 100 bp upstream of transcription initiation, but do contain a TTAA sequence 102 nucleotides upstream of the initiation codon. The 5' region of the gene (-243 to +551) is GC-rich and contains 80 CpG dinucleotides and four possible Sp1 (GGGCGG or CCGCCC) binding sites. Northern analysis has identified the salivary gland as a major site of expression. The derived amino acid sequence of the CA VII gene is 263 amino acids long and has 50, 56, and 49% identity with human CA I, CA II, and CA III, respectively. No differences were found at any of the 39 positions that have remained invariant in all mammalian CA isozymes sequenced to date. Based on analysis of interspecific somatic cell hybrids, the human CA VII gene, CA7, was assigned to chromosome 16, with localization to the long arm at the q21-23 region by in situ hybridization. This is in contrast to the location of the CA I, CA II, and CA III gene cluster on human chromosome 8 and that of the human CA VI gene on chromosome 1.

9/3,AB/31 (Item 31 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06992293 91329668 PMID: 2101687 Record Identifier: 91329668

Molecular cloning and sequencing of a cDNA for an auxin-repressed mRNA: correlation between fruit growth and repression of the auxin-regulated gene.

Reddy A S; Poovaiah B W

Department of Horticulture and Landscape Architecture, Washington State University, Pullman 99164-6414.

Plant molecular biology (NETHERLANDS) Feb 1990, 14 (2) p127-36

, ISSN 0167-4412 Journal Code: 9106343

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Other Citation Owner: NASA

Record type: Completed

A complementary DNA (cDNA) library has been constructed in lambda gt 10 from poly(A)+ mRNA isolated from auxin-deprived strawberry receptacles. By differential plaque filter hybridization, a cDNA (lambda SAR5) to an auxin-repressed mRNA has been isolated. The expression of the auxin-repressed gene is studied at various stages of normal fruit development and in fruits of variant strawberry genotype using lambda SAR5 as a probe. Northern analyses of RNA isolated from pollinated and unpollinated fruits of various developmental stages revealed that mRNA corresponding to the lambda SAR5 clone is repressed during normal fruit development, and the level of lambda SAR5 mRNA is regulated by endogenous auxin. Furthermore, results with both normal and variant genotype strawberry fruit indicate that there is a positive correlation between growth of strawberry fruit and repression of mRNA corresponding to the lambda SAR5 clone. The lambda SAR5 cDNA has been sequenced and is 723 nucleotides in length. The deduced protein has 111 amino acid residues with a molecular mass of 12.5 kDa. The putative polypeptide starts at nucleotide position 20 and ends at 352. The molecular weight of the predicted polypeptide is in agreement with the molecular weight of the in vitro translated polypeptide of hybrid selected mRNA. A comparison of the nucleotide and deduced amino acid sequence of lambda SAR5 with nucleotide and protein sequences in data banks has not revealed any homology to known proteins.

9/3,AB/32 (Item 32 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06897123 91210234 PMID: 1826905

Two genes, atpC1 and atpC2, for the gamma subunit of Arabidopsis thaliana chloroplast ATP synthase.

Inohara N; Iwamoto A; Moriyama Y; Shimomura S; Maeda M; Futai M

Department of Organic Chemistry and Biochemistry, Osaka University, Japan.

Journal of biological chemistry (UNITED STATES) Apr 25 1991, 266

(12) p7333-8, ISSN 0021-9258 Journal Code: 2985121R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Arabidopsis thaliana has two genes (atpC1, atpC2) coding for gamma subunits of chloroplast ATP synthase. The atpC1 and atpC2 were cloned and sequenced. They had no introns within the reading frames and coded for proteins of 373 and 386 amino acid residues, respectively, including putative transit sequences (50 and 60 amino acid residues, respectively). In contrast, the spinach gamma subunit gene had two introns within the reading frame. The mature sequences coded by the two genes of A. thaliana (atpC1, 323 residues; atpC2, 326 residues) were homologous with that of spinach (J. Miki, M. Maeda, Y. Mukohata, and M. Futai (1988) FEBS Lett. 232, 221-226): the homologies of gamma subunits coded by atpC1 and atpC2 were 72%, those of the subunits coded by atpC1 and spinach cDNA were 84%,

and those of the proteins coded by atpC2 and spinach cDNA were 71%. Like the spinach subunit, the gamma subunits coded by the two genes had unique regulatory domains not found in mitochondrial or bacterial subunits. **Poly(A)+** mRNAs corresponding to atpC1 (1.5 kilobases) and atpC2 (2.5 kilobases) were detected in illuminated plants, the amount of the former being at least 140 times that of the latter. The atpC1 mRNA was not found in dark-adapted plants. Nuclear protein(s) specifically bound to the upstream region of atpC1 was detected by gel shift assay and its binding was shown to be inhibited by the GT-1 element of the gene encoding the ribulose-1,5-bisphosphate carboxylase small subunit, which is expressed under illumination (P. J. Green, S. A. Kay, and N. H. Chau (1987) EMBO J. 6, 2543-2549). Consistent with these findings, an increased amount of the gamma subunit was detected immunochemically in illuminated plants.

9/3,AB/33 (Item 33 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06891775 91200205 PMID: 2015853

Isolation of cDNA for a *Xenopus* sperm-specific basic nuclear protein (SP4) and evidence for expression of SP4 mRNA in primary spermatocytes.

Hiyoshi H; Uno S; Yokota T; Katagiri C; Nishida H; Takai M; Agata K; Eguchi G; Abe S

Department of Biological Science, Faculty of Science, Kumamoto University, Japan.

Experimental cell research (UNITED STATES) May 1991, 194 (1)

p95-9, ISSN 0014-4827 Journal Code: 0373226

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

A cDNA library was prepared in lambda gt 11 from **poly(A)+** mRNA isolated from a pure population of *Xenopus* round spermatids and screened with an antibody against SP3-5 (sperm-specific proteins) of *Xenopus* sperm. Positive clones were sequenced and an arginine-rich clone, designated pXSP531, was obtained. The 473-nucleotide sequence of pXSP531 contained an open reading frame of 237 nucleotides which was preceded by a 5' untranslated region of 67 nucleotides. The 3' untranslated region contained 149 nucleotides, including a consensus polyadenylation signal (AAATAAAA). Twenty nucleotides of a **poly(A)** tail was contained in the pXSP531. SP3-5 were separated from each other by reverse-phase chromatography and sequenced. The amino acid sequence of the peptide fragments which were obtained by digestion of SP4 with V8 protease and separated by reverse-phase chromatography was identical to the sequence of the N-terminal 43 and C-terminal 15 amino acids deduced from the nucleotide sequence of pXSP531. This result demonstrates that pXSP531 encodes SP4. Northern hybridization of RNA extracted from primary spermatocytes and round spermatids on Days 0 and 6 with SP4 cDNA probe (pXSP531) showed that SP4 mRNA is present both in primary spermatocytes and in round spermatids as is protamine mRNA in the rainbow trout. The size of the SP4 mRNA in round spermatids on Day 0 was longer by 60 nucleotides compared to that in primary spermatocytes and that in spermatids on Day 6 was shorter by 30 nucleotides compared to that on Day 0. These size differences were due to differences in the length of the **poly(A)** tracts because digestion of **poly(A)** with ribonuclease H resulted in the shortening of mRNA to the same size for three stages.

9/3,AB/34 (Item 34 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06833282 91138958 PMID: 1995416

Occlusion of the HIV **poly(A)** site.

Weichs an der Glon C; Monks J; Proudfoot N J

Sir William Dunn School of Pathology, University of Oxford, UK.
Genes & development (UNITED STATES) Feb 1991, 5 (2) p244-53,
ISSN 0890-9369 Journal Code: 8711660
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

To investigate the selective use of **poly(A)** sites in the 3' long terminal repeat (LTR) but not the 5' LTR of retroviruses, we have studied the **poly(A)** site of the human immunodeficiency virus (HIV-1). Using hybrid HIV/alpha-globin gene constructs, we demonstrate that the HIV **poly(A)** site is inactive or occluded when adjacent to an active promoter, either the homologous HIV promoter or the alpha-globin gene promoter. Furthermore, this occlusion of the HIV **poly(A)** site occurs over a considerable distance of up to at least 500 bp. In contrast, two nonretroviral **poly(A)** sites [alpha-globin and a synthetic **poly(A)** site] are active when close to a promoter. We also show that a short fragment of approximately 60 nucleotides containing the HIV **poly(A)** site is fully active when placed at the 3' end of the human alpha-globin gene or within the rabbit beta-globin gene. This result rules out the requirement of more distant upstream elements for the activity of the HIV **poly(A)** site, as has been suggested for other viral **poly(A)** sites. Finally, we show that the GT-rich downstream region of the HIV **poly(A)** site confers **poly(A)** site occlusion properties on a synthetic **poly(A)** site. This result focuses attention on this more variable part of a **poly(A)** site in retroviruses as a possible general signal for **poly(A)** site occlusion.

9/3,AB/35 (Item 35 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06806194 91115092 PMID: 1899227

Identification of ecdysone response elements by analysis of the *Drosophila* Eip28/29 gene.

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Institute for Molecular and Cellular Biology, Indiana University, Bloomington 47405.

Genes & development (UNITED STATES) Jan 1991, 5 (1) p120-31,
ISSN 0890-9369 Journal Code: 8711660
Contract/Grant No.: GM37813; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

We have identified ecdysone-response elements (EcREs) by studying regulation of the steroid-responsive *Drosophila* Eip28/29 gene. First, functional assays of deletion mutants identified large sequence regions required for the response; then a blotting method using the specifically labeled steroid receptor as probe identified receptor-binding regions. Three short receptor-binding regions near Eip28/29 have been identified: Prox and Dist [521 and 2295 nucleotides, respectively, downstream of the **poly(A)** site] are probably required for the Eip28/29 response in cell lines; Upstream (-440) is unnecessary for that response. We have also demonstrated that an EcRE-containing region from hsp27 contains a receptor-binding site. Each of these four receptor-binding regions functions as an EcRE when placed upstream of an ecdysone nonresponsive promoter and each contains an imperfect palindrome, suggesting the consensus 5'-RG(GT)TCANTGA(CA)CY-3'. Furthermore, a synthetic 15-bp fragment containing an imperfect palindrome similar to the consensus is a fully functional EcRE. The presence of any of the EcREs leads, in the absence of hormone, to depressed gene expression. When hormone is added, it relieves this repression and causes additional activation. The similarity

of the EcRE sequence to response elements for estrogen, thyroid hormone, and retinoic acid receptors suggests that the steroid receptors and their signal transduction mechanisms have been strongly and broadly conserved.

9/3,AB/36 (Item 36 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06785327 91097705 PMID: 2176504

CAP binding sites reveal pyrimidine-purine pattern characteristic of DNA bending.

Barber A M; Zhurkin V B
Laboratory of Mathematical Biology NCI, National Institutes of Health, Bethesda, MD 20892.

Journal of biomolecular structure & dynamics (UNITED STATES) Oct 1990, 8 (2) p213-32, ISSN 0739-1102 Journal Code: 8404176

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

To investigate the intrinsic bending of DNA at sites where proteins bind, we analyzed catabolite gene activator protein (CAP) binding sites and various operators from the viewpoint of DNA bending flexibility. Theoretical conformational analysis. DNase I digestion and x-ray crystallography data indicate that bending of B-DNA is highly anisotropic and sequence-dependent. Certain dimers prefer to bend into the major groove ("major-philic") and others prefer to bend into the minor groove ("minor-philic" dimers). From these data we considered TA, CG, CA: TG and GG: CC as major-philic dimers and AT, AA: TT and GT: AC as minor-philic ones. Analysis of 31 CAP binding sites has identified strong major-philic tendencies 5-7 base pairs (bp) away from the center. In addition, we found minor-philic poly-A tracts extending 4-5 bp away from the proposed major-philic bends. Finally, to analyze the central regions we followed the lead of Shumilov and classified the DNA sites by their spacer lengths [V.Y. Shumilov, Mol. Biol. (Mosk) 21, 168-187 (1987)]. In this way, we identified two subsets of CAP binding sites: one with 6 bp between the TGTGA: TCACA consensus boxes (N6-set) and one with 8 central bp (N8-set). We discovered that the dimer at the center of an N6-set site was usually major-philic, whereas at the center of an N8-set site more often minor-philic. Analysis of phages 434, P22 lambda and trp operators revealed similar results. In conclusion, our data show that CAP binding sites have major-philic and minor-philic dimers at specific positions; the location of these dimers may facilitate wrapping of DNA around CAP. A similar pattern is seen in nucleosomes.

9/3,AB/37 (Item 37 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06778114 91090111 PMID: 1824668

Use of short sequence repeat DNA polymorphisms after PCR amplification to detect the parental origin of the additional chromosome 21 in Down syndrome.

Petersen M B; Schinzel A A; Binkert F; Tranebjaerg L; Mikkelsen M; Collins F A; Economou E P; Antonarakis S E

Department of Pediatrics, Johns Hopkins University School of Medicine, Baltimore, MD.

American journal of human genetics (UNITED STATES) Jan 1991, 48

(1) p65-71, ISSN 0002-9297 Journal Code: 0370475

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The origin of nondisjunction in trisomy 21 has so far been studied using

cytogenetic heteromorphisms and DNA polymorphisms using Southern blot analysis. Short sequence repeats have recently been described as an abundant class of DNA polymorphisms in the human genome, which can be typed using the polymerase chain reaction (PCR) amplification. We describe the usage of such markers on chromosome 21 in the study of parental origin of the additional chromosome 21 in 87 cases of Down syndrome. The polymorphisms studied were (a) two (GT)_n repeats and a poly(A) tract of an Alu sequence within the HMG14 gene and (b) a (GT)_n repeat of locus D21S156. The parental origin was determined in 68 cases by studying the segregation of polymorphic alleles in the nuclear families (either by scoring three different alleles in the proband or by dosage comparison of two different alleles in the proband). Our results demonstrate the usefulness of highly informative PCR markers for the study of nondisjunction in Down syndrome.

9/3,AB/38 (Item 38 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06723222 91033001 PMID: 2227420

Characterization of a gene encoding a manganese peroxidase from *Phanerochaete chrysosporium*.

Godfrey B J; Mayfield M B; Brown J A; Gold M H
Department of Chemical and Biological Sciences, Oregon Graduate Institute of Science and Technology, Beaverton 97006-1999.

Gene (NETHERLANDS) Sep 1 1990, 93 (1) p119-24, ISSN 0378-1119
Journal Code: 7706761

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The complete nucleotide (nt) sequence of a gene (mnp-1) encoding manganese peroxidase isozyme 1 (MnP-1) (pI = 4.9) from *Phanerochaete chrysosporium* has been determined. The sequence of 2539 bp includes 526 bp of 5'-flanking sequence and 368 bp 3' to the poly(A) site. Comparison of cDNA and genomic sequences indicates six introns varying in size from 57-72 bp. Intron splice-junction sequences all adhere to the GT ---AG rule. The positions of the introns show little similarity to the intron positions in the closely related lignin peroxidase-encoding genes. The 5' upstream region of the mnp-1 gene contains a TATAA element and three inverted CCAAT elements (ATTGG) at nt positions -81, -181, -195, and -304, respectively, relative to the start codon. In addition, the mnp-1 gene contains three putative heat-shock (HS) elements similar to the consensus C--GAA--TTC--G sequence, and two consensus metal response elements located within 500 bp upstream from the start codon. Furthermore, Northern-blot analysis demonstrates that mnp gene transcription is regulated by HS.

9/3,AB/39 (Item 39 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06711521 91024969 PMID: 1699521

Predicted structure of rabbit N-terminal, calcitonin and katacalcin peptides.

Martial K; Minvielle S; Jullienne A; Second N; Milhaud G; Lasmoles F
U 113 INSERM CNRS, CHU St. Antoine, Paris, France.
Biochemical and biophysical research communications (UNITED STATES) Sep 28 1990, 171 (3) p1111-4, ISSN 0006-291X Journal Code: 0372516

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Poly A rich RNA was extracted from rabbit thyroid and cDNA

obtained by the action of reverse transcriptase. The cDNA was used to construct a library in lambda GT 11. Screening of the library with a radio-labelled probe specific for human calcitonin allowed the isolation of a clone containing an open reading frame with a high homology with human and murine exon 4 of calcitonin/calcitonin gene-related peptide gene. This sequence codes for a typical calcitonin precursor. We deduced the amino acid sequence of rabbit N-terminal peptide, calcitonin and katecalcitonin.

9/3,AB/40 (Item 40 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06646024 90343792 PMID: 2383265

Evidence for an alternate splicing in the thyroperoxidase messenger from patients with Graves' disease.

Zanelli E; Henry M; Charvet B; Malthiery Y
Laboratoire de Biochimie Medicale, U.38 INSERM, Faculte de Medecine, Marseille, France.

Biochemical and biophysical research communications (UNITED STATES) Jul 31 1990, 170 (2) p735-41, ISSN 0006-291X Journal Code: 0372516

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

An initial lambda gt 11 cDNA library constructed from a human Graves' patient thyroid was screened with an immunopurified rabbit anti-human thyroperoxidase (hTPO) polyclonal antibody. A 869 bp clone was obtained. It presents a 130 bp deletion as compared to the published sequence and a 77 bp insertion in the 3' non-coding region. Screening of a pUC cDNA library from another Graves' patient thyroid exhibited the same 130 bp deletion in two other cDNA clones. PCR analysis of mRNA transcripts confirmed the presence of the two messengers in two other Graves' thyroid tissues. In all the cases, this new spliced mRNA species represents between 40% and 50% of the total hTPO mRNAs. With respect to the structure of the hTPO gene, the present deletion suggests an alternate splicing of exon 16. The juxtaposition of exon 17 to exon 15 encoding the transmembrane domain leads to a shift in the reading frame. By the use of a different stop codon, the spliced mRNA generates a modified 56 - COOH terminal aminoacids (aa) sequence.

9/3,AB/41 (Item 41 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06640179 90337314 PMID: 2379828

Sequences 5' to the polyadenylation signal mediate differential poly(A) site use in hepatitis B viruses.

Russnak R; Ganem D
Department of Microbiology, University of California Medical Center, San Francisco 94143.

Genes & development (UNITED STATES) May 1990, 4 (5) p764-76,
ISSN 0890-9369 Journal Code: 8711660

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Most genetic elements that employ reverse transcription generate a terminally redundant genomic RNA that serves as the template for this reaction. Because the identical polyadenylation signal is present in each terminally redundant segment, synthesis of this RNA requires that this signal be ignored on the first pass of the transcription machinery, then recognized and used on the second pass. We have studied the mechanism of this differential poly(A) site use in one family of retroviral elements, the hepatitis B viruses (hepadnaviruses). Our results indicate

that two features are involved: the presence of a variant **poly(A)** signal (TATAAA) and the participation of multiple sequences 5' to this signal that act to increase the efficiency of its use. Deletion of these upstream elements abolishes proper **poly(A)** site use, despite the presence of the **poly(A)** signal and downstream **GT** - and T-rich motifs known to be required for polyadenylation. Sequences from the corresponding regions of retroviral genomes can restore proper processing to these hepadnaviral deletion mutants. Thus, functionally analogous upstream elements exist in other classes of retroviral elements, including those employing the canonical AATAAA hexanucleotide signal.

9/3,AB/42 (Item 42 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06563613 90264393 PMID: 2160955
Spatial constraints on polyadenylation signal function.
Heath C V; Denome R M; Cole C N
Department of Biochemistry, Dartmouth Medical School, Hanover, New Hampshire 03756.
Journal of biological chemistry (UNITED STATES) Jun 5 1990, 265
(16) p9098-104, ISSN 0021-9258 Journal Code: 2985121R
Contract/Grant No.: CA-23018; CA; NCI; GM-33998; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Efficient cleavage and polyadenylation of eukaryotic messenger RNAs require at least two signal elements: an AAUAAA or closely related sequence located 7-30 base pairs (bp) upstream of the site of processing, and a G/U- or U-rich sequence located 3' to the cleavage site. The herpes simplex virus type 1 thymidine kinase (tk) gene contains two copies of the AATAAA hexanucleotide and a **GT**-rich region. We have shown that the first AATAAA and the **GT**-rich region are essential for efficient processing, both in vivo and in vitro, whereas the second AATAAA does not appear to play any role in the formation of tk mRNA 3' ends. The failure of a signal containing only the second AATAAA and the **GT**-rich element to signal cleavage and polyadenylation suggested that these two elements might be too close together to constitute a functional polyadenylation signal. The experiments described in this report were directed at determining the effects on mRNA 3' end formation of alterations in spacing between signal elements. Wild-type tk contains 19 bp between these two elements. Constructs were made in which an AATAAA and the **GT**-rich region were separated by various distances ranging from 7 to 43 bp. The quantity and location of 3' ends of the tk mRNA produced by these constructs in Cos-1 cells were measured by S1 nuclease protection analysis. Signal efficiency was gradually reduced as the separation between the two signal elements was increased; with a separation of 43 bp, the signal functioned at approximately one-eighth the efficiency of the parental construction. Bringing the two signals closer together resulted in decreased signal efficiency; with a separation of 7 or 9 bp, no tk mRNA polyadenylated within the normal region was produced. Altering the sequences between these two elements without changing the distance had small effects on processing efficiency.

9/3,AB/43 (Item 43 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06430617 90138913 PMID: 1689054
Murine beta 1,4-galactosyltransferase: both the amounts and structure of the mRNA are regulated during spermatogenesis.
Shaper N L; Wright W W; Shaper J H

Cell Structure and Function Laboratory, Oncology Center, Johns Hopkins University, Baltimore, MD 21205.

Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Jan 1990, 87 (2) p791-5, ISSN 0027-8424
Journal Code: 7505876

Contract/Grant No.: CA45799; CA; NCI; GM38310; GM; NIGMS; HD21648; HD; NICHD

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Previously we have shown that the gene encoding murine beta 1,4-galactosyltransferase (beta 1,4-GT; UDPgalactose:N-acetyl-D-glucosaminyl-glycopeptide 4-beta-D-galactosyltransferase, EC 2.4.1.38) is unusual in that it specifies two sets of mRNAs of about 3.9 and 4.1 kilobases (kb). Translation of the 3.9- and 4.1-kb mRNAs results in the predicted synthesis of two related membrane-bound forms of the protein of 386 amino acids (short form) and 399 amino acids (long form), respectively. In this study we have examined the expression of beta 1,4-GT during murine spermatogenesis. Spermatogonia contain a 4.1-kb transcript that is comparable in size to the beta 1,4-GT mRNA identified in somatic cells. During differentiation from spermatogonia (2n) to pachytene spermatocytes (4n), the amount of beta 1,4-GT mRNA is reduced to barely detectable levels. Continued differentiation to round spermatids (n) is coincident with a renewed production of beta 1,4-GT mRNA to levels comparable with those detected in spermatogonia. However, the characteristic 4.1-kb mRNA detected in spermatogonia is replaced by two truncated transcripts of 2.9 and 3.1 kb. By S1 nuclease analysis, the 2.9- and 3.1-kb transcripts were shown to encode the same open reading frame as the 4.1-kb transcript found in somatic cells. The shorter round spermatid transcripts arise as a consequence of the use of alternative poly(A) signals. Lastly, we show that, in direct contrast to all somatic tissues and cell lines examined to date, male germ cells synthesize only the long form of the beta 1,4-GT polypeptide.

9/3,AB/44 (Item 44 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

06408222 90097947 PMID: 2532303

E1A-induced enhancer activity of the poly(dG-dT).poly(dA-dC) element (GT element) and interactions with a GT-specific nuclear factor.

Berg D T; Walls J D; Reifel-Miller A E; Grinnell B W

Department of Molecular Biology, Lilly Research Laboratories, Lilly Corporate Center, Indianapolis, Indiana 46285.

Molecular and cellular biology (UNITED STATES) Nov 1989, 9 (11)
p5248-53, ISSN 0270-7306 Journal Code: 8109087

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The alternating sequence poly(dG-dT).poly(dA-dC) is a highly repeated sequence in the eucaryotic genome. We have examined the effect of trans-acting early viral proteins on the ability of the GT element to stimulate transcription of the adenovirus major late promoter (MLP). We find that the GT element alone does not activate expression from the MLP in either the presence or absence of another enhancer element. However, in the presence of the E1A gene products of either adenovirus type 5 or 2, the GT element activated expression from the MLP. The stimulatory activity of the GT element in the presence of E1A had the properties of an enhancer element, and the trans-activating effect on the GT element was additive in conjunction with the E1A-responsive BK virus enhancer. We also have demonstrated that a specific nuclear factor(s) binds to the GT element. However, the E1A protein(s) do not affect the

initial factor interaction(s) with the **GT** element. Overall, our data demonstrate that trans modulation of promoter activity can be mediated through the **GT** element.

9/3,AB/45 (Item 45 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06291179 89378732 PMID: 2570734

Definition of an efficient synthetic **poly(A)** site.
Levitt N; Briggs D; Gil A; Proudfoot N J
Sir William Dunn School of Pathology, University of Oxford, UK.
Genes & development (UNITED STATES) Jul 1989, 3 (7) p1019-25,
ISSN 0890-9369 Journal Code: 8711660
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

We constructed and analyzed a synthetic **poly(A)** (SPA) site that was based on the highly efficient **poly(A)** signal of the rabbit beta-globin gene. By use of the SPA, we demonstrate that the minimum sequences required for efficient polyadenylation are the AATAAA sequence and a **GT** /T-rich sequence with the correct spacing of 22-23 nucleotides between them. When placed downstream of the **poly(A)** site of the human alpha 2-globin gene, the SPA is used exclusively. We predict that the SPA, with its more extensive **GT**/T-rich sequence, is a more efficient **poly(A)** site than alpha-globin. Also, we compared the use of the SPA when it is placed either in the exon 3 or intron 2 of the rabbit beta-globin gene. When in the exonic position, SPA is used 10-fold more than the regular **poly(A)** site of rabbit beta-globin. In contrast, when it is in the intronic location, no detectable use of SPA is observed; however, the deletion of the donor site of intron 2 reactivates the intronic positioned SPA. These results indicate that the splicing of intron 2 in the rabbit beta-globin gene occurs ahead of polyadenylation and have important implications for termination of transcription. Polyadenylation, although required for termination of transcription, is not sufficient; therefore, additional termination signals for RNA polymerase II must exist.

9/3,AB/46 (Item 46 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06040774 89129447 PMID: 2464841

Cloning of the cDNA from normal brain and brain of patients with Alzheimer's disease in the expression vector lambda **GT** 11.

Octave J N; de Sauvage F; Macq A F; Maloteaux J M
Universite Catholique de Louvain, Laboratoire de Neurochimie, Brussels, Belgium.

Progress in neuro-psychopharmacology & biological psychiatry (ENGLAND)
1988, 12 (5) p813-20, ISSN 0278-5846 Journal Code: 8211617

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

1. RNA was purified from postmortem human brains, and the **poly A** + RNA was isolated by oligo dT cellulose. 2. Double stranded cDNA was synthesized using reverse transcriptase, RNase H and DNA polymerase. 3. cDNA was cloned in the lambda **GT** 11 expression vector, and libraries containing between 1 and 2 millions clones were obtained. 92 to 98% of the plaques contained a recombinant phage. 4. Such libraries will allow the molecular characterization of cDNA and corresponding proteins which play a key role in brain functions and in particular which could be involved in the etiology of Alzheimer's dementia.

9/3,AB/47 (Item 47 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05989211 89076497 PMID: 2462430

Human inter-alpha-trypsin inhibitor. Isolation and characterization of heavy (H) chain cDNA clones coding for a 383 amino-acid sequence of the H chain.

Salier J P; Diarra-Mehrpour M; Sesboue R; Bourguignon J; Martin J P
INSERM Unite 295, Faculte de Medecine de Rouen, France.

Biological chemistry Hoppe-Seyler (GERMANY, WEST) May 1988, 369
Suppl p15-8, ISSN 0177-3593 Journal Code: 8503054

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

A cDNA library cloned in lambda gt 11 expression vector was screened with specific anti-inter-alpha-trypsin inhibitor (ITI) heavy (H) chain antiserum. Among seven positive clones selected, two overlapping clones were sequenced. The corresponding consensus sequence encompasses a stretch of bases with one single open reading frame, and the deduced amino-acid sequence displays no homology with the full length cDNA-deduced amino-acid sequence of ITI-light (L) chain. Furthermore, analysis of poly A + mRNAs hybrid-selected by the corresponding cDNA from clone lambda gt11 revealed an immunoprecipitable polypeptide of Mr 91,000. Northern blot analysis showed a single population of mRNAs of 3.3 kb. These data provide new evidence for the presence of distinct H and L chains in the 180 kDa ITI molecule.

9/3,AB/48 (Item 48 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05986990 89073734 PMID: 3201745

Identification and comparison of Campoletis sonorensis virus transcripts expressed from four genomic segments in the insect hosts Campoletis sonorensis and Heliothis virescens.

Theilmann D A; Summers M D

Department of Biology, Texas A&M University, College Station 77843-2475.

Virology (UNITED STATES) Dec 1988, 167 (2) p329-41, ISSN
0042-6822 Journal Code: 0110674

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The Campoletis sonorensis virus (CsV; Polydnviridae) genome consists of at least 28 closed circular superhelical (SH) DNAs. In this study we used complete clones of four SH DNAs to analyze viral transcription both in the adult parasitic wasp host Campoletis sonorensis (Ichneumonidae) and in the lepidopteran host, Heliothis virescens (Noctuidae). CsV genes are expressed in parasitized H. virescens, but no viral transcripts had been characterized from C. sonorensis until this study. The clones of the SH DNAs B, H, M, and O1 were used to probe Northern blots of poly(A)+ RNA isolated from C. sonorensis reproductive tissue and from parasitized H. virescens larvae. All four SH DNAs hybridized to viral transcripts. SH-H, -M, and -O1 hybridized to messages expressed in both hosts. SH-B and -M hybridized to transcripts that were detected only in either C. sonorensis reproductive tissue or parasitized H. virescens larvae. These results suggest that some CsV genes are expressed in a host-specific manner. In a previous study we identified a family of imperfectly conserved tandemly repeated 540-bp repeat elements on SH-B, -H and -O1 (D. A. Theilmann and M. D. Summers, 1987 J. Virol. 61; 2589-2598). Hybridization of the 540-bp repeat regions to Northern blots showed that

they were all homologous to viral transcripts. A cDNA clone of a mRNA that is transcribed from the 540-bp repeat region of SH-B was isolated from a lambda gt 10 library and completely sequenced. The sequence data revealed that the 540-bp repeat element was contained within the open reading frame of this gene. These results indicate that transcribed sequences homologous to the 540-bp repeat elements represent a second gene family to be identified within the CsV genome.

9/3,AB/49 (Item 49 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05963396 89050186 PMID: 2847735

Cloning, nucleotide sequence and molecular evolution of a rabbit processed metallothionein MT-2 pseudogene.

Tam Y C; Hassan M; Chopra A; Thirion J P

Department of Microbiology, Faculty of Medicine, Centre Hospitalier Universitaire, Sherbrooke, Quebec, Canada.

Biochemical and biophysical research communications (UNITED STATES) Nov 15 1988, 156 (3) p1403-10, ISSN 0006-291X Journal Code: 0372516

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

A rabbit metallothionein-2 pseudogene (MT-2 psi) has been isolated from a partial rabbit genomic library. Its unusual sequence shows evidence of complex rearrangements involving recombination and deletion events. There are no intervening sequences, 3' poly A tract or 5' regulatory DNA sequences. The pseudogene is flanked by two sets of direct repeats (CT)3 GT (CT)4 and CTGG(G)CTC. They are most probably the sites of insertion of MT-2 psi in the rabbit genome. In addition, a number of repetitive DNA sequences are observed flanking the MT-2 psi gene. These are features of a processed retrogene.

9/3,AB/50 (Item 50 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05927383 89005726 PMID: 2458971

Cloning and nucleotide sequence of cDNA for the plastid glycerol-3-phosphate acyltransferase from squash.

Ishizaki O; Nishida I; Agata K; Eguchi G; Murata N

National Institute for Basic Biology, Okazaki, Japan.

FEBS letters (NETHERLANDS) Oct 10 1988, 238 (2) p424-30,
ISSN 0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The partial amino acid sequence and amino acid composition of acyl-(acyl-carrier-protein):glycerol-3-phosphate acyltransferase purified from squash cotyledons were determined. cDNAs encoding this enzyme were isolated from lambda gt 11 cDNA libraries made from poly(A)+ RNA of squash cotyledons by immunological selection and cross-hybridization. One of the resultant clones contained a cDNA insert of 1426 base pairs and an open reading frame of 1188 base pairs. The amino acid sequence deduced from the nucleotide sequence matched the partial amino acid sequence determined for the enzyme. The results suggest that a precursor protein of 396 amino acid residues is processed to the mature enzyme of 368 amino acid residues, losing a leader peptide of 28 amino acid residues. Relative molecular masses of the precursor and mature proteins were calculated to be 43,838 and 40,929 Da, respectively.

9/3,AB/51 (Item 51 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05847968 88275972 PMID: 2455863

[A new class of mobile genetic elements of *Drosophila melanogaster*]
Novyi klass mobil'nykh geneticheskikh elementov *Drosophila melanogaster*.
Vashakidze R P; Mzhaviia N Z; Kolchinskii A M; Anan'ev E V
Molekuliarnaia biologii (USSR) Mar-Apr 1988, 22 (2) p362-8,
ISSN 0026-8984 Journal Code: 0105454
Document type: Journal Article ; English Abstract
Languages: RUSSIAN
Main Citation Owner: NLM
Record type: Completed
Clone Dm A89 was obtained upon cloning of DNA fragments coding abundant
poly(A +)RNA's of *D. melanogaster*. Dm A89 was identified as a
new transposable element using in situ hybridization with polytene
chromosomes of two independent highly isogenic lines of *D. melanogaster*
oregon RC and **gt wa** Dm A89 hybridizes with approximately 20 sites in
each line. A portion of Dm A89 is homologous to the distal part of type I
ribosomal gene insertion sequence and is highly repetitive. Two other
sections of the clone have much less redundancy. The unity of the three
fragments is not casual, as revealed by cloning of some other genomic
sequences homologous to Dm A89. Dm A89 is actively transcribed throughout
the development of *D. melanogaster* and produces polyadenylated RNA 1.1 kb
long.

9/3,AB/52 (Item 52 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05817234 88243702 PMID: 2454224

Identification of a mutation that causes exon skipping during collagen
pre-mRNA splicing in an Ehlers-Danlos syndrome variant.
Weil D; Bernard M; Combates N; Wirtz M K; Hollister D W; Steinmann B;
Ramirez F

Department of Microbiology and Immunology, Morse Institute of Molecular
Genetics, State University of New York, Health Science Center at Brooklyn
11203.

Journal of biological chemistry (UNITED STATES) Jun 25 1988, 263
(18) p8561-4, ISSN 0021-9258 Journal Code: 2985121R
Contract/Grant No.: AR-38648; AR; NIAMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Recent biochemical studies have shown that the fibroblasts from a patient
with Ehlers-Danlos Syndrome Type VIIB produce nearly equal amounts of
normal and shortened pro-alpha 2(I) collagen chains (Wirtz, M.K.,
Glanville, R. W., Steinmann, B., Rao, V. H., and Hollister, D. (1987) J.
Biol. Chem. 262, 16376-16385). Compositional and sequencing studies of the
abnormal pro-alpha 2(I) chain identified an interstitial deletion of 18
residues corresponding to the N-telopeptide of the collagen molecule. Since
this region is encoded by a 54-base pair exon, number 6, the protein defect
could have been caused by gene deletion, abnormal pre-mRNA splicing, or
both. Here, in order to elucidate the molecular nature of this mutation we
have analyzed the sequences of pro-alpha 2(I) collagen cDNA and genomic
clones obtained from RNA and DNA of the patient's fibroblasts. Using
oligomer-specific cloning we identified a cDNA that contains a 54-base pair
deletion corresponding precisely to the sequence of exon 6. Identification
of the normal gene was based on the finding of an identical sequence
polymorphism in a normal cDNA and in the genomic clone derived from one of
the two collagen alleles. The other gene, instead, displayed a base
substitution (T to C) in the obligatory **GT** dinucleotide of the 5'
splice-site sequence of intron 6. Analysis of nearly 100 base pairs

immediately 5' to exons 5, 6, and 7, and 3' to exons 5 and 7 did not reveal any additional change. Therefore, the data strongly suggest that the observed GT-to-GC transition at the splice donor site of intron 6 generates an abnormally spliced mRNA in which the sequence of exon 5 is joined to the sequence of exon 7. Since skipping of exon 6 does not interfere with the coding frame of the mRNA, the resulting shortened polypeptide, albeit utilized in the assembly of a procollagen trimer, ultimately causes the Ehlers-Danlos Syndrome Type VII phenotype.

9/3,AB/53 (Item 53 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05731247 88144447 PMID: 3125548

Primary structure of prostaglandin G/H synthase from sheep vesicular gland determined from the complementary DNA sequence.

DeWitt D L; Smith W L

Department of Biochemistry, Michigan State University, East Lansing 48824.

Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Mar 1988, 85 (5) p1412-6, ISSN 0027-8424 Journal Code: 7505876

Contract/Grant No.: DK22042; DK; NIDDK; HL07404; HL; NHLBI

Erratum in Proc Natl Acad Sci U S A 1988 Jul;85(14) 5056

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Prostaglandin G/H synthase (8,11,14-icosatrienoate, hydrogen-donor:oxygen oxidoreductase, EC 1.14.99.1) catalyzes the first step in the formation of prostaglandins and thromboxanes, the conversion of arachidonic acid to prostaglandin endoperoxides G and H. This enzyme is the site of action of nonsteroidal anti-inflammatory drugs. We have isolated a 2.7-kilobase complementary DNA (cDNA) encompassing the entire coding region of prostaglandin G/H synthase from sheep vesicular glands. This cDNA, cloned from a lambda gt 10 library prepared from poly(A)+ RNA of vesicular glands, hybridizes with a single 2.75-kilobase mRNA species. The cDNA clone was selected using oligonucleotide probes modeled from amino acid sequences of tryptic peptides prepared from the purified enzyme. The full-length cDNA encodes a protein of 600 amino acids, including a signal sequence of 24 amino acids. Identification of the cDNA as coding for prostaglandin G/H synthase is based on comparison of amino acid sequences of seven peptides comprising 103 amino acids with the amino acid sequence deduced from the nucleotide sequence of the cDNA. The molecular weight of the unglycosylated enzyme lacking the signal peptide is 65,621. The synthase is a glycoprotein, and there are three potential sites for N-glycosylation, two of them in the amino-terminal half of the molecule. The serine reported to be acetylated by aspirin is at position 530, near the carboxyl terminus. There is no significant similarity between the sequence of the synthase and that of any other protein in amino acid or nucleotide sequence libraries, and a heme binding site(s) is not apparent from the amino acid sequence. The availability of a full-length cDNA clone coding for prostaglandin G/H synthase should facilitate studies of the regulation of expression of this enzyme and the structural features important for catalysis and for interaction with anti-inflammatory drugs.

9/3,AB/54 (Item 54 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05716262 88152493 PMID: 2450052

The structure and expression of neuron-specific enolase gene.

Sakimura K; Kushiya E; Takahashi Y; Suzuki Y

Department of Neuropharmacology, Niigata University, Japan.

Gene (NETHERLANDS) 1987, 60 (1) p103-13, ISSN 0378-1119
Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Neuron-specific (gamma gamma) enolase (NSE) is an isoenzyme form of glycolytic enzyme, enolase. We isolated genomic clones for NSE and clarified NSE gene structures. The NSE-gene spanned about 9 kb and consisted of twelve exons and eleven introns. Multiple transcriptional start points were identified by a combination of S1 nuclease mapping and primer extension analysis. In the 5'-flanking region we found a TATA-like sequence TCTATAGGC which was only partially homologous to the consensus sequence, but we did not find a CAAT box. The sequence in the immediate 5'-flanking region was of a relatively high G + C content and contained GC-box-like clusters that did not correspond to the typical GC box. In addition, we found seven classes of the repeated sequences. In the introns 1, 5 and 10 there were tandem repeats (GT)³³, (GT)²¹ and (GT)²⁴, respectively. The 3' end contains a single polyadenylation site and an identifier sequence 2 kb downstream from the poly(A)-addition site. The in vitro cell-free transcription of the truncated genomic DNA fragment using HeLa cell extract showed that the transcription start points have been correctly identified and the putative promoter sequences appear to be functional.

9/3,AB/55 (Item 55 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05554941 87304251 PMID: 2441988

Multiple mRNA species code for the catalytic subunit of the cAMP-dependent protein kinase from LLC-PK1 cells. Evidence for two forms of the catalytic subunit.

Adavani S R; Schwarz M; Showers M O; Maurer R A; Hemmings B A

European journal of biochemistry / FEBS (GERMANY, WEST) Sep 1 1987, 167 (2) p221-6, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We present evidence for the existence of two forms of the catalytic (C) subunit of the cAMP-dependent protein kinase. A lambda gt-11 cDNA library constructed from poly(A)-rich RNA from the porcine kidney cell line, LLC-PK1, was screened using a 1.5-kb EcoRI fragment from a bovine cDNA for the C subunit. Two independent classes of cDNAs were identified on the basis of partial restriction map and sequence data. These two cDNAs, lambda CAT4 and lambda CAT3, apparently encode two forms of C subunit designated C alpha and C beta, respectively. The nucleotide sequence of the C alpha and C beta cDNAs revealed differences in the coding region and particularly in the 3' untranslated region. However, the deduced amino acid sequences of C alpha and C beta subunits were 96% homologous to the sequences so far determined. Specific probes from the 3' coding region of the two cDNA species were used to investigate C subunit mRNA expression in LLC-PK1 cells. Northern analysis showed a major mRNA species of 2.8 kb with the C alpha probe while the C beta probe detected two mRNA species of 5.0 kb and 3.8 kb. These data were supported by genomic blot analysis which showed distinct hybridization patterns with either the C alpha or C beta probes. All the available evidence suggests that at least two distinct genes encode the C subunit which are expressed in LLC-PK1 cells.

9/3,AB/56 (Item 56 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05340634 87064784 PMID: 2431304

Isolation and characteristics of cDNA clones containing simple (GT)n/(CA)n sequences of an animal genome]

Poluchenie i kharakteristika klonov kDNK, soderzhashchikh "prostye" posledovatel'nosti (GT)n/(CA)n genoma zhivotnykh.

Tokarskaia O N; Dzhumanova E T; Kupriianova N S; Ivanov P L; Ryskov A P
Molekuliarnaia genetika, mikrobiologiya i virusologiya (USSR) Sep 1986, (9) p24-9, ISSN 0208-0613 Journal Code: 9315607

Document type: Journal Article ; English Abstract

Languages: RUSSIAN

Main Citation Owner: NLM

Record type: Completed

9/3,AB/57 (Item 57 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

05335325 87089822 PMID: 2879221

Fine-structure analysis of the processing and polyadenylation region of the herpes simplex virus type 1 thymidine kinase gene by using linker scanning, internal deletion, and insertion mutations.

Zhang F; Denome R M; Cole C N

Molecular and cellular biology (UNITED STATES) Dec 1986, 6 (12)

p4611-23, ISSN 0270-7306 Journal Code: 8109087

Contract/Grant No.: GM33998; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Most eucaryotic mRNAs are polyadenylated. In higher eucaryotes, the sequence AATAAA is located 7 to 30 base pairs (bp) upstream from the site of processing and polyadenylation and is a critical part of the signal for processing and polyadenylation. Efficient cleavage and polyadenylation also require sequences downstream of polyadenylation sites. The herpes simplex virus type 1 thymidine kinase (tk) gene contains two copies of the AATAAA hexanucleotide and a GT box (18 of 19 consecutive residues are G or T) previously shown to be required for efficient processing and polyadenylation of tk mRNA (C. N. Cole and T. P. Stacy, Mol. Cell. Biol., 5:2104-2113). To define further the sequence requirements for efficient polyadenylation, we prepared linker scanning, internal deletion, and small insertion mutations in the polyadenylation region of the tk gene. These mutations were analyzed by S1 nuclease protection analysis of cytoplasmic RNA isolated from transfected Cos-1 monkey kidney cells. When the proximal AATAAA was deleted, no tk mRNA polyadenylated in the normal region was detected, whereas replacement of the second AATAAA with an XbaI linker had no effect on polyadenylation. When various portions of the GT box were replaced with linker, the amount of tk mRNA produced was reduced to 23 to 82% of the normal amount, but polyadenylation in the normal region was never abolished. Thus, no single portion of the GT box was absolutely required. In some cases, extended transcripts, polyadenylated at a cryptic site within pBR322, were detected. A spacing of 6 bp between AATAAA and the GT box was too short for efficient processing and polyadenylation. A spacing of 30 bp appeared to work almost as efficiently as did the wild-type spacing of 18 bp. Taken together, these results indicate that efficient polyadenylation requires both AATAAA and downstream GT-rich sequences. In addition, processing and polyadenylation are affected both qualitatively and quantitatively by sequences at polyadenylation sites and at more distant locations.

9/3,AB/58 (Item 58 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

05328559 87080763 PMID: 2431926

Expression cloning of a cDNA encoding the type II regulatory subunit of the cAMP-dependent protein kinase.

Hemmings B A; Schwarz M; Adavani S R; Jans D A

FEBS letters (NETHERLANDS) Dec 15 1986, 209 (2) p219-22,

ISSN 0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We report here the isolation and sequence of a cDNA for the type II regulatory subunit of the cAMP-dependent protein kinase (cAMP-PK) from a lambda gt-11 cDNA library derived from a porcine epithelial cell line (LLC-PK1). The cDNA was detected by immunological screening using an affinity purified polyclonal antibody for bovine RII. DNA sequence analysis of the 467 bp EcoRI insert confirmed the identity of the clone, because the deduced amino acid sequence corresponded to the published sequence for the bovine RII protein. Northern analysis of total RNA from the LLC-PK1 cells indicated a single mRNA species of about 6.0 kb, probably derived from a single copy gene.

9/3,AB/59 (Item 59 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

05300771 87053869 PMID: 3023066

Molecular cloning and sequencing of the human erythrocyte 2,3-bisphosphoglycerate mutase cDNA: revised amino acid sequence.

Joulin V; Peduzzi J; Romeo P H; Rosa R; Valentin C; Dubart A; Lapeyre B; Blouquit Y; Garel M C; Goossens M; et al

EMBO journal (ENGLAND) Sep 1986, 5 (9) p2275-83, ISSN

0261-4189 Journal Code: 8208664

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The human erythrocyte 2,3-bisphosphoglycerate mutase (BPGM) is a multifunctional enzyme which controls the metabolism of 2,3-diphosphoglycerate, the main allosteric effector of haemoglobin. Several cDNA banks were constructed from reticulocyte mRNA, either by conventional cloning methods in pBR322 and screening with specific mixed oligonucleotide probes, or in the expression vector lambda gt 11. The largest cDNA isolated contained 1673 bases [plus the poly(A) tail], which is slightly smaller than the size of the intact mRNA as estimated by Northern blot analysis (approximately 1800 bases). This cDNA encodes for a protein of 258 residues; the protein yielded 34 tryptic peptides which were subsequently isolated by h.p.l.c. Our nucleotide sequence data were entirely confirmed by the amino acid composition of these tryptic peptides and reveal several major differences from the published sequence; the revised amino acid sequence of human BPGM is presented. These findings represent the first step in the study of the expression and regulation of this enzyme as a specific marker of the erythroid cell line.

9/3,AB/60 (Item 60 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

05235199 86308096 PMID: 3091848

A biomolecular approach to the study of the expression of specific genes in the retina.

McGinnis J F; Leveille P J

Journal of neuroscience research (UNITED STATES) 1986, 16 (1)

p157-65, ISSN 0360-4012 Journal Code: 7600111

Contract/Grant No.: HD-05615; HD; NICHD
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The central nervous system contains a number of populations of neurons that are morphologically and functionally distinct. To study the genes responsible for the development and maintenance of proteins with unique structural and biochemical properties, polyspecific antisera were produced against normal mouse retinal proteins and used in combination with the rd (retinal degeneration) neurological mutant of the mouse to immunologically identify specific retinal proteins. Western transfer analysis of the proteins present in normal and in mutant retinas identified three classes of neural proteins: those found only in normal retina; those found in normal and in photoreceptorless retinas but not in other tissues; and those found in both normal and mutant retinas, as well as in brain, but not elsewhere. Some of these class 1 proteins were shown to be present in the retinas of other species, including humans, suggesting their importance in the process of vision. The poly A+ RNA was isolated from the retinas of normal mice and used to generate a cDNA expression library in lambda gt -11. This library was screened with polyspecific antisera absorbed with the proteins present in mutant retina, and a number of immunologically positive plaques were cloned. Four of these were shown to code for rhodopsin, the major visual protein in mammalian retinas. The approach described is applicable to other systems in order to generate specific immunological and recombinant DNA probes for examining the expression of specific genes during development and differentiation.

9/3,AB/61 (Item 61 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05144595 86216149 PMID: 3011081

Amino acid sequence of human histidine-rich glycoprotein derived from the nucleotide sequence of its cDNA.

Koide T; Foster D; Yoshitake S; Davie E W

Biochemistry (UNITED STATES) Apr 22 1986, 25 (8) p2220-5,

ISSN 0006-2960 Journal Code: 0370623

Contract/Grant No.: HL 16919; HL; NHLBI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

A lambda gt 11 library containing cDNA inserts prepared from human liver mRNA has been screened with an affinity-purified antibody to human histidine-rich glycoprotein (HRG) and then with a restriction fragment isolated from the 5' end of the largest cDNA insert obtained by antibody screening. A number of positive clones were identified and shown to code for HRG by DNA sequence analysis. A total of 2067 nucleotides were determined by sequencing 3 overlapping cDNA clones, which included 121 nucleotides of 5'-noncoding sequence, 54 nucleotides coding for a leader sequence of 18 amino acids, 1521 nucleotides coding for the mature protein of 507 amino acids, a stop codon of TAA, and 352 nucleotides of 3'-noncoding sequence followed by a poly(A) tail of 16 nucleotides. The length of the noncoding sequence of the 3' end differed in several clones, but each contained a polyadenylation or processing sequence of AATAAA followed by a poly(A) tail. More than half of the amino acid sequence of HRG consisted of five different types of internal repeats. Within the last 3 internal repeats (type V), there were 12 tandem repetitions of a 5 amino acid segment with a consensus sequence of Gly-His-His-Pro-His. This repeated portion, referred to as a "histidine-rich region", contained 53% histidine and showed a high degree of similarity to a histidine-rich region of high molecular weight kininogen.

9/3,AB/62 (Item 62 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05116534 86186906 PMID: 2421730

Induction of UDP-glucuronyl transferase mRNA in embryonic chick livers by phenobarbital.

Jackson M R; Kennedy S M; Lown G; Burchell B

Biochemical pharmacology (ENGLAND) Apr 1 1986, 35 (7) p1191-8,

ISSN 0006-2952 Journal Code: 0101032

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Administration of phenobarbital to chick embryos increased hepatic microsomal UDP-glucuronyltransferase activity some 25-fold. The large phenobarbital-induced increase of UDP-glucuronyltransferase activity was correlated to an equivalent increase of immunochemically measurable UDP-glucuronyltransferase protein. Poly(A+) RNA isolated from the livers of chick embryos treated with either phenobarbital or saline was translated in vitro. Immunochemical analysis of the translation products indicated that phenobarbital induced a 30-fold increase in UDP-GT mRNA. Fractionation of hepatic poly(A+) RNA from phenobarbital-treated chick embryos by sucrose density gradient centrifugation indicated that the size of the UDP-GT mRNA was 21S. These data show that phenobarbital induction of chick embryo liver UDP-glucuronyltransferase activity correlates with a similar large increase in the level of translatable mRNA for this enzyme.

9/3,AB/63 (Item 63 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

05067703 86140140 PMID: 3005291

Structure of rodent helix-destabilizing protein revealed by cDNA cloning.

Cobianchi F; SenGupta D N; Zmudzka B Z; Wilson S H

Journal of biological chemistry (UNITED STATES) Mar 15 1986, 261

(8) p3536-43, ISSN 0021-9258 Journal Code: 2985121R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

A cDNA library of newborn rat brain poly(A+) RNA in lambda gt 11 was screened with a synthetic oligonucleotide probe corresponding to a five amino acid sequence in the N-terminal region of the calf helix-destabilizing protein, UPl. Six positive phage were isolated after testing 2 X 10(5) recombinants, and each phage was plaque purified. Four of these phage clones were positive with a second oligonucleotide probe corresponding to a 5 amino acid sequence in the C-terminal region of calf UPl; one of the clones positive with both probes was selected for detailed study. This phage, designated lambda HDP-182, contained a 1706-base pair cDNA insert corresponding to an mRNA with a poly(A) sequence at the 3' terminus and a single open reading frame starting 63 bases from the 5' terminus and extending 988 bases. The 3' untranslated region of the mRNA contained 718 bases, including an AAUAAA signal 21 bases from the poly(A) sequence and a 16-residue poly(U) sequence flanked on each side by oligonucleotide repeats. Primer extension analysis of newborn rat brain poly(A+) RNA suggested that the cDNA insert in lambda HDP-182 was full length except for about 35 nucleotide residues missing from the 5' end untranslated region, and Northern blot analysis revealed one relatively abundant mRNA species of approximately the same size as the cDNA insert. The 988-residue open reading frame in the cDNA predicted a 34,215-dalton protein of 320 amino

acids. Residues 2 through 196 of this rat protein are identical to the 195-residue sequence of the calf helix-destabilizing protein, UP1. The 124-amino acid sequence in the C-terminal portion of the 34,215-dalton protein is not present in purified calf UP1. This 124-residue sequence has unusual amino acid content in that it is 11% asparagine, 15% serine, and 40% glycine and consists of 16 consecutive oligopeptide repeats. Computer-derived secondary structure predictions for the 34,215-dalton protein revealed two distinct domains consisting of residues 1 through approximately 196 and residues approximately 197 to 320, respectively.

9/3,AB/64 (Item 64 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

04961684 86033784 PMID: 2997165

Genomic DNA sequence for human C-reactive protein.

Lei K J; Liu T; Zon G; Soravia E; Liu T Y; Goldman N D

Journal of biological chemistry (UNITED STATES) Oct 25 1985, 260

(24) p13377-83, ISSN 0021-9258 Journal Code: 2985121R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The gene for the prototype acute phase reactant, C-reactive protein, has been isolated from two lambda phage libraries containing inserted human DNA fragments using synthetic oligonucleotide probes. Nucleotide sequence analysis indicates that after coding for a signal peptide of 18 amino acids and the first two amino acids of the mature protein, there is an intron of 278 base pairs followed by the nucleotide sequence for the remaining 204 amino acids. The intron is unusual in that it contains on the positive strand a **poly(A)** stretch 16 nucleotides long and a **poly(GT)** region 30 nucleotides long which could adopt the Z-form of DNA. The nucleotide sequence reported here confirms the amino acid sequence of mature C-reactive protein as originally reported except that it codes for an additional 19 amino acids beginning at position 62. Thus DNA sequence analysis predicts that the mature protein consists of 206 amino acids rather than 187 as originally reported. The mRNA cap site is located 104 nucleotides from the start of the signal peptide and there is a 3' noncoding region 1.2 kilobase pairs in length. The gene has a typical promoter containing the sequences TATAAAT and CAAT 29 and 81 base pairs upstream, respectively, of the cap site.

9/3,AB/65 (Item 65 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

04667986 85046483 PMID: 6093780

Isolation of an evolutionarily conserved epidermal growth factor receptor cDNA from human A431 carcinoma cells.

Simmen F A; Gope M L; Schulz T Z; Wright D A; Carpenter G; O'Malley B W

Biochemical and biophysical research communications (UNITED STATES) Oct 15 1984, 124 (1) p125-32, ISSN 0006-291X Journal Code: 0372516

Contract/Grant No.: CA 16672; CA; NCI; CA 24071; CA; NCI; RR-05425; RR; NCRR

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Complementary DNA corresponding to total **poly(A)**+RNA from the human A431 epidermoid carcinoma cell line was cloned in the phage expression vector lambda **gt** 11. An epidermal growth factor (EGF) receptor cDNA clone was obtained by screening of the expression library with a rabbit polyclonal antibody (IgG), raised to the purified A431 EGF receptor, in combination with [125I]protein A of *S. aureus*. The cloned cDNA

was able to select, by hybridization, messenger RNA which was translated in *Xenopus* oocytes and yielded an immunoprecipitable EGF receptor protein of Mr = 160,000. The insert of this cDNA (pHEGFR-1), is approximately 880 base pairs in length and encodes the carboxyterminal portion of the EGF receptor protein. Its sequence is evolutionarily conserved among vertebrates as shown by hybridization to unique chromosomal DNA sequences from human, baboon, dog, rat, mouse and frog.

9/3,AB/66 (Item 66 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

04630432 85006903 PMID: 6148343

Isolation, characterization, and DNA sequence of the rat somatostatin gene.

Tavianini M A; Hayes T E; Magazin M D; Minth C D; Dixon J E
Journal of biological chemistry (UNITED STATES) Oct 10 1984, 259
(19) p11798-803, ISSN 0021-9258 Journal Code: 2985121R
Contract/Grant No.: AM 18024; AM; NIADDK; AM0734021; AM; NIADDK; GM 07211
; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The gene encoding rat somatostatin has been isolated from a lambda phage gene library. Phage harboring the gene were identified by plaque hybridization using a nick-translated fragment derived from the cDNA for rat somatostatin. The transcriptional unit includes exons of 238 and 367 base pairs (bp) separated by one intron of 621 bp. The intron is located between the codons for Gln (-57) and Glu (-56) of prosomatostatin. Analysis of the nucleotide sequence 5' to the start of transcription reveals a number of sequences which may be involved in the expression of somatostatin. A variant of the "TATA" box, TTAAAA, lies 26 bp upstream from the start of transcription, and a sequence homologous to the "CAAT" box (GGCTAAT) is 92 bp upstream from the transcription start. A long alternating purine-pyrimidine stretch, (GT)₂₅, which is similar to Z DNA-forming sequences in other genes, lies 628 bp 5' to the transcription start and is flanked by small repeats. Hybridization analysis shows that this region is highly repeated in the genome and that homologous sequences are located approximately 2 kilobase pairs downstream from the poly(A) addition site. Southern hybridization of the lambda clone with probes derived from brain or liver poly(A+) RNA demonstrates that another transcribed sequence lies about 7 kilobase pairs downstream from the poly(A) addition site of the rat somatostatin gene. Analysis of rat DNA suggests that there may be restriction-site polymorphisms in or near the gene or that additional somatostatin-hybridizing sequences may exist in the genome.

9/3,AB/67 (Item 67 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

04608758 84272638 PMID: 6087320

Molecular cloning of human terminal deoxynucleotidyltransferase.

Peterson R C; Cheung L C; Mattaliano R J; Chang L M; Bollum F J
Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Jul 1984, 81 (14) p4363-7, ISSN 0027-8424 Journal Code: 7505876

Contract/Grant No.: GM31393; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

A cDNA of the human terminal deoxynucleotidyltransferase (TdT; "terminal

transferase," EC 2.7.7.31) was isolated from a human lymphoblastoid cell cDNA library in lambda gt 11 by using immunological procedures. Four inserts containing 723 to 939 base pairs were recloned in pBR322 for hybridization and preliminary sequence studies. mRNA selected by hybridization to recombinant DNA was translated to a 58-kDa peptide that specifically immunoprecipitated with rabbit antibodies to calf terminal transferase and mouse monoclonal antibody to human terminal transferase. Blot hybridization of total poly(A)+ RNA from KM3 (TdT+) cells with nick-translated pBR322 recombinant DNA detected a message of about 2000 nucleotides, sufficient to code for the 580 amino acids in the protein. mRNA from terminal transferase- cells gave no signal in hybrid selection or RNA blot hybridization. The complete sequence of the 939-base-pair insert sequence was obtained from deletions cloned in pUC8. The DNA sequence contains an open reading frame coding for 238 amino acids, about 40% of the protein. Three peptides isolated by HPLC from tryptic digests of succinylated 58-kDa calf thymus terminal transferase were sequenced, providing 20, 18, and 22 residues of peptide sequence. A search of the translated sequence of the 939-base-pair insert shows three regions beginning after arginine that have greater than 90% homology with the sequence determined from the calf thymus terminal transferase peptides. These results provide unambiguous evidence that the human terminal transferase sequence has been cloned.

9/3,AB/68 (Item 68 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

04452120 84135765 PMID: 6365917

The conserved 5 S rRNA complement to tRNA is not required for translation of natural mRNA.

Zagorska L; Van Duin J; Noller H F; Pace B; Johnson K D; Pace N R
Journal of biological chemistry (UNITED STATES) Mar 10 1984, 259
(5) p2798-802, ISSN 0021-9258 Journal Code: 2985121R
Contract/Grant No.: GM-17129; GM; NIGMS; GM-20147; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

We have tested a putative base-paired interaction between the conserved GT psi C sequence of tRNA and the conserved GAAC47 sequence of 5 S ribosomal RNA by in vitro protein synthesis using ribosomes containing deletions in this region of 5 S rRNA. Ribosomes reconstituted with 5 S rRNA possessing a single break between residues 41 and 42, deletion of residues 42-46, or deletion of residues 42-52 were tested for their ability to translate phage MS2 RNA. Initiator tRNA binding, aminoacyl-tRNA binding, ppGpp synthesis, and miscoding were also tested. All of the measured functions could be carried out by ribosomes carrying the deleted 5 S rRNAs. The sizes and relative amounts of the polypeptides synthesized by MS2 RNA-programmed ribosomes were identical whether or not the 5 S RNA contained deletions. Aminoacyl-tRNA binding and miscoding were essentially unaffected. Significant reduction in ApUpG (but not poly(A,U,G) or MS2 RNA)-directed fMet-tRNA binding and ppGpp synthesis were observed, particularly in the case of the larger (residues 42-52) deletion. We conclude that if tRNA and 5 S rRNA interact in this fashion, it is not an obligatory step in protein synthesis.

9/3,AB/69 (Item 69 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

03753091 82025551 PMID: 6269745

Ribosomal insertion-like elements in Drosophila melanogaster are interspersed with mobile sequences.

Dawid I B; Long E O; DiNocera P P; Pardue M L

Cell (UNITED STATES) Aug 1981, 25 (2) p399-408, ISSN
0092-8674 Journal Code: 0413066
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Sequences homologous to the type 1 ribosomal DNA insertion occur in the chromocenter and in one location on the fourth chromosome of *Drosophila melanogaster*. Ribosomal insertion-like elements frequently occur in the form of tandem repeats and are often interspersed with nonhomologous DNA. Sequences that interrupt of flank insertion-like elements are members of diverged repeated DNA families. Members of five of these interspersed sequence families are located at multiple euchromatic sites as well as in the chromocenter. The euchromatic sites differ greatly in the *gt*-1 and *gt*-X11 stocks of *D. melanogaster*, suggesting that these sequence families are mobile in the genome. No long inverted repeats were detected in any of these interspersed sequences. One sequence, called 101F, interrupts a ribosomal insertion-like element; the nucleotide sequences across the boundaries between 101F and ribosomal insertion have been determined. A stretch of 13 base pairs that is present once in the ribosomal insertion is repeated at the ends of the 101F sequence, suggesting a target site duplication. Within the 101F element, no extended direct or inverted repeat sequence exists. The interspersed repeated sequences studied are transcribed into rare, heterogeneous, poly(A)-lacking nuclear RNA molecules. In one case, we showed that both strands of a flanking sequence are transcribed, but to a different extent. With respect to structural features and the nature of their transcripts, the sequences described here are distinct from other known transposable elements in *Drosophila*.

9/3,AB/70 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11192326 BIOSIS NO.: 199799813471
Biochemical properties of hepatitis C virus NS5B RNA-dependent RNA polymerase and identification of amino acid sequence motifs essential for enzymatic activity.
AUTHOR: Lohmann Volker; Koerner Frank; Herian Ulrike; Bartenschlager Ralf
(a)
AUTHOR ADDRESS: (a)Inst. Virol., Johannes-Gutenberg Univ. Mainz, Obere Zahlbacher Str. 67, 55131 Mainz**Germany
JOURNAL: Journal of Virology 71 (11):p8416-8428 1997
ISSN: 0022-538X
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The NS5B protein of the hepatitis C virus (HCV) is an RNA-dependent RNA polymerase (RdRp) (S.-E. Behrens, L. Tomei, and R. De Francesco, EMBO J. 15:12-22, 1996) that is assumed to be required for replication of the viral genome. To further study the biochemical and structural properties of this enzyme, an NS5B-hexahistidine fusion protein was expressed with recombinant baculoviruses in insect cells and purified to near homogeneity. The enzyme was found to have a primer-dependent RdRp activity that was able to copy a complete in vitro-transcribed HCV genome in the absence of additional viral or cellular factors. Filter binding assays and competition experiments showed that the purified enzyme binds RNA with no clear preference for HCV 3'-end sequences. Binding to homopolymeric RNAs was also examined, and the following order of specificity was observed: poly(U) *gt* poly(G) *gt* poly(A) *gt* poly(C). An inverse order was found for the RdRp activity, which used poly(C) most efficiently as a template but was inactive on poly(U) and poly(G), suggesting that a high

binding affinity between polymerase and template interferes with processivity. By using a mutational analysis, four amino acid sequence motifs crucial for RdRp activity were identified. While most substitutions of conserved residues within these motifs severely reduced the enzymatic activities, a single substitution in motif D which enhanced the RdRp activity by about 50% was found. Deletion studies indicate that amino acid residues at the very termini, in particular the amino terminus, are important for RdRp activity but not for RNA binding. Finally, we found a terminal transferase activity associated with the purified enzyme. However, this activity was also detected with NS5B proteins with an inactive RdRp, with an NS4B protein purified in the same way, and with wild-type baculovirus, suggesting that it is not an inherent activity of NS5B.

1997

9/3,AB/71 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10937826 BIOSIS NO.: 199799558971

Functional expression of rat renal cortex taurine transporter in *Xenopus laevis* oocytes: Adaptive regulation by dietary manipulation.

AUTHOR: Han Xiaobin; Budreau Andrea M; Chesney Russel W(a)

AUTHOR ADDRESS: (a)Dep. Pediatr., Univ. Tennessee, LeBonheur Children's Medical Center, 50 North Dunlap St., Memphis**USA

JOURNAL: Pediatric Research 41 (5):p624-631 1997

ISSN: 0031-3998

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Renal brush border taurine transport adapts to changes in the dietary intake of sulfur amino acids with increased rates after dietary restriction and reduced transport after dietary surplus. The *Xenopus laevis* oocyte expression system was used to define the renal adaptive response to dietary manipulation. Injection of **poly(A)**+ RNA isolated from rat kidney cortex resulted in a time- and dose-dependent increase in NaCl-aurine cotransport in oocytes. The K-m of the expressed taurine transporter was 22.5 μ M. In oocytes, injection of 40 ng of **poly(A)**+ RNA from kidneys of low taurine diet (LTD)-fed rats elicited 2-fold the taurine uptake of normal taurine diet (NTD)-fed rats and **gt** 3-fold the uptake of high taurine diet (HTD)-fed rats. Northern blots of rat kidneys using a riboprobe derived from an rB16a (rat brain taurine transporter) subclone revealed 6.2- and 2.4-kb transcripts, the abundance of which were increased or decreased in LTD- or HTD-fed rats, respectively, as compared with NTD-fed rats. A approx 70-kD protein was detected by Western blot using an antibody derived from a synthetic peptide corresponding to a conserved intracellular segment of rB16a. The abundance of the approx 70-kD protein was increased or decreased in LTD- or HTD-fed rats, respectively, as compared with NTD-fed rats. In conclusion, expression of the rat renal taurine transporter is regulated by dietary taurine at the level of mRNA accumulation and protein synthesis.

1997

9/3,AB/72 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10928145 BIOSIS NO.: 199799549290

Molecular tools for population and ecological genetics in coniferous trees.

AUTHOR: Morgante Michele; Pfeiffer Antonella; Costacurta Antonia; Olivieri

Angelo M
AUTHOR ADDRESS: Dipartimento Produzione Vegetale Tecnologie Agrarie,
Univ. Udine, Via delle Scienze 208, I-33100 Ud**Italy
JOURNAL: Phyton (Horn) 36 (4):p129-138 1996
ISSN: 0079-2047
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: In order for molecular markers to be used in the population genetics of forest trees they have to meet certain requirements such as the ease and speed of genotyping, the codominance of alleles, the reproducibility over time and space, the high information content and the possibility of easily exchanging marker information. None of the many molecular marker systems available fully meets all these requirements. However after taking into account advantages and disadvantages of each of the systems we decided to focus our attention on the use of simple sequence repeats (SSRs or microsatellites) because they are codominant, reproducible, highly informative and easy to exchange. We have been isolating AC/GT and AG/CT SSRs from the Norway spruce (*Picea abies* K.) nuclear genome. We isolated several hundreds positive clones from a small-insert genomic library and following sequence analysis we designed primers for 36 of them, 24 containing AG and 12 AC SSRs. After testing them on a panel of spruce individuals 25% of the primer pairs produced a single-locus hypervariable pattern, with the remaining ones giving either a single monomorphic product (18%) or very poor amplification (19%) or amplification of multiple bands (38%). Segregation in accordance with a simple Mendelian model of inheritance was demonstrated for all the loci amplified with the primer pairs giving a simple variable pattern. We screened a panel of 19 spruce trees at these loci. The average number of alleles per locus was 14 and expected heterozygosity 0.80, with up to 23 alleles per locus and heterozygosities exceeding 0.94. This shows that nuclear SSRs can be very useful markers in the population genetics of trees even though the overall efficiency of the marker identification process is quite low due to the high percentage of primer pairs producing complex or "dirty" patterns. We attribute this phenomenon to the high complexity of the spruce genome. Other methods, including the construction of libraries highly enriched for SSR sequences, that we developed in order to make SSR retrieval and typing easier and faster will be discussed. We recently extended the use of PCR amplified SSR markers to the chloroplast genome. We demonstrated that mononucleotide poly(A/T) stretches are frequent in the chloroplast genomes of plants and show high levels of between and within population variation, making them ideal tools for cytoplasmic population genetics overcoming the difficulties in finding within species variation that are frequently encountered when analysing the cpDNA molecule by RFLPs or PCR-PFLPs. We will discuss the possible applications of such markers for studying gene flow and for paternity analysis.

1996

9/3,AB/73 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10844527 BIOSIS NO.: 199799465672
The renal electrogenic Na⁺: HCO₃-cotransporter.
AUTHOR: Boron Walter F(a); Heidiger Matthias A; Boulpaep Emile L; Romero Michael F
AUTHOR ADDRESS: (a)Dep. Cellular Molecular Physiology, Yale Univ. Sch. Med., New Haven, CT 06520**USA
JOURNAL: Journal of Experimental Biology 200 (2):p263-268 1997
ISSN: 0022-0949
RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The electrogenic Na⁺:HCO₃⁻ cotransporter (symporter) is the major transporter for HCO₃⁻ reabsorption across the basolateral membrane of the renal proximal tubule and also contributes significantly to Na⁺ reabsorption. We expression-cloned the salamander renal electrogenic Na⁺:Bicarbonate Cotransporter (NBC) in *Xenopus laevis* oocytes. After injecting **poly(A)**⁺ RNA, fractionated **poly(A)**⁺ RNA or cRNA, we used microelectrodes to monitor membrane potential (V_m) and intracellular pH (pH_i). All solutions contained ouabain to block the Na⁺/K⁺ pump (P-ATPase). After applying 1.5% CO₂/10 mmol l⁻¹ HCO₃⁻ (pH 7.5) and allowing pH_i to stabilize from the CO₂-induced acidification, we removed Na⁺. In native oocytes or water-injected controls, removing Na⁺ hyperpolarized the cell by -5 mV and had no effect on pH_i. In oocytes injected with **poly(A)**⁺ RNA, removing Na⁺ transiently depolarized the cell by -10 mV and caused pH_i to decrease; both effects were blocked by 4,4'-diisothiocyano-2,2'-stilbenedisulfonate (DIDS) and required HCO₃⁻. We enriched the signal by electrophoretic fractionation of the **poly(A)**⁺ RNA, and constructed a size-selected cDNA library in pSPORT1 using the optimal fraction. Screening the Ambystoma library yielded a single clone (aNBC). Expression was first obvious 3 days after injection of NBC cRNA. Adding CO₂/HCO₃⁻ induced a large (gt 50 mV) and rapid hyperpolarization, followed by a partial relaxation as pH_i stabilized. Subsequent Na⁺ removal depolarized the cell by more than 40 mV and decreased pH_i. aNBC is a full-length clone with a start Met and a **poly(A)**⁺ tail; it encodes a protein with 1025 amino acids and several putative membrane-spanning domains. aNBC is the first member of a new family of Na⁺-linked HCO₃⁻ transporters. We used aNBC to screen a rat kidney cDNA library, and identified a full-length cDNA clone (rNBC) that encodes a protein of 1035 amino acids. rNBC is 86% identical to aNBC and can be functionally expressed in oocytes.

1997

9/3,AB/74 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10801560 BIOSIS NO.: 199799422705

Glucoamylase gene fusions alleviate limitations for protein production in *Aspergillus awamori* at the transcriptional and (post)translational levels.

AUTHOR: Gouka Robin J; Punt Peter J; Van Den Hondel Cees A M J J(a)
AUTHOR ADDRESS: (a)TNO Nutr. Food Res. Inst., Dep. Mol. Genetics Gene Technol., P.O. Box 360, NL-3700AJ Zeist**Netherlands
JOURNAL: Applied and Environmental Microbiology 63 (2):p488-497 1997
ISSN: 0099-2240
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: In this study we have analyzed the effects of a glucoamylase gene fusion on the mRNA levels and protein levels for the human interleukin-6 gene (hil6) and the guar alpha-galactosidase gene (aglA). Previously it was shown that production of nonfused alpha-galactosidase and hIL-6 in *Aspergillus awamori* was limited at transcriptional and (post)translational levels, respectively (R. J. Gouka, P. J. Punt, J. G. M. Hessing, and C. A. M. J. J. van den Hondel, Appl. Environ. Microbiol. 62: 1951-1957, 1996). Vectors were constructed which contained either the hil6 or aglA gene fused to the *Aspergillus niger* glucoamylase gene (glaA) under control of the efficient 1,4-beta-endoxyranase A promoter and transcription terminator. For comparison, the vectors were integrated in a single copy at the pyrG locus of *A. awamori*. A glaA fusion to the 5' end of the hil6 gene resulted in a large increase in hIL-6 yield, whereas

with a glaA fusion to the 3' end of the hil6 gene, almost no protein was produced. Nevertheless, the steady-state mRNA levels of both fusions were very similar and not clearly increased compared to those of a strain expressing nonfused hIL-6. Fusions of glaA to the 5' end of the wild-type guar aglA gene resulted in truncated mRNA lacking almost 900 bases (gt 80%) of the aglA sequence. When the coding sequence of the wild-type aglA gene was replaced by a synthetic aglA gene with optimized Saccharomyces cerevisiae codon usage, full-length mRNA was obtained. Compared to a nonfused synthetic aglA gene, a glaA fusion with the synthetic aglA gene resulted in a 25-fold increase in the mRNA level and, as a consequence, a similar increase in the alpha-galactosidase protein level. The truncated transcripts derived from the wild-type aglA gene were further analyzed by nuclear run-on transcription assays. These experiments indicated that transcription elongation in the nucleus proceeded at least 400 bases downstream of the site where the truncation was determined, indicating that transcription elongation or premature termination was not the reason for the generation of truncated mRNAs. As the truncated mRNA also contained a poly(A) tail, truncation most likely occurs by incorrect processing of the aglA mRNA in the nucleus.

1997

9/3,AB/75 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10696925 BIOSIS NO.: 199799318070
Genomic and cDNA sequence tags of the hyperthermophilic archaeon
Pyrobaculum aerophilum.
AUTHOR: Voelkl Paul; Markiewicz Peter; Baikalov Claudia; Fitz-Gibbon Sorel;
Stetter Karl O; Miller Jeffrey H(a)
AUTHOR ADDRESS: (a)Dep. Micorbiol. Molecular Genetics, Molecular Biol
Inst., Univ. California, 405 Hilgard Ave., Lo**USA
JOURNAL: Nucleic Acids Research 24 (22):p4373-4378 1996
ISSN: 0305-1048
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The hyperthermophilic archaeum, Pyrobaculum aerophilum, grows optimally at 100 degree C with a doubling time of 180 min. It is a member of the phylogenetically ancient Thermoproteales order, but differs significantly from all other members by its facultatively aerobic metabolism. Due to its simple cultivation requirements and its nearly 100% plating efficiency, it was chosen as a model organism for studying the genome organization of hyperthermophilic ancient archaea. By a G+C content of the DNA of 52 mol%, sequence analysis was easily possible. At least some of the mRNA of P. aerophilum carried poly-A tails facilitating the construction of a cDNA library. 245 sequence tags of a poly-A primed cDNA library and 55 sequence tags from a 1-2 kb Sau3AI-fragment containing genomic library were analyzed and the corresponding amino acid sequences compared with protein sequences from databases. Fourteen percent of the cDNA and gt 9% of genomic DNA sequence tags revealed significant similarities to proteins in the databases. Matches were obtained to proteins from archaeal, bacterial and eukaryal sources. Some sequences showed greatest similarity to eukaryal rather than to bacterial versions of proteins, other matches were found to proteins which had previously only been found in eukaryotes.

1996

9/3,AB/76 (Item 7 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
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10691975 BIOSIS NO.: 199799313120

Structural and functional characterization of human potassium channel subunit beta-1 (KCNA1B).

AUTHOR: Leicher T; Roeper J; Weber K; Wang X; Pongs O(a)

AUTHOR ADDRESS: (a)Zentrum fuer Mol. Neurobiol., Inst. fuer Neurale Signalverarbeitung, Martinistrasse 52, D-20246 **Germany

JOURNAL: Neuropharmacology 35 (7):p787-795 1996

ISSN: 0028-3908

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Voltage-activated Shaker-related potassium channels (K-v1) consist of alpha and beta subunits. We have analysed the structure of the human KCNA1B (hK-v-beta-1) gene. KCNA1B is **gt** 250 kb in size and encodes at least three K-v-beta-1 splice variants. The K-v-beta-1 open reading frame is divided into 14 exons. In contrast, genes coding for family members of KCNA (K-v1-alpha) subunits are markedly smaller and have intronless open reading frames. The expression of K-v1-alpha and K-v-beta mRNA was compared in Northern blots of **poly(A+)** RNA isolated from various human brain tissues. The results suggest an intricate and cell-specific regulation of K-v1-alpha and K-v-beta mRNA synthesis such that distinct combinations of alpha and beta subunits would occur in different nuclei of the brain. The splice variants hK-v-beta-1.1 and hK-v-beta-1.2 were functionally characterized in coexpression studies with hK-v1.5-alpha subunits in 293 cells. It is shown that they confer rapid inactivation on hK-v1.5 channels with different potencies. This may be due to differences in their amino terminal sequences and/or inactivating domains. It is also shown that the amino terminal K-v-beta-1.1 and K-v1.4-alpha inactivating domains compete with each other, probably for the binding to the same receptor site(s) on K-v1-alpha-subunits.

1996

9/3,AB/77 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10634662 BIOSIS NO.: 199699255807

Interaction of polyadenylic acid (5') with histone H1 or protamine.

AUTHOR: Kuo Wu-Nan(a); Chambers Maxine C; Jn-Baptiste Junior B

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JOURNAL: Biochemistry and Molecular Biology International 40 (2):p365-372

1996

ISSN: 1039-9712

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The interaction between polyadenylic acid (5') (**poly (A)**) and histone (or protamine) was analyzed by electrophoretic retardation of **poly (A)**-histone (or protamine) complex in agarose gel. The potency of interaction was protamine **gt** histone H1, arginine-rich histone **gt** other histones. The catalytic subunit of cyclic AMP-dependent protein kinase effectively decreased the electrophoretic retardation of **poly(A)**-histone H1. The interaction between **poly(A)** and histone H1 was also detected by the drastically enhanced absorbance around 340 nm. The findings may implicate a regulatory role of histone H1 on mRNAs through its binding on

poly(A) tails.

1996

9/3,AB/78 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10622172 BIOSIS NO.: 199699243317

Molecular cloning, sequencing and expression analysis of a fatty acid transport gene in rat heart induced by ischemic preconditioning and oxidative stress.

AUTHOR: Maulik Nilanjana; Das Dipak K(a)

AUTHOR ADDRESS: (a)Cardiovascular Div., Dep. Surg., Univ. Connecticut Sch. Med., Farmington, CT 06030-1110**USA

JOURNAL: Molecular and Cellular Biochemistry 160-161 (0):p241-247

1996

ISSN: 0300-8177

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: In this study, ischemia and oxidative stress-inducible gene expression in heart was examined by subtractive hybridization technique. Total RNA was isolated from ventricular muscle fragments of normal and oxidative stress-induced hearts. Poly (A)+ RNA was purified followed by the construction of a plasmid cDNA library. This was followed by the subtractive screening of oxidative stress-induced cDNA library. The positive colonies were amplified and the plasmid isolated. An aliquot was subjected to restriction cutting with Bam H1 and EcoRI; the fragments corresponding to cDNA insert were separated by electrophoresis, radiolabeled by random-primed DNA synthesis, and used as probes in standard Northern blotting experiments. An aliquot containing the plasmid from the confirmed positives was then subjected to bidirectional partial DNA sequencing (using M13 and T7/T3a primers) by the chain-extension/chain termination method. These sequences were subjected to a computerized search for homologies against all sequences in the updated worldwide Gen Bank and EMBL sequence databases followed by restriction mapping and reading frame identification. Out of 24 putative positive colonies screened, one clone was matched with gt 97% homology with FAT gene that has been implicated in binding or transport of long chain fatty acids. cDNA probe synthesized from this clone identified two major transcripts of 4.8 and 2.9 kb. Additional experiments were then performed where isolated perfused rat hearts were subjected to the following treatments: (1) 5 min ischemia; (2) 10 min ischemia; (3) 20 min ischemia; (4) 5 min ischemia followed by 10 min reperfusion (ischemic preconditioning); and (5) 5 min ischemia followed by 10 min reperfusion, repeated four times (4 x preconditioning). RNAs were extracted from these hearts and hybridized with the FAT cDNA probe. The results indicated that FAT gene was induced by oxidative stress, ischemic preconditioning, but not by ischemia.

1996

9/3,AB/79 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10619560 BIOSIS NO.: 199699240705

Characterization of the NTPase activity of Japanese encephalitis virus NS3 protein.

AUTHOR: Kuo Ming-Der; Chin Chuan; Hsu Shu-Ling; Shiao Jen-Yin; Wang

Teen-Meei; Lin Ju-Hung(a)
AUTHOR ADDRESS: (a)Inst. Preventive Med., Natl. Defense Med. Cent., P.O.
Box 90048-700, Sanhsia, Taipei**Taiwan
JOURNAL: Journal of General Virology 77 (9):p2077-2084 1996
ISSN: 0022-1317
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Japanese encephalitis (JE) virus NS3 protein and two N-terminally truncated (DELTA-1-148 and DELTA-1-323) forms of NS3 were engineered and expressed in *E. coli* as fusion proteins with a histidine tag at the N terminus. The purified recombinant protein his-NS3 and his-NS3-(DELTA-1-148) were found to possess NTPase activity which was stimulated by single-stranded RNA, whereas NS3-(EPSILON-D-1-323) did not. The requirements for MgCl₂ and MnCl₂ and the salt and pH were determined and shown to be slightly different from those of the NTPases of other flaviviruses. Poly(U) and poly(C) were better than poly(A) at stimulating the NTPase activities, in contrast to other flaviviral NTPases. The substrate preference was in the order GTP gt ATP mchgt UTP gt CTP. Interestingly, we found that Ca²⁺ could not substitute for Mg²⁺; on the contrary, it inhibited NTPase activity. The removal of the N-terminal 148 amino acids enhanced NTPase activity, but further deletion of the region (amino acids 148-323) completely abolished the activity. Therefore, amino acids 148-323 contain a critical region required for NTPase activity.

1996

9/3,AB/80 (Item 11 from file: 5)
DIALOG(R)File 5:BIOSIS Previews(R)
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10572895 BIOSIS NO.: 199699194040
Characterization of RNA binding activity and RNA helicase activity of the hepatitis C virus NS3 protein.

AUTHOR: Gwack Yousang; Kim Dong Wook; Han Jang H; Choe Joonho(a)
AUTHOR ADDRESS: (a)Dep. Biol. Sci., Korea Advanced Inst. Sci. Technol.,
Taejon 305-701**South Korea
JOURNAL: Biochemical and Biophysical Research Communications 225 (2):p
654-659 1996
ISSN: 0006-291X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The Hepatitis C Virus (HCV) NS3 protein has RNA binding activity, RNA-stimulated NTPase activity, and RNA helicase activity. The RNA binding activity of the C-terminal domain of the HCV NS3 protein is less sensitive to pH, KCl, and MgCl₂ than NTPase and the RNA helicase activity. The overall order of the binding of homoribopolymer for the NS3 protein was poly(U) mchgt poly(A) gt poly(G), poly(C). The minimal RNA binding size of the HCV NS3 protein was determined using a gel retardation assay and is estimated between 7 nt and 20 nt. The HCV RNA helicase unwinds RNA/DNA heteroduplexes as well as RNA/RNA duplexes and it catalytically translocates in the 3' to 5' direction.

1996

9/3,AB/81 (Item 12 from file: 5)
DIALOG(R)File 5:BIOSIS Previews(R)
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10562799 BIOSIS NO.: 199699183944

Isolation and sequencing of the rho gene from *Streptomyces lividans* ZX7 and characterization of the RNA-dependent NTPase activity of the overexpressed protein.

AUTHOR: Ingham Colin J(a); Hunter Iain S; Smith Margaret C M

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JOURNAL: Journal of Biological Chemistry 271 (36):p21803-21807 1996

ISSN: 0021-9258

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The gene for transcription termination factor Rho was isolated from *Streptomyces lividans* ZX7. It encoded a 77-kDa polypeptide (Rho 77) with considerable homology to known Rho factors. An atypical hydrophilic region of 228 residues was found within the N-terminal RNA-binding domain. Only Rho from *Micrococcus luteus* and *Mycobacterium leprae* (closely related GC-rich Gram-positive bacteria) had an analogous sequence. Rho 77 was overexpressed in *Escherichia coli* and purified using an N-terminal hexahistidine-tag. Rho 77 displayed a broad RNA-dependent ATPase activity, with poly(C) RNA being no more than 4-fold more effective than poly(A). This contrasts with the ATPase activity of Rho from *E. coli* which is stimulated primarily by poly(C) RNA. Rho 77 was a general RNA-dependent NTPase, apparent K_m values for NTPs were: GTP 0.13 mM, ATP 0.17 mM, UTP 1.1 mM, and CTP **gt** 2 mM. Rho 77 poly(C)-dependent ATPase activity was inhibited by heparin, unlike the *E. coli* Rho. The antibiotic bicyclomycin inhibited the *in vitro* RNA-dependent ATPase activity of Rho 77, did not inhibit growth of streptomycetes but delayed the development of aerial mycelia. N-terminal deletion analysis to express a truncated form of Rho (Rho 72, 72 kDa) indicated that the first 42 residues of Rho 77 were not essential for RNA-dependent NTPase activity and were not the targets of inhibition by heparin or bicyclomycin.

1996

9/3,AB/82 (Item 13 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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10475810 BIOSIS NO.: 199699096955

Inhibition of glycosylation decreases Na⁺/H⁺ exchange activity, blocks NHE-3 transport to the membrane, and increases NHE-3 mRNA expression in LLC-PK-1 cells.

AUTHOR: Soleimani Manoocher(a); Singh Gurinder; Bookstein Crescence; Rao Mrinalini C; Chang Eugene B; Dominguez Jesus H

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JOURNAL: Journal of Laboratory and Clinical Medicine 127 (6):p565-573

1996

ISSN: 0022-2143

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Recent studies have shown that NHE-3 is the luminal Na⁺/H⁺ exchanger isoform in cultured renal proximal tubule cells LLC-PK-1 and OK (J Biol Chem 1994;269:15613-8). The purpose of the current experiments was to study the role of NHE-3 glycosylation on antiporter activity in LLC-PK-1 cells. Treatment of LLC-PK-1 cells with 1.5 μ -g/ml tunicamycin for 24 hours, which blocks glycosylation in the endoplasmic reticulum,

significantly decreased antiporter activity as assessed by acid-stimulated sodium 22 uptake (9.52 ± 1.0 nmol/mg protein in control cells vs 5.85 ± 0.7 nmol/mg protein in tunicamycin-treated cells, $p < 0.01$, $n = 4$) and sodium-dependent pH-1 recovery from an acid load (0.46 ± 0.05 pH/min in control cells vs 0.35 ± 0.04 pH/min in tunicamycin-treated cells, $p < 0.02$, $n = 6$). Lactate dehydrogenase (LDH) concentration in the medium was the same in both groups ($p > 0.05$), indicating that the inhibitory effect of tunicamycin was not caused by cell toxicity. Northern hybridization of **poly(A)+** RNA from LLC-PK-1 cells illustrated that in tunicamycin-treated cells, NHE-3 mRNA expression increased threefold over control cells. Immunoblots of luminal membranes from control LLC-PK-1 cells with specific NHE-3 antiserum showed a doublet at 94 to 95 kd and a band at 90 kd. Luminal membranes from tunicamycin-treated cells showed only one strong band at 95 kd. NHE-3 immunoblots of whole cell extract from tunicamycin-treated cells showed that in addition to the 95 kd protein, an 87 kd band was also detected. These results are consistent with the possibility that the two bands in the 94 and 90 kd areas became deglycosylated and did not reach the membrane in the presence of tunicamycin. We conclude that glycosylation of the Na⁺/H⁺ exchanger isoform NHE-3 is essential for antiporter activity in LLC-PK-1 cells. The results further suggest that glycosylation of NHE-3 mediates the translocation and insertion of this exchanger in the plasma membrane.

1996

9/3,AB/83 (Item 14 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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10427055 BIOSIS NO.: 199699048200
 Effects of alcohols and food additives on glutamate receptors expressed in Xenopus oocytes: Specificity in the inhibition of the receptors.
 AUTHOR: Aoshima Hitoshi
 AUTHOR ADDRESS: Dep. Chem., Fac. Liberal Arts, Yamaguchi Univ., 1677-1 Yoshida, Yamaguchi 753**Japan
 JOURNAL: Bioscience Biotechnology and Biochemistry 60 (3):p434-438

1996

ISSN: 0916-8451
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: To study the effects of food additives on glutamate receptors, they were expressed in Xenopus oocytes that received an injection of **poly(A)+** mRNAs prepared from rat brain. The response of the receptors elicited by kainate (KA) and N-methyl-D-aspartate (NMDA) was measured electrophysiologically in the presence and absence of food additives. Both responses elicited by KA and NMDA were inhibited similarly by addition of additives such as caffeine, vanillin or saccharin. However, inhibition of KA-elicited response by food additives followed a competitive inhibition scheme with two binding sites, while that of NMDA-elicited response followed a simple noncompetitive inhibition scheme. Inhibition constants of food additives for both responses were more than 1 mM. So it is unlikely that food additives taken with processed food interrupt signal transmission under physiological conditions. The specificity of inhibition of both responses was examined by adding various compounds to the bathing solutions containing the agonist. Increase of the number of hydroxyl groups in alcohols with the chain of three carbon atoms decreased the potency of inhibition. Potency of the inhibition depended on the species of functional groups. The order of potency of the inhibition by compounds with a chain of six carbon atoms was alcohol = diamine **gt** aldehyde

gt carboxylic acid. Hexanol inhibited the receptors more strongly than (3Z)-hexen-1-ol. NMDA-elicited response showed little selectivity in inhibition by structural isomers of pentanol, while KA-elicited response showed some selectivity in inhibition by the structural isomers.

1996

9/3,AB/84 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10415067 BIOSIS NO.: 199699036212
CAMP-activation of amiloride-sensitive Na⁺ channels from guinea-pig colon expressed in *Xenopus* oocytes.
AUTHOR: Liebold Katja M; Reifarth Frank W; Clauss Wolfgang; Weber Wolf-Michael(a)
AUTHOR ADDRESS: (a)Inst. Animal Physiol., Justus-Liebig-Univ., Wartweg 95, D-35392 Giessen**Germany
JOURNAL: Pfluegers Archiv European Journal of Physiology 431 (6):p913-922
1996

ISSN: 0031-6768
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Guinea-pig distal colonic mRNA injection into *Xenopus laevis* oocytes resulted in expression of functional active epithelial Na⁺ channels in the oocyte plasma membrane. Poly(A)⁺ RNA was extracted from distal colonic mucosa of animals fed either a high-salt (HS) or a low-salt (LS) diet. The electrophysiological properties of the expressed amiloride-sensitive Na⁺ conductances were investigated by conventional two-electrode voltage-clamp and patch-clamp measurements. Injection of poly(A)⁺ RNA from HS-fed animals (from hereon referred to as HS-poly(A)⁺ RNA) into oocytes induced the expression of amiloride-sensitive Na⁺ conductances. On the other hand, oocytes injected with poly(A)⁺ RNA from LS-fed animals (LS-poly(A)⁺ RNA) expressed a markedly larger amount of amiloride-blockable Na⁺ conductances. LS-poly(A)⁺ RNA-induced conductances were completely inhibitable by amiloride with a K_i of 77 nM, and were also blocked by benzamil with a K_i of 1.8 nM. 5-(N-Ethyl-N-isopropyl)-amiloride (EIPA), even in high doses (25 μM), had no detectable effect on the Na⁺ conductances. Expressed amiloride-sensitive Na⁺ channels could be further activated by cAMP leading to nearly doubled clamp currents. When Na⁺ was replaced by K⁺, amiloride (1 μM) showed no effect on the clamp current. Single-channel analysis revealed slow gating behaviour, open probabilities (P_o) between 0.4 and 0.9, and slope conductances of 3.8 pS for Na⁺ and 5.6 pS for Li⁺. The expressed channels showed to be highly selective for Na⁺ over K⁺ with a permeability ratio P_{Na}/P_K gt 20. Amiloride (500 nM) reduced channel P_o to values lt 0.05. All these features make the guinea-pig distal colon of LS-fed animals an interesting mRNA source for the expression of highly amiloride-sensitive Na⁺ channels in *Xenopus* oocytes, which could provide new insights in the regulatory mechanism of these channels.

1996

9/3,AB/85 (Item 16 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10385286 BIOSIS NO.: 199699006431

Molecular cloning of the gene for human leukotriene C-4 synthase:
Organization, nucleotide sequence, and chromosomal localization to 5q35.
AUTHOR: Penrose John F(a); Spector Jeremy; Baldasaro Mathew; Xu Kongyi;
Boyce Joshua; Arm Jonathan P(a); Austen K Frank; Lam Bing K
AUTHOR ADDRESS: (a)Seeley G. Mudd Build., 250 Longwood Ave., Room 610,
Boston, MA 02115**USA
JOURNAL: Journal of Biological Chemistry 271 (19):p11356-11361 1996
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Leukotriene C-4 (LTC-4) synthase catalyzes the conjugation of LTA-4 with reduced GSH to form LTC-4, the parent of the receptor active cysteinyl leukotrienes implicated in the pathobiology of bronchial asthma. Previous cloning of the cDNA for human LTC-4 synthase demonstrated significant homology of its amino acid sequence to that of 5-lipoxygenase activating protein (FLAP) but none to that of the GSH S-transferase super-family. Genomic cloning from a P1 library now reveals that the gene for LTC-4 synthase contains five exons (ranging from 71 to 257 nucleotides in length) and four introns, which in total span 2.52 kilobase pairs in length. The intron/exon junctions of LTC-4 synthase align identically with those of FLAP; however, the small size of the LTC-4 synthase gene contrasts with the **gt** 31-kilobase pair size reported for FLAP. Confirmation of the LTC-4 synthase gene size to ensure that no deletions had occurred during the cloning was obtained by two overlapping polymerase chain reactions from genomic DNA, which provided products of the predicted sizes. Primer extension analysis with **poly(A)+** RNA from culture-derived human eosinophilic granulocytes or the KG-1 myelogenous cell line revealed multiple transcriptional start sites with prominent signals at 66, 69 and 96 base pairs 5' of the ATG translation start site. The 5'-flanking region revealed a GC-rich promotor sequence consistent with an SP-1 site and consensus sequences for AP-1 and AP-2 enhancer elements, 24, 807 and 877 bp, respectively, 5' from the first transcription initiation site. Southern blot analysis of a genomic DNA (with full-length cDNA as well as 5' and 3' oligonucleotide probes) confirmed the size of the gene and indicated a single copy gene in normal human genomic DNA. Fluorescent in situ hybridization mapped LTC-4 synthase to chromosomal location 5q35, which is in close proximity to the cluster of genes for cytokines and receptors involved in the regulation of cells central to allergic inflammation and implication in bronchial asthma.

1996

9/3,AB/86 (Item 17 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10384605 BIOSIS NO.: 199699005750
Analysis of polymorphism for an Alu element on the Y chromosome (YAP) in Korean population.
AUTHOR: Ryu Kyoung-Hwa; Kim Wook(a)
AUTHOR ADDRESS: (a)Dep. Biol., Dankook Univ., Cheonan 330-714**South Korea
JOURNAL: Korean Journal of Genetics 18 (1):p39-47 1996
ISSN: 0254-5934
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Korean; Non-English
SUMMARY LANGUAGE: Korean; English

ABSTRACT: A simple polymorphism resulting from the recent insertion of an

Alu element, referred to as the Y Atu polymorphic (YAP) element, on the long arm (Yq11) of the Y chromosome has been proved to be useful for the human population studies. We have examined the Y Alu insertion polymorphism using PCR based detection method in Korean population. A total of 204 unrelated males were analyzed to raise the possibility of tracing paternal lineages and male-mediated gene flow between Korea and Japan. The frequency of YAP' element was found to be 0.98% (2/204). Therefore, almost Korean revealed to have YAP element (gt 99%) similar to those of most Asian populations with the exception of high frequency of YAP element in Japanese. We cloned these two Korean YAP elements derived from PCR products by ligating into pCRII plasmids and subsequently sequenced to determine the Y haplotype based on the length of the 3'-terminal poly(A) region of the sequence. The first clone, designated p(YAP)KB1 appeared to have 41 dA-nucleotides and the second one, p(YAP)KK1 was found to have 50 dA-nucleotides. Based on these results, they seem to belong to the type 3a which is frequently found in Japanese population. It might be suggested that these YAP' chromosomes provide an explanation for the admixture recently from Japan. Therefore the rate of admixture for YAP' chromosomes from Japan to Korea appeared to be extremely low than that of a large infusion of YAP chromosomes with the Yayoi migration starting 2,300 years ago from Korea. Finally, all of these results support the hybridization theory that modern Japanese populations have resulted from the ancient Jomon people (YAP) and Yayoi immigrants (YAP) from Korea.

1996

9/3,AB/87 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10377320 BIOSIS NO.: 199698832238
Characterization of ovine stem cell factor messenger ribonucleic acid and protein in the corpus luteum throughout the luteal phase.
AUTHOR: Gentry P C; Smith G W; Anthony R V; Zhang Z; Long D K; Smith M F(a)
AUTHOR ADDRESS: (a)Dep. Animal Sciences, 160 Animal Sci. Res. Cent.,
Columbia, MO 65211**USA
JOURNAL: Biology of Reproduction 54 (5):p970-979 1996
ISSN: 0006-3363
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Stem cell factor (SCF) is a growth factor known to have profound effects on the proliferation, migration, differentiation, and survival of numerous cell types, including those of the ovary. The objectives of the present study were to identify and characterize expression of this growth factor in the ovine corpus luteum (CL). A 952-bp cDNA was amplified from Day 3 (Day 0 = estrus) ovine luteal total cellular (tc) RNA by reverse transcriptase-polymerase chain reaction and determined to encode SCF. Northern analysis of Day 10 luteal poly(A)+ RNA indicated one major transcript of approximately 6.5 kb. SCF mRNA was localized within Day 3 and Day 10 CL by in situ hybridization and was expressed throughout luteal tissue on both days examined. To assess expression throughout the luteal phase, SCF mRNA was quantified by ribonuclease protection assay in tcRNA collected on Days 3, 7, 10, 13, and 16; values did not differ across days (p gt 0.10). Similarly, SCF mRNA was quantified in tcRNA isolated from pools of Day 10 large and small steroidogenic cells (n = 4 and 3, respectively); levels did not differ (p gt 0.10) between cell types. In addition, SCF protein was detected in CL on Days 3 and 10, and was expressed in a cell-specific manner in cells with morphological characteristics of large and small luteal cells. These data indicate that SCF may be involved in communication among steroidogenic

cells and/or between steroidogenic and nonsteroidogenic cells of the CL.

1996

9/3,AB/88 (Item 19 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10326754 BIOSIS NO.: 199698781672

Experimental and theoretical study of electrostatic effects on the isoelectric pH and the pK-a of the catalytic residue His-102 of the recombinant ribonuclease from *Bacillus amyloliquefaciens* (Barnase).

AUTHOR: Bastyns Katrin; Froeyen Matheus; Fernando Diaz Jose; Volckaert Guido; Engelborghs Yves(a)

AUTHOR ADDRESS: (a)Laboratory Chemistry Biological Dynamics Celestijnenlaan 200 D, B-3001 Leuven**Belgium

JOURNAL: Proteins Structure Function and Genetics 24 (3):p370-378

1996

ISSN: 0887-3585

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Barnase, the guanine specific ribonuclease of *Bacillus amyloliquefaciens*, was subjected to mutations in order to alter the electrostatic properties of the enzyme. Ser-85 was mutated into Glu with the goal to introduce an extra charge in the neighborhood of His-102. A double mutation (Ser-85-Glu and Asp-86-Asn) was introduced with the same purpose but without altering the global charge of the enzyme. A similar set of mutations was made using Asp at position 85. For all mutants the pI was determined using the technique of isoelectric focusing and calculated on the basis of the Tanford-Kirkwood theory. When Glu was used to replace Ser-85, the correlation between the experimental and the calculated values was perfect. However, in the Ser-85-Asp mutant, the experimental pI drop is bigger than the calculated one, and in the double mutant (Ser-85-Asp and Asp-86-Asn) the compensation is not achieved. The effect of the mutations on the pK-a of His-102 can be determined from the pH dependence of the k-cat/K-M for the hydrolysis of dinucleotides, e.g., GpC. The effect can also be calculated using the method of Honig. In this case the agreement is very good for the Glu-mutants and the single Asp-mutant, but less for the double Asp-mutant. The global stability of the Asp-mutants is, however, the same as the wild type, as shown by stability studies using urea denaturation. Molecular dynamics calculations, however, show that in the double Asp-mutant His-102 (H+) swings out of its pocket to make a hydrogen bridge with Gln-104 which should cause an additional pK-a rise. The effect of the Glu-mutations was also tested on all the kinetic parameters for GpC and the cyclic intermediate G_{gt}p at pH 6.5, for RNA at pH 8.0, and for poly(A) at pH 6.2. The effect of the mutations is rather limited for the dinucleotide and the cyclic intermediate, but a strong increase of the K-M is observed in the case of the single mutant (extra negative charge) with polymeric substrates. These results indicate that the extra negative charge has a strong destabilizing effect on the binding of the polymeric substrates in the ground state and the transition state complex. A comparison with the structure of bound tetranucleotides (Buckle, A.M. and Fersht, A.R., Biochemistry 33:1644-1653,1994) shows that the extra negative charge points towards the P2 Site.

1996

9/3,AB/89 (Item 20 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
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10266683 BIOSIS NO.: 199698721601

Demonstration and characterization of a transport system capable of lysine and leucine absorption that is encoded for in porcine jejunal epithelium by expression of mRNA in *Xenopus laevis* oocytes.

AUTHOR: Matthews J C; Wong E A; Bender P K; Webb K E Jr(a)

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JOURNAL: Journal of Animal Science 74 (1):p127-137 1996

ISSN: 0021-8812

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Defolliculated *Xenopus laevis* oocytes were injected with size-fractionated poly(A)+ RNA (RNA) isolated from the jejunal epithelium of growing pigs (average BW 33.8 kg) to identify proteins capable of Na+-independent amino acid transport. The ability of oocytes to absorb L-lysine (lysine) or L-leucine (leucine) from Na+- free media was quantified in oocytes after injection of RNA fractions or water. Specific RNA fractions were identified that induced saturable uptake of lysine (K-t = 52 mu-M) and leucine (K-t = 97 mu-M), whereas endogenous oocyte uptake was not saturable. Induced uptake of .05 mM lysine by oocytes was inhibited (P lt .05) 68.1% by 5 mM leucine and 38.9% by .2 mM L-cystine (cystine). Induced uptake of .05 mM leucine was inhibited (P lt .05) 83.1% by 5 mM lysine and 23.2% by .2 mM cystine. Although not significant (P gt .05), 5 mM L-glutamate (glutamate) quantitatively stimulated the induced uptake of .05 mM lysine by 18.8% and the induced uptake of .05 mM leucine by 60%. To identify mRNA species responsible for this b-o,+ transporter-like activity, oocytes were co-injected with the RNA fractions and degenerate DNA oligomers complementary (antisense) to the cloned human kidney b-o,+ amino acid transporter, or (as a negative control) with a DNA oligomer complementary to the rabbit intestinal Na+/glucose cotransporter, or with water. Only those oocytes injected with two specific RNA fractions and the antisense DNA oligomer complementary to the b-o,+ transporter displayed reduced (P lt .05) uptake of lysine (45.7, 55.4%) and leucine (44.1, 65.9%). These results indicate that messenger RNA encoding for a protein capable of stimulating the competitive absorption of lysine and leucine is expressed by the jejunal epithelia of growing pigs.

1996

9/3,AB/90 (Item 21 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10244430 BIOSIS NO.: 199698699348

A candidate gene for mild mental handicap at the FRAXE fragile site.

AUTHOR: Chakrabarti Lisa; Knight Samantha J L; Flannery Angela V; Davies Kay E(a)

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JOURNAL: Human Molecular Genetics 5 (2):p275-282 1996

ISSN: 0964-6906

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The cytogenetic expression of the folate sensitive fragile site, FRAXE, is due to the expansion of a GCC repeat in proximal Xq28 of the

human X chromosome and is associated with a mild form of mental handicap. Normal individuals have 6-35 copies of the repeat whereas cytogenetically positive, developmentally delayed males have **gt** 200 copies and show methylation of the associated CpG island. Through the use of conserved sequences adjacent to the FRAXE GCC repeat, we have isolated a 1495 bp cDNA which begins 331 bp distal to the FRAXE site and extends to a region **gt** 170 kb distal in Xq28. The cDNA sequence possesses both a putative start of translation and a **poly-A** tail. The predicted protein has amino acid motifs which share significant homologies with the human AF-4 gene which encodes a putative transcription factor. On northern analysis, the cDNA detects a 9.5 kb transcript in human brain, placenta and lung. This transcript is present in multiple human brain tissues, but is more abundant in the hippocampus and the amygdala, thus providing possible functional insights. RT-PCR of normal adult brain RNA provides evidence for the existence of the 1495 bp transcript represented by the isolated cDNA.

1996

9/3,AB/91 (Item 22 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10235253 BIOSIS NO.: 199698690171

Proteins C1 and C2 of heterogeneous nuclear ribonucleoprotein complexes bind RNA in a highly cooperative fashion: Support for their contiguous deposition on Pre-mRNA during transcription.

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JOURNAL: Biochemistry 35 (4):p1212-1222 1996

ISSN: 0006-2960

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Proteins C1 and C2 together comprise about one-third the protein mass of mammalian core 40S heterogeneous nuclear ribonucleoprotein particles (40S hnRNP) and exist as heterotetramers of (C1)-3C2. On the basis of nonequilibrium binding studies, it has been suggested that the C proteins specifically bind oligo(U)- and poly(U)-rich sequences, and preferentially associate with uridine-rich regions near the 3' termini of many introns. We describe here a more quantitative characterization of the equilibrium binding properties of native and recombinant C protein to homoribopolymers using fluorescence spectroscopy. Like C protein from HeLa cells, the recombinant proteins spontaneously oligomerize to form tetramers with the same hydrodynamic properties as native protein. Near-stoichiometric binding titrations of the fluorescent homoribopolymer polyethenoadenosine (poly(r(epsilon-A))) with recombinant (C1)-4 and (C2)-4 homotetramers along with competition binding assays with **poly(A)** and **poly(C)** indicate that the binding site size (n) is between 150 and 230 nucleotides. This site size range is in close agreement with that previously determined for native C protein through hydrodynamic and ultrastructural studies (apprx 230 nucleotides). (C1)-4 and (C2)-4 bind **poly(G)** with intrinsic affinities (K_i) of 10^{-9} M $^{-1}$, which are a hundredfold higher than their affinities for **poly(U)**. In opposition to report,) that C protein does not bind **poly(A)** and **poly(C)**, we find that the C proteins bind these substrates with moderate K_i , but with high cooperativity (ω). The overall affinity ($K\omega$) for the binding of both proteins to **poly(A)** and **poly(C)** is 10-fold higher **gt** 10^{-8} but **lt** 10^{-9} M $^{-1}$ than their affinities for **poly(U)**. The highLY cooperative binding of C protein to

these substrates provides a mechanistic basis for the distribution of C protein along the length of nucleic acid substrates.

1996

9/3,AB/92 (Item 23 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10177473 BIOSIS NO.: 199698632391
Artificial neural network method for discriminating coding regions of eukaryotic genes.
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JOURNAL: Computer Applications in the Biosciences 11 (5):p497-501

1995

ISSN: 0266-7061
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: This paper describes the application of artificial neural networks to discriminating the coding system of eukaryotic genes. We choose **gt** 300 genes from eight eukaryotic organisms: human, mouse, rat, horse, ox, sheep, soybean and rabbit, from which we build up different discrimination models relevant to their promoter regions, **poly (A)** signals, splice site locations of introns and noose structures. The result shows that as long as the coding length is definite, the only correct coding region can be chosen from the large number of possible solutions discriminated by neural networks.

1995

9/3,AB/93 (Item 24 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10138021 BIOSIS NO.: 199698592939
Molecular cloning and sequence analysis of the rat liver carnitine octanoyltransferase cDNA, its natural gene and the gene promoter.
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JOURNAL: Biochimica et Biophysica Acta 1264 (2):p215-222 1995
ISSN: 0006-3002
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The full-length cDNA and the natural gene for rat peroxisomal carnitine octanoyltransferase (COT) have been isolated and sequenced. The 2681 bp long cDNA contains an open reading frame for 613 amino acids, resulting in a protein with a deduced molecular weight of 70 301, and a C-terminal peroxisomal targeting sequence (Ala-His-Leu). The isolated COT cDNA has 51 bp of the 5' untranslated region (UTR), 791 bp of 3' UTR, two putative polyadenylation sites, and a **poly(A-19-23)** tail. Screening of a rat genomic DNA library in the lambda phage with the COT cDNA probe resulted in the isolation of seven overlapping clones, together containing the complete COT gene with seventeen exons. All of the exon-intron boundary sequences conform to the **GT-AG** rule. The COT gene appears to spread over 40 to 60 kbp region of the rat genome.

The transcription initiation site of the COT gene was determined through primer extension, and the promoter sequence up to the position -1140 was established. The promoter lacks the canonical TATA box and a promoter-reporter construct containing the sequence encompassing -1140 to +84 base positions and the firefly luciferase reporter cDNA yielded about 100-fold increase in promoter activity in transfected hepatoma cells. Some of the consensus sequences for putative cis elements present in the promoter sequence are: the two CCAAT motifs for CTF/NF1/CBP binding (at -284 and -93), two GC boxes for Sp1 binding (at -160 and -68), two AP2 sites (at -359 and -25), a half site (TGACCT) for the peroxisome proliferator activated receptor (PPAR) binding at -737 within a partial palindromic sequence region. Potential regulatory elements such as several palindromes and repeat motifs for five different sequence segments, are also identified.

1995

9/3,AB/94 (Item 25 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10020868 BIOSIS NO.: 199598475786
Analysis of gene expression in small numbers of purified hemopoietic cells by RT-PCR.
AUTHOR: Ziegler Benedikt L(a); Lamping Christa P; Thoma Stefan J; Fliender T M
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JOURNAL: Stem Cells (Dayton) 13 (SUPPL. 1):p106-116 1995
ISSN: 1066-5099
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Primitive hemopoietic stem cells represent the most probable targets for genetic alterations due to exposure to ionizing irradiation or chemical carcinogens. We have applied a two-step protocol for the purification of CD34+HLA-DR-/low hemopoietic progenitor cells from cord blood (CB). CD34+ cells were isolated by monoclonal antibody (mAb) against CD34 (My10) and immunomagnetic beads. Beads were cleaved off the CD34+ cells by enzymatic treatment with chymopapain. Due to chymopapain-resistance of epitopes recognized by the used mAbs purity control of CD34+ cells and separation into CD34+HLA-DR-/low and CD34+HLA-DR+ subsets could be performed by using flow cytometry. Two miniaturized procedures were applied to isolate poly(A)+ mRNA for the reverse transcription polymerase chain reaction (RT-PCR) from small numbers of CD34+HLA-DR-/low cells. In five experiments, the mean purity of immunomagnetically isolated CD34+ cells was 93.8% +/- 3.9. Flow cytometry sorting of CD34+ cells resulted in pure CD34+HLA-DR-/low populations (purity gt 98.8%; range 98.8% to 99.9%; viability gt 96%) with an average yield of 2600 +/- 800 cells/5 times 10⁻⁷ low density CB cells. By RT-PCR using both poly(A)+ mRNA isolation procedures, sequences corresponding to CD34 and beta-2-microglobulin were amplified from as few as 20 cells. Furthermore, a sequence-independent RT-PCR (SIP-RT-PCR) was applied to amplify the cDNA derived from five erythroblasts isolated from a burst-forming unit-erythroid (BFU-E). Upon hybridization, full-length c-fos message was detected in the SIP-RT-PCR amplified material. Our data demonstrate that gene expression can be detected at the transcriptional level in small numbers of hemopoietic progenitor cells. In addition, the SIPRT-PCR may allow the amplification of unique mRNA species when subtractive hybridization procedures are performed. The presented data should be useful to analyze gene expression in rare subsets of radiation-exposed

immature hemopoietic stem/progenitor cells.

1995

9/3,AB/95 (Item 26 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10006200 BIOSIS NO.: 199598461118

Molecular characterization of a reduced glutathione transporter in the lens.

AUTHOR: Kannan Ram(a); Yi Jian R; Zlokovic Berislav V; Kaplowitz Neil
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JOURNAL: Investigative Ophthalmology & Visual Science 36 (9):p1785-1792

1995

ISSN: 0146-0404

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Purpose: To characterize glutathione (GSH) transporter in the lens. Methods: Poly (A)+RNA isolated from bovine lens was injected into Xenopus laevis oocytes. Oocytes were incubated for 1 hour in either NaCl or sucrose medium containing tracer GSH, and cell-associated radioactivity was determined. Glutathione efflux was determined in lens mRNA injected oocytes preloaded with GSH. Relationship of lens GSH transporter to the two recently cloned sodium-independent hepatic membrane GSH transporters was studied by Northern blot and reverse transcription-polymerase chain reaction (RT-PCR) analyses. Bovine lens mRNA also was probed for gamma glutamyl transpeptidase (GGT) by RT-PCR Results: Uptake of tracer 35S-GSH could be demonstrated in X. laevis oocytes injected with poly (A)+RNA from bovine lens. Glutathione transport was carrier mediated (K-m apprx 1.3 mM) and was sodium independent. High-performance liquid chromatography confirmed that the molecular form of uptake was predominantly (gt 98%) as it was for GSH. Poly (A)+RNA-injected oocytes preloaded with 16.5 nmol GSH-oocyte showed GSH efflux at a rate of 2.6 nmol/oocyte per hour. When bovine lens poly (A)+RNA was hybridized with the cDNA probe for the sodium-independent rat canalicular GSH transporter (RcGshT), the transcript for RcGshT was observed. RT-PCR confirmed the presence of RcGshT and showed the absence of rat sinusoidal GSH transporter (RsGshT) and GGT mRNA in rat lens. Conclusions: The authors have demonstrated for the first time that lens contains mRNA for RcGshT and expresses a low-affinity GSH transporter in oocytes. Glutathione efflux from the apical side of the anterior epithelium and progressive uptake, and inward efflux into cortical fibers, might be explained by expression of RcGshT alone or in combination with as yet unidentified GSH transporters.

1995

9/3,AB/96 (Item 27 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09993474 BIOSIS NO.: 199598448392

Stimulation by alkylxanthines of chloride efflux in CFPAC-1 cells does not involve A-1 adenosine receptors.

AUTHOR: Jacobson Kenneth A(a); Guay-Broder Colleen; Van Galen Philip J M; Gallo-Rodriguez Carola; Melman Neli; Jacobson Marlene A; Eidelman Ofer; Pollard Harvey B

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JOURNAL: Biochemistry 34 (28):p9088-9094 1995
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A series of 8-substituted derivatives of 1,3,7-alkylxanthines was synthesized as potential activators of chloride efflux from a human epithelial cell line (CFPAC) expressing the cystic fibrosis transmembrane regulator (CFTR) AF508 mutation. Their interactions with rat brain A-1 and A-2a receptors were also studied in radioligand binding experiments. Substitution was varied at the xanthine 1-, 3-, 7 and 8-positions. 1,3-Dipropyl-8-cyclopentylxanthine (CPX) stimulated Cl⁻ efflux in the 10⁻⁸ M range with a maximal effect reaching 200% of control and diminishing at higher concentrations. The potent adenosine antagonist 8-(4-((((2-aminoethyl)amino)carbonyl)methyl)oxy)phenyl)-1,3-dipropylxanthine, nonselective at human A-1 and A-2a receptors, was inactive in Cl⁻ efflux. 1,3-Diallyl-8-cyclohexylxanthine (DAX) was highly efficacious in stimulating chloride efflux with levels reaching **gt** 300% of control, although micromolar concentrations were required. 1,3,7-Trimethyl-8-(3-chlorostyryl)xanthine, an A-2a-selective adenosine antagonist, was only weakly active. Caffeine, which acts as a nonselective adenosine antagonist in the range of 10⁻⁵ M, was active in Cl⁻ efflux in the low nanomolar range but with low efficacy. Thus, among the xanthine derivatives of diverse structure, there was no correlation between potency in Cl⁻ efflux and adenosine antagonism. **Poly(A)**+ RNA isolated from CFPAC-1 cells showed no hybridization to a human A_{2A} receptor cDNA probe, excluding this receptor as a mediator of CPX-elicited Cl⁻ efflux. Thus, this action of xanthines in stimulating Cl⁻ efflux in CFPAC cells, which express a defective CFTR, represents a novel site of action apparently unrelated to adenosine receptors.

1995

9/3,AB/97 (Item 28 from file: 5)
DIALOG(R) File 5:Biosis Previews(R)
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09950327 BIOSIS NO.: 199598405245
Trinucleotide Repeats at the rad Locus: Allele Distributions in NIDDM and Mapping to a 3-cM Region on Chromosome 16q.
AUTHOR: Doria Alessandro; Caldwell James S; Ji Linong; Reynet Christine; Rich Stephen S; Weremowicz Stanislaw; Morton Cynthia C; Warram James H; Kahn C Ronald; Krolewski Andrzej S(a)
AUTHOR ADDRESS: (a)Sect. Epidemiol. Genet., Joslin Diabetes Cent., One Joslin Place, Boston, MA 02215**USA
JOURNAL: Diabetes 44 (2):p243-247 1995
ISSN: 0012-1797
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A 10-allele polymorphism was identified in rad (ras associated with diabetes), a gene that is overexpressed in non-insulin-dependent diabetes mellitus (NIDDM) muscle. The polymorphism, designated RAD1, consists of a variable number of trinucleotide repeats (GTT and ATT) located in the **poly(A)** region of an intronic Alu sequence. Based on the number of GTT and ATT repetitions, the alleles can be grouped into four classes (I-IV). RAD1 allele frequencies were determined in 210 NIDDM patients and 133 nondiabetic control subjects, all Caucasians. One allele (number 8, class III) accounted for **gt** 80% of the chromosomes in both groups. However, an excess of minor alleles,

all belonging to class I, II, or IV, was observed among NIDDM chromosomes (P lt 0.025), suggesting a possible association between RAD1 and NIDDM predisposition. To promote further studies to test the hypothesis that genetic variability at the rad locus contributes to NIDDM, we mapped rad on the human genome. Using the fluorescence in situ chromosomal hybridization technique, rad was unequivocally assigned to chromosomal band 16q22. In families that were informative for RAD1, the rad locus was mapped within a 3-cM region defined by the markers D16S265, D16S186, and D16S397 (logarithm of odds scores = 10.08, 10.9, and 10.84 at recombination fractions of 0.024, 0.001, and 0.03, respectively). The high degree of heterozygosity of these markers will allow large-scale family studies to be performed to test the presence of linkage between rad and NIDDM.

1995

9/3,AB/98 (Item 29 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09921821 BIOSIS NO.: 199598376739
Stable chelating linkage for reversible immobilization of oligohistidine tagged proteins in the BIAcore surface plasmon resonance detector.
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JOURNAL: Journal of Immunological Methods 183 (1):p65-76 1995
ISSN: 0022-1759
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We describe a stable chelating linkage for the reversible immobilization of oligohistidine tagged proteins in the flow cell of the 'BIAcore' surface plasmon resonance (SPR) biosensor. The carboxymethylated dextran surface of the flow cell was covalently derivatized with N-(5-amino-1-carboxypentyl)iminodiacetic acid (NTA ligand) via its single primary amino group, and the derivatized surface charged with Ni-2+. 6His-VP55, an N-terminally tagged derivative of the catalytic subunit of the heterodimeric vaccinia virus poly(A) polymerase, was immobilized to this surface in a manner that was dependent upon the immobilized NTA ligand, the prior injection of Ni-2+ at a concentration of gt 10-5 M and the 6His tag, and which was reversible upon injection of EDTA. The stability of immobilization varied inversely with the amount of 6His-VP55 immobilized and was greatest in buffer of pH 8.0 or greater, containing NaCl at a concentration of 0.1 M. Utilizing these conditions, 6His-VP55 remained stably immobilized during 60 min of buffer flow at moderate flow rates. VP39, the stimulatory subunit of vaccinia poly(A) polymerase, interacted with the immobilized 6His-VP55. apprx 99% of immobilized 6His-VP55 molecules were available for VP39 binding, in contrast to the apprx 40% availability for 6His-VP55 molecules immobilized covalently, via primary amino groups. Three additional proteins, tagged at either the N- or C-terminus with oligohistidine, were shown to be stably immobilized via the chelating linkage. This simple method permits immobilization of proteins in the BIAcore biosensor via a commonly employed affinity tag, in a stable and reversible manner, and requires only a single biosensor flow cell for the iterative generation of immobilized protein surfaces.

1995

9/3,AB/99 (Item 30 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
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09920797 BIOSIS NO.: 199598375715

Parathyroid hormone/parathyroid hormone related peptide receptor gene transcripts are expressed from tissue-specific and ubiquitous promoters.
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JOURNAL: Nucleic Acids Research 23 (11):p1948-1955 1995

ISSN: 0305-1048

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Parathyroid hormone (PTH) and PTH related peptide (PTHrP) stimulate diverse physiological responses in a number of tissues by binding to the same receptor. We have previously cloned the gene encoding the mouse PTH/PTHrP receptor (PTHR), and have identified a promoter region. The first exon transcribed from this promoter contains untranslated sequence and is followed by an exon encoding signal sequence and the first amino acids of the mature polypeptide. We have now identified and characterized a second promoter region, located **gt** 3 kb upstream of the original. Four partial cDNA clones, amplified from mouse kidney RNA by reverse transcription followed by the polymerase chain reaction, contain sequence corresponding to two previously unidentified exons composed of untranslated sequence. The second (3') of the two exons is spliced to the previously identified signal sequence exon. These cDNAs are highly homologous to the 5' end of a cDNA isolated from human kidney, strongly suggesting that the promoter region is conserved between mouse and humans. RNase protection and primer extension experiments have identified several transcriptional start sites extending over a region of approx 100 bp. Unlike the previously identified promoter, this promoter is not (G+C)-rich. It lacks a consensus TATA element, but does contain a consensus CCAAT box. We have determined the expression patterns of both promoters by RNase protection with total and **poly A+** RNA from several mouse tissues. The newly identified promoter is highly tissue specific, being strongly active in kidney and weakly active in liver, but not expressed in the other tissues studied. The previously identified (G+C)-rich promoter is expressed in all tissues studied. This indicates that the PTHR gene expression is controlled by regulatory signals specific to kidney and liver, as well as signals functioning in a wide variety of cell types. These results may provide insight into certain defects in PTH signalling found in humans.

1995

9/3,AB/100 (Item 31 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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09912754 BIOSIS NO.: 199598367672

Estradiol increases amounts of messenger ribonucleic acid for gonadotropin-releasing hormone receptors in sheep.

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JOURNAL: Biology of Reproduction 53 (1):p179-185 1995

ISSN: 0006-3363

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Two experiments were conducted simultaneously to investigate regulation of amounts of mRNA for GnRH receptors during the periovulatory period in sheep. In the first experiment, amounts of mRNA for GnRH receptors were measured before and after the preovulatory surge of LH following regression of the CL by prostaglandin F-2alpha (PGF-2alpha). So that the time of the preovulatory surge of LH could be accurately predicted, ewes received two injections of PGF-2alpha on Day 14 of the estrous cycle. Anterior pituitary glands were collected from 5 control ewes on Day 14 of the estrous cycle (0 h after PGF-2alpha) and at 48, 72, and 96 h after PGF-2alpha (5 ewes per group). The second experiment was conducted to investigate the effects of 17-beta-estradiol on amounts of mRNA for GnRH receptors. On Day 14 of the estrous cycle, 20 ewes were ovariectomized (OVX); 15 of these ewes received estradiol implants when they were OVX (OVXEI). Sixteen hours after OVX, anterior pituitary glands were collected from 5 OVX and 5 OVXEI ewes, and the remaining OVXEI ewes received an i.m. injection of estradiol (25 mu-g in corn oil; OVXEI + E) to induce a preovulatory-like surge of LH. Anterior pituitary glands were collected from OVXEI + E ewes 18 or 54 h after injection of estradiol (n = 5 per group). Half of each anterior pituitary gland was used to measure the number of GnRH receptors. Poly(A)+ RNA was isolated from the remaining half of each anterior pituitary gland, applied to slot blots, and hybridized with a radioactive cDNA probe encoding the ovine GnRH receptor. Amounts of GnRH receptor mRNA were elevated (p lt 0.05) approximately 2-fold 48 h after PGF-2alpha (i.e., prior to the onset of the preovulatory surge of LH) compared to 0, 72, or 96 h after PGF-2alpha. Acute (i.e., 16 h) removal of ovarian hormones did not influence amounts of mRNA for GnRH receptors (p gt 0.05) compared to the amount on Day 14 of the estrous cycle. Administration of estradiol implants to OVX ewes for 16 h increased (p lt 0.05) amounts of mRNA for GnRH receptors approximately 1.6-fold as compared to the amount in ewes OVX for 16 h or that on Day 14 of the estrous cycle. There were, however, no further increases (p gt 0.05) in GnRH receptor mRNA after injection of estradiol to induce a preovulatory-like surge of LH. We conclude that removal of ovarian hormones was not sufficient to increase amounts of mRNA for GnRH receptors. In contrast, estradiol increased amounts of mRNA for GnRH receptors in OVXEI ewes. Ovarian hormones other than estradiol do not appear to be required for the increase in GnRH receptor mRNA that occurs prior to the preovulatory surge of LH in ewes.

1995

9/3,AB/101 (Item 32 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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09877388 BIOSIS NO.: 199598332306
 Acute effects of spinal cord injury on the pituitary-testicular hormone axis and Sertoli cell functions: A time course study.
 AUTHOR: Huang H F S(a); Linsenmeyer T A; Li M T; Giglio W; Anesetti R; Von Hagen J; Ottenweller J E; Serenas C; Pogach L
 AUTHOR ADDRESS: (a)Dep. Surg., Sect. Urol., UMD-N.J. Med. Sch., 185 S. Orange Ave., Newark, NJ 07103-2757**USA
 JOURNAL: Journal of Andrology 16 (2):p148-157 1995
 ISSN: 0196-3635
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: The present study investigated the time course of the onset of the abnormalities in spermatogenesis following spinal cord injury, and their relationship to changes in the pituitary testicular hormonal axis and Sertoli cell function. Spinal cord injury (SCI) was induced in adult male rats by surgical transection of the spinal cord at the level of T9

and L1 vertebrae. Animals were killed 3, 7, and 14 days after the operation. As early as 3 days following SCI, abnormalities in spermatogenesis, including delayed spermiation and vacuolization of the nucleus of spermatids, were noted in both the T9 and L1 animals. By 14 days, other lesions, including phagocytosis of mature spermatids, incomplete cellular associations, and total regression of seminiferous epithelium, became apparent. Concurrently a transient but significant ($P < 0.05$) suppression of serum follicle-stimulating hormone (FSH) occurred in the T9 animals. and a suppression of serum luteinizing hormone (LH) occurred in both the T9 and the L1 animals 3 days after the surgery. This was accompanied by a suppression of testicular and serum testosterone levels ($P < 0.05$, $P < 0.01$, respectively). Most of the hormonal parameters had recovered and were not different from those of sham-operated animals by 14 days ($P > 0.10$). Northern blot analysis of testicular poly(A)⁺ RNA revealed a transient but significant reduction in the steady-state level of the 2.7-kilobase (kb) Sertoli cell transferrin mRNA transcript in both the T9 and the L1 animals 3 days after the operation ($P < 0.05$). On the other hand, the 1.7-kb androgen binding protein (ABP) mRNA remained unaffected during the 2-week study period. The steady-state level of mRNA transcripts for spermatogenic cell-specific hemiferrin and spermatid specific transition protein 2 and protamine 1 also remained unchanged. These results suggest that spinal cord injury will result in a temporary, but profound, effect on the pituitary-testicular hormone axis. These changes may impair certain aspects of Sertoli cell function that could render these cells incapable of supporting normal spermatogenesis. However, the severity of spermatogenic lesions and the disparate responses of the two major Sertoli cell proteins make it unlikely that hormone deficiency is the only mechanism responsible for the impaired spermatogenesis following spinal cord injury.

1995

9/3,AB/102 (Item 33 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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09816685 BIOSIS NO.: 199598271603
 Synthesis of dicationic diarylpyridines as nucleic-acid binding agents.
 AUTHOR: Kumar A; Rhodes R A; Sychala J; Wilson W D; Boykin D W(a); Tidwell R R; Dykstra C C; Hall J E; Jones S J; Schinazi R F
 AUTHOR ADDRESS: (a)Dep. Chem., Georgia State Univ., Atlanta, GA 30303**USA
 JOURNAL: European Journal of Medicinal Chemistry 30 (2):p99-106 1995
 ISSN: 0223-5234
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: The syntheses of
 2,6-bis(4-(4,5-dihydro-1H-imidazol-2-yl)phenyl)pyridine 7,
 2-(4-(4,5-dihydro-1H-imidazol-2-yl)phenyl)-6-(3-(4,5-dihydro-1H-imidazol-2-yl)phenyl)pyridine 8 and
 2,6-bis(3-(4,5-dihydro-1H-imidazol-2-yl)phenyl)pyridine 9 in five steps from the appropriately substituted bromoacetophenone are described. 3,5-Bis(4-(4,5-dihydro-1H-imidazol-2-yl)phenyl)pyridine 13 is also reported, prepared in four steps from 4-bromophenylacetonitrile. The preparation of 2,5-bis(4-(4,5-dihydro-1H-imidazol-2-yl)phenyl)pyridine 18 from 4-bromoacetophenone in six steps is presented. The dictations bind to poly dA cntdot dT in the order 7 **gt** 13 **gt** 18 **gt** 8 **gt** 9; the order of binding to poly A cntdot U is 7 **gt** 13 **gt** 8 **gt** 9; 18 essentially does not bind to the RNA model. Only 7 inhibits topoisomerase II at millimolar concentrations. The dicationic compounds that were tested against Pneumocystis carinii

in the immunosuppressed rat model show only modest activity and are moderately toxic. Some of the compounds demonstrated modest anti-HIV-1 activity and selectivity in primary lymphocytes.

1995

9/3,AB/103 (Item 34 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09779975 BIOSIS NO.: 199598234893
Structure, expression, and chromosomal localization of the type I human vasoactive intestinal peptide receptor gene.
AUTHOR: Sreedharan Sunil P(a); Huang Jin-Xing; Cheung Mei-Chi; Goetzl Edward J
AUTHOR ADDRESS: (a)Div. Allergy Immunol., UB8B, Univ. California, San Francisco, CA 94143-0711**USA
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 92 (7):p2939-2943 1995
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Vasoactive intestinal peptide (VIP) and other members of the pituitary adenylyl cyclase-activating peptide (PACAP) and secretin neuroendocrine peptide family are recognized with specificity by related G protein-coupled receptors. We report here the cloning, characterization, and chromosomal location of the gene encoding the human type I VIP receptor (HVR1), also termed the type II PACAP receptor. The gene spans approx 22 kb and is composed of 13 exons ranging from 42 to 1400 bp and 12 introns ranging from 0.3 to 6.1 kb. Primer extension analysis with poly(A)+ RNA from human HT29 colonic adenocarcinoma cells indicated that the transcription initiation site is located at position -110 upstream of the first nucleotide (+1) of the translation start codon, and 75 nt downstream of a consensus CCAAT-box motif. The G+C-rich 5' flanking region contains potential binding sites for several nuclear factors, including Sp1, AP2, ATF, interferon regulatory factor 1, NF-IL6, acute-phase response factor, and NF-kappa-B. The HVR1 gene is expressed selectively in human tissues with a relative prevalence of lung gt prostate gt peripheral blood leukocytes, liver, brain, small intestine gt colon, heart, spleen gt placenta. kidney, thymus, testis. Fluorescence in situ hybridization localized the HVR1 gene to the short arm of human chromosome 3 (3p22), in a region associated with small-cell lung cancer.

1995

9/3,AB/104 (Item 35 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

09764938 BIOSIS NO.: 199598219856
Polyadenylation helps regulate mRNA decay in Escherichia coli.
AUTHOR: O'Hara Eileen B; Chekanova Julian A; Ingle Caroline A; Kushner Ze'eva R; Peters Erica; Kushner Sidney R(a)
AUTHOR ADDRESS: (a)Dep. Genetics, Life Sci. Building, Univ. Georgia, Athens, GA 30602-7223**USA
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 92 (6):p1807-1811 1995
ISSN: 0027-8424
DOCUMENT TYPE: Article

RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: As part of our genetic analysis of mRNA decay in *Escherichia coli* K-12, we examined the effect of the *pcnB* gene (encoding **poly(A)** polymerase I) on message stability. Eliminating **poly(A)** polymerase I (DELTA-*pcnB*) dramatically stabilized the *lpp*, *ompA*, and *trxA* transcripts. The half-lives of individual mRNAs were increased in both a DELTA-*pcnB* single mutant and a DELTA-*pcnB* *pnp-7 rnb-500 rne-1* multiple mutant. We also found mRNA decay intermediates in DELTA-*pcnB* mutants that were not detected in control strains. By end-labeling total *E. coli* RNA with (32P) pCp and T4 RNA ligase and then digesting the RNA with RNase A and T-1, we showed that many RNAs in a wild-type strain contained **poly(A)** tails ranging from 10 nt to **gt** 50 nt long. When polynucleotide phosphorylase, RNase II, and RNase E were absent, the length (**gt** 100 nt) and number (10- to 20-fold) of the **poly(A)** tails increased. After transcription initiation was stopped with rifampicin, polyadenylation apparently continued. Deleting the structural gene for **poly(A)** polymerase I (*pcnB*) reduced the amount of 3'-terminal **poly(A)** sequences by **gt** 90%. We propose a model for the role of polyadenylation in mRNA decay.

1995

9/3,AB/105 (Item 36 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09683844 BIOSIS NO.: 199598138762

An exon encoding the mouse growth hormone binding protein (mGHBP) carboxy terminus is located between exon 7 and 8 of the mouse growth hormone receptor gene.

AUTHOR: Zhou Yihua; He Li; Kopchick John J(a)

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Ohio Univ., Athens, OH 45701**USA

JOURNAL: Receptor 4 (4):p223-227 1994

ISSN: 1052-8040

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: A C57 black/6 mouse genomic library was screened for mGHR/BP using a mGHR cDNA hybridization probe. Two clones (mGHR-GA and mGHR-GB) were isolated. mGHR-GA contained an insert of 16 kb and hybridized only to exon 4 whereas mGHR-GB possessed an insert of 20 kb and hybridized to exons 6-10 of the mGHR cDNA. Oligonucleotide sequencing analysis confirmed that the mGHR-GA contained exon 4 and that the mGHR-GB possessed mGHR/BP genomic sequences from intron V through the 3' region of mGHR. In addition, mGHR-GB also contained a region, designated exon 8A, encoding the carboxy terminus of mGHBP. This exon is located between exons 7 and 8 of mGHR/BP gene. Two **poly(A)** additional signal sequences were found 54 bp downstream of the stop codon of mGHBP. Additionally, introns between exons 3/4 and 4/5 are **gt** 12 and **gt** 3 kb, respectively. Also, introns between exons 5/6, 6/7, 7/8A, 8A/8 (3' region of mGHBP), 8/9, 9/10, and the 3' region of mGHR are approx **gt** 3 kb, 4 kb, 287 bp, 1569 bp, 6 kb, 265 bp, and **gt** 3 kb, respectively. This study supports the hypothesis that mGHBP is generated by alternative splicing of a common primary mGHR transcript. It also demonstrates differences and similarities between mGHR/BP and hGHR genes.

1994

9/3,AB/106 (Item 37 from file: 5)
DIALOG(R) File 5:Biosis Previews(R)
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09641862 BIOSIS NO.: 199598096780

Characterization of one novel venom protease with beta-fibrinogenase activity from the Taiwan habu (*Trimeresurus mucrosquamatus*): Purification and cDNA sequence analysis.

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JOURNAL: Biochemical and Biophysical Research Communications 205 (3):p 1707-1715 1994

ISSN: 0006-291X

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Several fibrinogenolytic proteases were isolated from the venom of Taiwan habu, *Trimeresurus mucrosquamatus*, a snake species belonging to the Crotalidae family. One protease with strong fibrinogenolytic activity was further purified to homogeneity through multiple-step chromatographies including ion-exchange chromatography, gel permeation and reversed-phase HPLC. In vitro, the purified enzyme cleaved beta-chain of fibrinogen molecules efficiently and showed relatively lower activity on alpha-chain, with almost no activity on gamma-chain even after a long period of incubation. Further characterization indicated that it is a single-chain polypeptide with molecular weight of about 28,000. Its stability at high temperatures (gt 90 degree C) distinguished it from the previously reported venom fibrinogenases. N-Terminal sequence analysis revealed that it is similar to batroxobin and ancrod, which were shown to possess either fibrinogen-clotting or antithrombotic effect. Polymerase chain reaction (PCR) was employed to amplify cDNAs constructed from the poly(A)+RNA of fresh venom glands of the same snake species to facilitate the cloning and sequencing of this important fibrinogenase. Sequencing several positive clones corresponding to the coding sequence of the enzyme revealed the existence of a family of novel thrombin-like fibrinogenases in the Taiwan habu, which are heat-stable and may be useful as strong antithrombotic agents.

1994

9/3,AB/107 (Item 38 from file: 5)
DIALOG(R) File 5:Biosis Previews(R)
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09597943 BIOSIS NO.: 199598052861

Characterization of a Y-1-preferring NPY/PYY receptor in HT-29 cells.

AUTHOR: Mannon Peter J(a); Mervin Sabrena J; Sheriff-Carter Katrina D

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JOURNAL: American Journal of Physiology 267 (5 PART 1):pG901-G907

1994

ISSN: 0002-9513

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Equilibrium binding studies showed that butyrate-treated HT-29 cells express a high-affinity 125I-labeled peptide YY (125I-PYY) binding site with a dissociation constant of 0.32 +/- 0.12 nM (mean +/- SE, n = 4). This site was Y-1 preferring because neuropeptide Y (NPY) and the Y-1-selective agonist (Leu-31,Pro-34)NPY were equipotent to PYY at displacing 125I-PYY; PYY-(13-36) and pancreatic polypeptide were gt

1,000- and 10,000-fold less potent at displacing the radioligand. PYY and (Leu-31,Pro-34)NPY inhibited forskolin-stimulated adenosine 3',5'-cyclic monophosphate production 63% and 48%, respectively, with a half-maximal inhibitory concentration between 0.1 and 1.0 nM. PYY and (Leu-31,Pro-34)NPY had no effect on release of intracellular calcium alone or on the increase in intracellular calcium concentration caused by carbachol or neurotensin. Northern blot analysis of poly(A)+ RNA from HT-29 cells demonstrated a single transcript of 2.5 kb that hybridized to a human Y-1-receptor cDNA probe. Sequence analysis of a reverse transcription-polymerase chain reaction product amplified with primers based on human Y-1-receptor cDNA confirmed that these cells contained mRNA encoding the human Y-1 receptor. These studies show that butyrate-treated HT-29 cells constitutively express the Y-1-preferring NPY/PYY receptor and Y-1 mRNA and provide a new model for studies of PYY-regulated epithelial cell function and tissue-specific expression of the human Y-1-receptor gene.

1994

9/3,AB/108 (Item 39 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09593540 BIOSIS NO.: 199598048458
Molecular characterization of a mouse prostaglandin D receptor and functional expression of the cloned gene.
AUTHOR: Hirata Masakazu; Kakizuka Akira; Aizawa Megumi; Ushikubi Fumitaka; Narumiya Shuh(a)
AUTHOR ADDRESS: (a)Dep. Pharmacol., Kyoto University Med., Kyoto 606**Japan
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 91 (23):p11192-11196 1994
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Prostanoid receptors belong to the family of G protein-coupled receptors with seven transmembrane domains. By taking advantage of nucleotide sequence homology among the prostanoid receptors, we have isolated and identified a cDNA fragment and its gene encoding a mouse prostaglandin (PG) D receptor by reverse transcription polymerase chain reaction and gene cloning. This gene codes for a polypeptide of 357 amino acids, with a calculated molecular weight of 40,012. The deduced amino acid sequence has a high degree of similarity with the mouse PGI receptor and the EP-2 subtype of the PGE receptor, which together form a subgroup of the prostanoid receptors. Chinese hamster ovary cells stably expressing the gene showed a single class of binding sites for (3H)PGD-2 with a K-d of 40 nM. This binding was displaced by unlabeled ligands in the following order: PGD-2 gt BW 245C (a PGD agonist) gt BW A868C (a PGD antagonist) gt STA-2 (a thromboxane A-2 agonist). PGE-2, PGF-2alpha, PGF-2alpha, and iloprost showed little displacement activity at concentrations up to 10 mu-M. PGD-2 and BW 245C also increased cAMP levels in Chinese hamster ovary cells expressing the receptor, in a concentration-dependent manner. BW A868C showed a partial agonist activity in the cAMP assay. Northern blotting analysis with mouse poly (A)' RNA identified a major mRNA species of 3.5 kb that was most abundantly expressed in the ileum, followed by lung, stomach, and uterus.

1994

9/3,AB/109 (Item 40 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
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09592665 BIOSIS NO.: 199598047583

The processive reaction mechanism of ribonuclease II.

AUTHOR: Cannistraro Vincent J; Kennell David(a)

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JOURNAL: Journal of Molecular Biology 243 (5):p930-943 1994

ISSN: 0022-2836

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Ribonuclease II is a processive 3' exoribonuclease in Escherichia coli. It degraded substrates with 3'-OH or 2',3'-cyclicP ends slightly faster than those with 3'-P or 2'-P groups with a turnover number of apprx 70 nt/s at 37 degree C. RNase II does not degrade DNA but the specificity for ribose was not for the cleavage bond but rather for ribo-bonds three to four nucleotides (nt) upstream, which could explain why the limit digest is a dimer. Oligonucleotides (oligos) of deoxy(C) were reversible competitive inhibitors of the enzyme and indicated a strong upstream binding site (apprx 15 to 27 nt from the 3' end). These oligos could protect RNase II from inactivation by heat or from diethylpyrocarbonate, an agent that preferentially reacts with His residues. Compared to oligo(dC), oligos of (dA) were at least 500 times less effective inhibitors of RNase II. Using mixed oligo(dAdC) inhibitors, an obligatory 3' to 5' direction of binding into the catalytic site was shown. From the reaction kinetics of RNase II under different conditions it was concluded that the enzyme recognition differs for poly(A), poly(C) and poly(U). Poly(C) was degraded more slowly than poly(A) or poly(U) with a 3.5 times slower V-max, while rate differences between small oligos were extreme; oligo(A)-7 was degraded gt 100 times faster than oligo(C)-y. Ethanol, which weakens hydrophobic interactions, increased the reaction velocity of poly(C) to that of poly(A) and poly(U). It had no effect on the reaction velocities of poly(A) or poly(U), but decreased the binding of poly(A) markedly. Oligo(A) was bound more strongly to a hydrophobic column than was oligo(C). Salt which affects charge interactions, decreased the binding affinity and/or association rate of poly(C) to RNase II, had a lesser effect on poly(U), but the reactions of poly(A) were unaffected even in much higher concentrations of salt. A clue to the slower reaction velocity of poly(C) was shown when the reaction intermediates were viewed by PAGE. At lower temperatures of reaction (lt 25 degree C), there were more intense bands separated by discrete distances of apprx 12 nt during the degradation of poly(C) by RNase II. Chase experiments showed that these stops were accounted for by dissociation of poly(C) from the enzyme. They were not seen when poly(C) was degraded at 37 degree C or degraded in the presence of 20% ethanol at any temperatures, nor were they seen when poly(A) or poly(U) was degraded even at low temperatures. However, all substrates showed dissociation when the oligo became less than 10 to 15 nt. A model was proposed to account for these observations. Poly(C) is bound very strongly by ionic bonds, apprx 15 to 27 nt from the 3' end, to an anchor site on RNase II, while the 3' end is pulled (threaded) through the catalytic site as the end nucleotides are cleaved off. Under conditions favoring the stacked single-strand structure, the helix is stretched to generate a progressively increasing force on the anchor site binding. After apprx 12 nt, that binding is broken and the enzyme dissociates. With conditions that favor the random coil (higher temperature or ethanol) these stops are not seen. This is the case with poly(U), which tends to be a randomly coiled single strand under all these conditions. Poly(A) has a stronger helix-coil than poly(C), but binding to the anchor site is by weak hydrophobic

interactions. Without strong anchor site binding, **poly(A)** threads through the enzyme without periodic dissociations. However, all substrates start dissociating with each cleavage when they become so small that the anchor site cannot be filled by nucleotides. In this model the energy for progression is provided by the pulling force on the substrate at the catalytic site.

1994

9/3,AB/110 (Item 41 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09589405 BIOSIS NO.: 199598044323
Ethonium interaction with single-chain homopolynucleotides.
AUTHOR: Sorokin V A(a); Valeev V A; Gladchenko G O; Blagoi Yu P; Ryazanova O A; Sukhodub L F
AUTHOR ADDRESS: (a)Phys.-Tech. Inst. Low Temp., Acad. Sci. Ukr., Kharkov**
Ukraine
JOURNAL: Biopolimery i Kletka 10 (2):p61-68 1994
ISSN: 0233-7657
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Russian; Non-English
SUMMARY LANGUAGE: Russian; Ukrainian; English

ABSTRACT: The interaction of single-chain homopolynucleotides and individual ribo- and desoxyribonucleotides with the effective antimicrobial preparation ethonium belonging to the group of nonintercalating substances is studied by the method of differential UV spectroscopy. Under conditions close to the physiological ones (pH 6, 0.1 M Na⁺), ethonium does not bind to heteroatoms of individual nucleotides. However, in polymers ethonium is found to interact strongly with N(7) and N(1) of **poly(A)**, N(3) of poly(C) and O(4) of poly(U). The affinity of ethonium for three atoms is much higher than for the oxygens of the phosphate groups of polymers. Its nucleotide selectivity of binding corresponds to the row: **poly(A)** gtorsim poly(U) gt poly(C). Ethonium cannot substitute protons at N(3) of poly(U) and O(2) of poly(C) ribose, neither it interacts with O(2) of this polynucleotide.

1994

9/3,AB/111 (Item 42 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09556678 BIOSIS NO.: 199598011596
A single-strand-specific nuclease from a fraction of wheat chloroplast stromal protein.
AUTHOR: Monko Magdalena; Kuligowska Elzbieta; Szarkowski J W
AUTHOR ADDRESS: Inst. Biochem. Biophysics, Polish Academy Sci., 02-532 Warszawa**Poland
JOURNAL: Phytochemistry (Oxford) 37 (2):p301-305 1994
ISSN: 0031-9422
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A single-strand-specific nuclease from the stroma fraction of wheat chloroplasts was purified to homogeneity. The nuclease exhibits an activity within a wide pH range of 5.0-7.5, its M-r is 20000. The enzyme

degrades DNA and RNA endonucleolytically, producing fragments with 3'-OH and 5'-phosphate termini. The nuclease shows no absolute requirement for added divalent cations. The enzyme catalyses hydrolysis of synthetic polyribonucleotides in the following order: poly(U) **gt** poly(A) **gt** poly(C) **gt** poly(G). Polydeoxynucleotides except poly(dA) and poly(dT) remain intact. Supercoiled, covalently closed circular phi-X174 DNA and plasmid pBR322 DNA are converted initially to the open-circular (relaxed) form and subsequently to the linear form.

1994

9/3,AB/112 (Item 43 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09536678 BIOSIS NO.: 199497545048

The human microsomal epoxide hydrolase gene (EPHX1): Complete nucleotide sequence and structural characterization.

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JOURNAL: Genomics 23 (2):p433-442 1994

ISSN: 0888-7543

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Human microsomal epoxide hydrolase (mEH) is a xenobiotic-metabolizing enzyme that detoxifies reactive epoxides to more water soluble dihydrodiol compounds. We have isolated and sequenced clones that encode the entire human mEH gene (EPHX1). The primary nuclear transcript, extending from the start of transcription to the site of **poly(A)** addition, is 20,271 nucleotides in length. The human mEH gene contains 9 exons, separated by 8 introns; canonical intron/exon boundary sites are observed at each junction. The introns vary in size from 335 to 6696 bp and contain numerous repetitive DNA elements, including 18 Alu sequences (each **gt** 100 nucleotides in length) within 4 introns. Alu sequences were classified with respect to subfamily assignment. Two thousand eighteen nucleotides 5' of the transcription start and 2501 nucleotides 3' of the **poly(A)** addition sites were also sequenced. To evaluate the human mEH promoter, chimeric constructs were prepared linking portions of the 5' mEH flanking sequence (up to -693 bp) to a CAT reporter gene, followed by transient transfection in both COS-1 and HepG2 cells. Results from these expression experiments suggest that the human mEH gene contains a weak core promoter and that inclusion of DNA sequences 5' of the minimal promoter region negatively regulates constitutive transcription.

1994

9/3,AB/113 (Item 44 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09536345 BIOSIS NO.: 199497544715

Molecular cloning and characterization of the hamster preproenkephalin A cDNA.

AUTHOR: Beaulieu Martin; Ouellette Michel; Desgroseillers Luc; Brakier-Gingras Lea(a)

AUTHOR ADDRESS: (a)Dep. Biochim., Univ. Montreal, Montreal, PQ H3C 3J7**
Canada

JOURNAL: DNA and Cell Biology 13 (9):p933-940 1994
ISSN: 1044-5498
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The cDNA for hamster preproenkephalin A (ENK) was cloned from an adrenal gland cDNA library constructed in the lambda ZapII vector. A nearly full-length cDNA was obtained and its 5' end region was completed using the technique of rapid amplification of cDNA ends (RACE). The coding and 3' untranslated regions of the hamster ENK cDNA share a high sequence identity with the rat, human, and bovine cDNAs, whereas the sequence identity is lower for the 5' untranslated region. Southern blot analysis of genomic DNA digests showed that a single copy of the ENK gene is present in the hamster haploid genome. Northern blot analysis of poly(A)+RNA from various hamster tissues indicated the following rank order for ENK messenger RNA abundance: adrenal glands gt right atrium gt brain gt left atrium gt right ventricle gt ventricular septum gt left ventricle, whereas primer extension analysis showed a single, identical transcriptional initiation site for the ENK mRNA in all these tissues. The sequence of the 5' untranslated region of the heart ENK cDNA was found to be identical to that from adrenal glands. This rules out the possibility that structural divergences in the 5' untranslated region of the heart ENK mRNA could decrease its translation efficiency and contribute to the very low level of enkephalin-containing peptides in the heart, compared to the adrenal glands.

1994

9/3,AB/114 (Item 45 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09503749 BIOSIS NO.: 199497512119
Cloning and characterization of multiple forms of the human kidney ROM-K potassium channel.
AUTHOR: Shuck Mary E; Bock Jeff H; Benjamin Christopher W; Tsai Ti-Dao; Lee Kai S; Slightom Jerry L; Bienkowski Michael J(a)
AUTHOR ADDRESS: (a)Upjohn Lab., 301 Henrietta, Kalamazoo, MI 49007**USA
JOURNAL: Journal of Biological Chemistry 269 (39):p24261-24270 1994
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The rat kidney ROM-K1 potassium channel cDNA was used to clone the homolog from human kidney using a combination of cDNA cloning, reverse transcriptase-polymerase chain reaction (RT-PCR), and primer extension cloning methods. In addition to the human species homolog of ROM-K1, four additional transcripts that are formed by alternative splicing of a single human gene were also characterized (hROM-K2 to hROM-K5). All five transcripts share a common 3' exon that encodes the majority of the channel protein and in three of the isoforms translation is initiated at a start codon contained within this exon (hROM-K2, hROM-K4, and hROM-K5). The two other transcripts contain additional exons that potentially extend the open reading frame by either 19 amino acid residues (hROM-K1) or by 17 amino acid residues (hROM-K3). Comparison of the translation products from the three representative transcripts (hROM-K1, hROM-K2, and hROM-K3) confirmed that hROM-K1 gave the largest product (41.6 kDa) and was translated more efficiently than either hROM-K2 or hROM-K3. Also, despite the presence of several additional canonical acceptor sites for Asn-linked glycosylation relative to rat

ROM-K1, all three channel polypeptides were glycosylated to a similar extent in the in vitro translation reactions when canine pancreatic microsomes were included. A survey of the tissue distribution of expression of the various forms in selected human tissues showed that the core-exon linked to all four possible 5' exons are detected almost exclusively in kidney. The core-exon was also detected in human kidney and lower amounts were detected in skeletal muscle **gt** pancreas **gt** spleen **gt** brain = heart **gt** liver RNAs by RT-PCR. Alternatively, Northern blot analysis of **poly(A)**+ RNAs from these same tissues revealed a 2.8-kilobase transcript only in kidney. Heterologous expression of either the hROM-K1, hROMK2, or hROM-K3 channel transcripts in *Xenopus* oocytes led to the expression of K+-selective, Ba-2+-sensitive inwardly rectifying channels as measured by whole cell currents. At this level of analysis, the channel properties of the individual forms could not be distinguished.

1994

9/3,AB/115 (Item 46 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09489914 BIOSIS NO.: 199497498284
Creatine kinase (CK) in skeletal muscle energy metabolism: A study of mouse mutants with graded reduction in muscle CK expression.
AUTHOR: Van Deursen Jan(a); Ruitenbeek Wim; Heerschap Arend; Jap Paul(a); Ter Laak Henk; Wieringa Be(a)
AUTHOR ADDRESS: (a)Dep. Cell Biol. Histology, Fac. Med. Sci., Univ. Nijmegen, P.O. Box 9101, 6500 HB Nijmegen**Netherlands
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 91 (19):p9091-9095 1994
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: To understand better the role of the creatine kinase (CK)/phosphocreatine system in muscle bioenergetics, a series of mouse mutants with subnormal muscle CK (M-CK) expression has been generated. Here we compare the phenotypes of mice deficient in M-CK (M-CK-/-) and M-CK leaky-mutant mice, which carry a targeted insertion of a hygromycin B-**poly(A)** resistance cassette in the second M-CK intron. Mice homozygous for this M-CK allele (M-CK-I/I) have a 3-fold reduction of dimeric muscle CK enzyme activity, whereas compound heterozygotes with the null M-CK allele (M-CK-I/-) display a 6-fold reduction. Unlike M-CK-/- mice, these mutants have no increased glycogen content or glycogen consumption in their fast fibers. The intermyofibrillar mitochondrial volume of these fibers is also normal, suggesting that energy transport via the CK/phosphocreatine system may function at low myofibrillar M-band CK levels. Conversely, the flux of energy through the CK reaction is still not visible by means of ³¹P NMR spectroscopy, indicating that relatively high levels of M-CK expression (**gt** 34% of normal) are required to generate CK fluxes detectable by this technique. The ability of muscles to perform burst activity is also subnormal and closely correlates with the level of M-CK expression.

1994

9/3,AB/116 (Item 47 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09418473 BIOSIS NO.: 199497426843

Expression of a rabbit renal ascorbic acid transporter in *Xenopus laevis* oocytes.

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JOURNAL: American Journal of Physiology 267 (1 PART 1):pC301-C306

1994

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LANGUAGE: English

ABSTRACT: We examined the expression of renal ascorbic acid transporters in *Xenopus laevis* oocytes after microinjection of cells with **poly(A)**+ RNA extracted from rabbit kidney cortex. Concomitant expression of the Na⁺-glucose cotransporter served as a control in these studies. Injection of **poly(A)**+ RNA into oocytes produced over a fivefold increase in the uptake of (14C)ascorbic acid (570 μ M) compared with water-injected cells. Size fractionation of the kidney cortex mRNA by sucrose gradient revealed that the mRNA species that induced ascorbic acid transporter expression in oocytes was present in a fraction centered around 2.0 kilobases (kb) and had a size range of 1.8-3.1 kb. Injection of the active fraction into oocytes produced a **gt** 40-fold increase in ascorbic acid uptake compared with water-injected controls. Expression of ascorbic acid transporter(s) was noticeable as early as 2 days after injection and was maximal after 7 days; it was also dependent on the amount of mRNA injected into oocytes. The induced uptake of (14C)ascorbic acid after injection of mRNA into oocytes was 1) Na⁺ dependent, as indicated by the almost complete lack of transport on removal of Na⁺ from the incubation medium; 2) significantly inhibited by unlabeled ascorbic acid and its structural analogue isoascorbic acid but not by D-glucose; and 3) saturable as a function of increasing the substrate concentration in the incubation medium (100-1,000 μ M), with an apparent K_m of 258 \pm 72.5 μ M and a maximum velocity of 29.6 \pm 2.8 pmol cndtdot oocyte⁻¹ cndtdot 2 h⁻¹. These data demonstrate that *X. laevis* oocytes are a suitable system to functionally express the mammalian renal ascorbic acid transporter. Furthermore, because of the similar properties of Na⁺ dependence, substrate specificity, and kinetics, the expressed ascorbic acid transporter appears to be that of the brush-border membrane of the renal reabsorptive cells, where it represents a major reabsorptive mechanism.

1994

9/3,AB/117 (Item 48 from file: 5)

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09415105 BIOSIS NO.: 199497423475

Characterization of bicuculline/baclofen-insensitive (rho-like)

gamma-aminobutyric acid receptors expressed in *Xenopus* oocytes. II.

Pharmacology of gamma-aminobutyric acid-A and alpha-aminobutyric acid-B receptor agonists and antagonists.

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JOURNAL: Molecular Pharmacology 43 (4):p609-625 1993

ISSN: 0026-895X

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: **Poly(A)**+ RNA from mammalian retina expresses

bicuculline/baclofen-insensitive gamma-aminobutyric acid (GABA) receptors in *Xenopus* oocytes with properties similar to those of homooligomeric GABA-rho-1 receptors. The pharmacological profile of these rho-like receptors was extended by measuring sensitivities to various GABA-A and GABA-B receptor ligands. For direct comparison the same compounds were also assayed with GABA-A receptors expressed by rat brain RNA. The potency sequence for heterocyclic GABA analogues at the GABA-rho-like receptors was GABA (1.3) **gt** muscimol (2.3) **gt** isoguvacine (100) (approximate EC-50 in parentheses; all EC-50 and K-b values given in μ -M). Both muscimol and isoguvacine were partial agonists at the p-like receptors. 4,5,6,7-Tetrahydroisoxazolo(5,4-c)pyridin-3-ol (K-b simeq 32), piperidine-4-sulfonic acid (K-b simeq 85), and isonipecotic acid (K-b simeq 1000) acted primarily as competitive antagonists, showing little or no activity as agonists. The sulfonic acid GABA analogue 3-aminopropanesulfonic acid was also a competitive antagonist (K-b simeq 20). Conformationally restricted GABA analogues trans- and cis-4-aminocrotonic acid (TACA and CACA) were agonists at the rho-like receptors. TACA (EC-50 simeq 0.6) had twice the potency of GABA and was 125 times more potent than CACA (EC-50 simeq 75). Z-3-(Amidinothio)propenoic acid, an isothiuronium analogue of GABA, had little activity as an agonist but instead acted as a competitive antagonist (K-b simeq 20). At concentrations of **gt** 100 μ -M, bicuculline did have some weak competitive inhibitory effects on the GABA-rho-like receptors (K-b simeq 6000), but it was at least 5000 times more potent at GABA-A receptors. Strychnine (K-b simeq 70) and SR-95531 (K-b simeq 35) also were competitive inhibitors of the rho-like receptors but were, respectively, 20 and 240 times more potent at GABA-A receptors. The GABA-B receptor ligands baclofen, phaclofen, and saclofen (1-100 μ -M) had no appreciable effects on the rho-like receptors. In contrast, 3-aminopropylphosphonic acid, the phosphonic acid analogue of GABA, acted as a competitive antagonist (K-b simeq 10), and 3-aminopropylphosphinic acid and 3-aminopropyl(methyl)-phosphinic acid were moderately potent antagonists (K-b simeq 1.7 and 0.8, respectively). delta-Aminovaleric acid was also an antagonist (K-b simeq 20), whereas 4-aminobutylphosphonic acid, the phosphonic acid analogue of delta-aminovaleric acid, was only a weak inhibitor (K-b simeq 600). In terms of structure-activity relationships, our experiments suggest that incorporation of the carboxyl or amino groups of GABA into 3-isoxazolo or piperidine rings either reduces agonist potency at the GABA-rho-like receptors or results in analogues that act as competitive antagonists. Similarly, substitution of the carboxyl group for sulfonic acid or of the amino group for isothiuronium generates antagonists. The relative activities of TACA and CACA clearly suggest that GABA interacts with the rho-like receptors in extended conformations and appears to distinguish these receptors from previously postulated GABA-c receptor sites. The 4-chlorophenyl substituent of baclofen and related GABA-B receptor antagonists almost wholly prohibits functionally relevant interactions with the rho-like receptors. However, some phosphonic and phosphinic analogues of GABA, normally categorized as selective GABA-B receptor agonists, show a clear potential for acting as antagonists. These results should be useful for designing drugs that interact selectively with mammalian bicuculline/ baclofen-insensitive GABA receptors and for investigating the mechanisms by which ligands interact with GABA-gated Cl⁻ channels.

1993

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 DIALOG(R)File 5:BIOSIS Previews(R)
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09413658 BIOSIS NO.: 199497422028
 Characterization of bicuculline/baclofen-insensitive gamma-aminobutyric

acid receptors expressed in *Xenopus* oocytes. I. Effects of Cl⁻ channel inhibitors.

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JOURNAL: Molecular Pharmacology 42 (1):p165-173 1992

ISSN: 0026-895X

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Poly(A)⁺ RNA from bovine retina expressed gamma-aminobutyric acid (GABA)-activated membrane current responses in *Xenopus* oocytes, consisting of two pharmacologically distinct components. One component (I-G-Aret) was mediated by GABA-A receptors, and the other component (K-G-BR) by atypical GABA receptors that were resistant to inhibition by bicuculline and insensitive to activation by baclofen. To further characterize the bicuculline/baclofen-insensitive GABA receptors, electrical recordings were made measuring the sensitivity of I-G-BR to two Cl⁻ channel inhibitors, t-butylbicyclophosphorothionate (TBPS) and picrotoxin. For purposes of comparison, effects of TBPS and picrotoxin were also assayed on currents mediated by GABA-A receptors expressed in oocytes by rat cerebral cortex RNA (I-G-Actx). The main finding of this study was that TBPS was a surprisingly weak inhibitor of ICBR, whereas I-G-Actx was potently suppressed. Assays on maximum responses indicated that I-G-Actx was at least 500 times more sensitive to TBPS than was I-G-BR (IC₅₀ values of approximately 0.2 μ M and \gt 50 μ M, respectively). Moreover, inhibition of I-G-Actx by micromolar concentrations of TBPS was largely insurmountable, whereas the weak inhibitory effects on I-G-BR showed strong dependence on agonist concentration. For example, 10 μ M TBPS reduced maximum I-G-Actx by \gt 90%, an effect that was not significantly reversed by 10-fold increases in the concentration of agonist. In contrast, the same concentration of TBPS caused a 2-fold increase in the EC₅₀ for ICBR but had only marginal (\lt 5%) inhibitory effects on maximum responses. Picrotoxin inhibited both types of current, but assays on maximum responses indicated that I-G-Actx was approximately 30 times more sensitive than I-G-BR (IC₅₀ values of approximately 1 and 30 μ M, respectively). Inhibitory effects of picrotoxin on ICBR again showed strong dependence on agonist concentration, but in this case there was also a clear insurmountable component. Comparisons between I-G-Actx and I-G-Aret suggested that GABA-A receptors expressed by either brain or retina RNA showed approximately the same sensitivity to TBPS and picrotoxin. Our experiments indicate that the bicuculline/baclofen-insensitive GABA receptors expressed by retina RNA differ markedly from GABA-A receptors in their sensitivity to TBPS and picrotoxin. Defining the structural features responsible for these differences at the molecular level will provide a further means of investigating the complex mechanisms underlying interactions between inhibitors and GABA-activated Cl⁻ channels.

1992

9/3,AB/119 (Item 50 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09412576 BIOSIS NO.: 199497420946

Increased voltage-dependent calcium influx produced by alpha-1B-adrenergic receptor activation in rat medullary thyroid carcinoma 6-23 cells.

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JOURNAL: Molecular Pharmacology 45 (4):p591-598 1994
ISSN: 0026-895X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We characterized norepinephrine (NE)-activated Ca-2+ influx in the rat medullary thyroid carcinoma (rMTC) 6-23 cell line using fura-2. NE caused a sustained increase in the intracellular Ca-2+ concentration ((Ca-2+)-i), which was completely reversed by addition of nifedipine or removal of extracellular Ca-2+. Bay K8644, KCl-induced depolarization, and ATP also increased (Ca-2+)-i in rMTC 6-23 cells, effects that were also reversed by nifedipine. Release of intracellular Ca-2+ by thapsigargin was not blocked by nifedipine, and NE caused nifedipine-sensitive increases in (Ca-2+)-i even in the presence of thapsigargin. NE-stimulated increases in (Ca-2+)-i were mimicked by the alpha-1-adrenergic receptor (AR) agonist phenylephrine but not by the beta-AR agonist isoproterenol. The response to NE was blocked by the alpha-AR antagonist phentolamine and by pretreatment with the alpha-1B-selective alkylating agent chloroethylclonidine (CEC) but was not blocked by alpha-1A-selective concentrations of the subtype-selective antagonist 5-methylurapidil. alpha-1-AR binding sites labeled by 125I-BE 2254 in membranes from this cell line were highly sensitive to inactivation by CEC (gt 80%), and competition with subtype-selective antagonists suggested the presence of a homogeneous population of alpha-1B-ARs. NE, epinephrine, and phenylephrine, but not KCl, ATP, or isoproterenol, caused large increases in (3H)inositol phosphate (InsP) formation in these cells. This (3H)InsP response was greatly reduced by CEC pretreatment, and competitive antagonists blocked this response with an alpha-1B-like pharmacology. Northern blots of poly(A)+ RNA from rMTC 6-23 cells showed single transcripts hybridizing to the hamster alpha-1B-AR (2.2-kilobase) and less prominently to the rat alpha-1D-AR (4.0-kilobase) cDNAs but no detectable hybridization to the bovine alpha-1C-AR cDNA. The phospholipase C inhibitor U-73122 reduced the (3H) InsP response to NE in a concentration-dependent manner but had little or no effect on the NE-induced increases in (Ca-2+)-i. Phorbol myristate acetate also increased (Ca-2+)-i in rMTC 6-23 cells, although this response was not blocked by nifedipine. We conclude that activation of alpha-1B-like ARs (including possibly both alpha-1B- and alpha-1D-ARs) increases voltage-dependent Ca-2+ influx in rat rMTC 6-23 cells. This effect appears to be independent of release of intracellular Ca-2+, activation of phospholipase C, and/ or activation of protein kinase C. This cell line should be very useful in defining the mechanisms underlying the known effects of alpha-1-ARs on voltage-gated Ca-2+ influx, which plays an important functional role in vascular smooth muscle.

1994

9/3,AB/120 (Item 51 from file: 5)
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09405046 BIOSIS NO.: 199497413416

Detection and characterization of triple-helical
pyrimidine-purine-pyrimidine nucleic acids with vibrational circular
dichroism.

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JOURNAL: Biochemistry 33 (28):p8428-8435 1994
ISSN: 0006-2960
DOCUMENT TYPE: Article
RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Vibrational circular dichroism (VCD) spectra were measured in the C dbd O stretching region for poly(U)*poly(A) cntdot poly(U), poly(dT)*poly(dA) cntdot poly(dT), and poly(U)*poly(dA) cntdot poly(dT). These VCD spectra of the triple-helical structure were dramatically different from those of the corresponding duplexes. The VCD indicates that a very similar base-pair structure is present in these triplexes. The same sign pattern was found for poly(C+)*poly(I) cntdot poly(C), which implies a generality of structure than can result from the steric constraint of the triple helix conformation. By contrast, the corresponding duplexes are quite different in terms of their VCD. The transitions between triplex, duplex, and single-stranded forms were studied as a function of temperature and interpreted using factor analysis. The relative stabilities of the triplexes lie in the order RNA gt DNA gt hybrid. Nondegenerate dipole-coupling calculations for a U*A.U oligomer were carried out for the C dbd O stretching modes to model the spectral changes observed. The experimental absorbance spectra indicate that the bases have nonequivalent H-bonds which can be achieved if a reverse Hoogsteen base-pairing scheme is assumed. The computational VCD results with such a scheme were in better qualitative agreement with experiment than those using the expected Hoogsteen base-pairing scheme.

1994

9/3,AB/121 (Item 52 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09396461 BIOSIS NO.: 199497404831
Cloning and biological function of laminin in Hydra vulgaris.
AUTHOR: Sarra Michael P Jr(a); Yan Li; Grens Ann; Zhang Xiaoming; Agbas Abdalbaki; Huff Jacquelyn K; St John P L; Abrahamson Dale R
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JOURNAL: Developmental Biology 164 (1):p312-324 1994
ISSN: 0012-1606
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The Cnidarian, hydra, lends itself to studies related to the role of extracellular matrix (ECM) components in development because of its high regenerative capacity and its simple structure, which is organized as an epithelial bilayer with an intervening ECM termed the mesoglea. Previous immunocytochemical and biochemical studies have established that hydra mesoglea contains many of the major matrix components (e.g., fibronectin, laminin, type IV collagen, and heparan sulfate proteoglycan) associated with the ECM of vertebrate and more complex invertebrate species. Additional studies have also established that ECM components have a critical role in hydra development as monitored during head regeneration and morphogenesis of hydra cell aggregates. In the present study a monoclonal antibody (mAb52) raised to isolated hydra mesoglea was used as a probe in additional functional studies and to screen a cDNA expression library made from poly(A)+ RNA isolated from Hydra vulgaris. Immunofluorescent analysis indicated that mAb52 was localized along the entire longitudinal axis of adult polyps in what is termed the subepithelial zones of hydra mesoglea. Cytochemical studies found these subepithelial zones to be rich in anionic sites. Previous studies have shown that mAb52 blocks hydra cell aggregate development and experiments in the current study have shown that mAb52 also blocks in vivo interstitial cell (I-cell) migration in hydra grafts. Sequence analysis of cDNA clones isolated using mAb52 indicated that the protein encoded by

these clones had structural homology with mammalian and *Drosophila* laminin B1 chain and hybridized to a single 6.75-kb band on Northern blots of total hydra RNA. One interesting difference in hydra laminin B1 was the presence of a FTGTQ amino acid sequence in place of the vertebrate YIGSR cell binding domain. Under nonreducing conditions, polyclonal antibodies against FTGTQ bound to the same **gt** 200-kDa band on Western blots of mesoglea as mAb52 and also immunolocalized to the subepithelial zones. Under reducing conditions, anti-FTGTQ antibodies bound to a single band with a mass of approximately 200 kDa. In addition, FTGTQ peptide inhibited adhesion of dissociated hydra cells to mesoglea and anti-FTGTQ antibodies inhibited hydra cell binding to substrates coated with mesoglea or FTGTQ peptide. Anti-FTGTQ antibodies also inhibited in vivo I-cell migration in hydra grafts. Given the early divergence of Cnidarians during evolution, these studies indicate the highly conserved nature of laminin and provide additional information regarding the critical role of ECM components during hydra development.

1994

9/3,AB/122 (Item 53 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09350331 BIOSIS NO.: 199497358701

Multiple instability-regulating sites in the 3' untranslated region of the urokinase-type plasminogen activator mRNA.

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JOURNAL: Molecular and Cellular Biology 14 (7):p4920-4928 1994

ISSN: 0270-7306

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RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: In LLC-PK-1 cells urokinase-type plasminogen activator (uPA) mRNA has a short half-life. it is stabilized by inhibition of protein synthesis and by downregulation of protein kinase C (PKC) **gt** In the present study on uPA mRNA metabolism, we focused our attention on the 3' untranslated region (3'UTR) of the uPA mRNA, as this region is long and highly conserved among several mammalian species, including mice and humans. To investigate the possible role of the 3'UTR of uPA mRNA in mRNA metabolism, we inserted this region into the 3'UTR of the rabbit beta-globin gene that is linked to the cytomegalovirus promoter and stably transfected it into LLC-PK₁ cells. While the parental globin mRNA was stable, the chimeric mRNA was degraded as rapidly as endogenous uPA mRNA, suggesting that the 3'UTR of uPA mRNA contains most of the information required for its rapid turnover. Further analysis showed that there are at least three independent determinants of instability in the 3'UTR; one is an AU-rich sequence located immediately 3' of the **poly(A)** addition signal, and one is a sequence containing a stem structure. One determinant seems to require ongoing RNA synthesis for its activity. All chimeric unstable globin mRNAs became stable in the presence of cycloheximide, a protein synthesis inhibitor, suggesting that the stabilization of mRNA by protein synthesis inhibition is not through a specific sequence in the mRNA. In PKC-downregulated cells, globin mRNAs with the complete 3'UTR or the AU-rich sequence were stabilized, suggesting that PKC downregulation stabilizes uPA mRNA through the AU-rich sequence. Here we discuss the significance of multiple, independently acting instability determinants in the regulation of uPA mRNA metabolism.

1994

9/3,AB/123 (Item 54 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09318380 BIOSIS NO.: 199497326750
Atrial natriuretic factor (ANF) binds to thyrotropin-regulated receptors in FRTL-5 cells and increases thyroglobulin mRNA.
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JOURNAL: Peptides (Tarrytown) 15 (3):p475-481 1994
ISSN: 0196-9781
DOCUMENT TYPE: Article
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LANGUAGE: English

ABSTRACT: Thyrotropin (TSH) regulation of atrial natriuretic factor (ANF) receptors was studied in the rat thyroid follicular cell line, FRTL-5. Exposure of FRTL-5 cells to 1 mU/ml TSH for 7 days resulted in a tenfold increase in ANF receptors (B-max = 188 fmol/mg protein) compared with control (B-max = 18 fmol/mg protein), without affecting binding affinity. An identical treatment of porcine thyrocytes with TSH resulted in a 50% decrease in ANF binding sites. Displacement binding studies indicated that **gt** 80% of the ANF receptors in FRTL-5 cells belong to the ANF-R-1 (guanylate cyclase-coupled) receptor subtype. By contrast, **gt** 98% of the ANF receptors in porcine thyrocytes were of the ANF-R-2, or clearance, receptor subtype. Intracellular cGMP content was increased thirty-sixfold in FRTL-5 cells by 1 mu-M ANF, but only 2.5-fold in porcine thyrocytes. cAMP levels were unaffected by ANF in either cell type. Northern blot analysis of **poly A** mRNA extracted from FRTL-5 cells incubated 2 days in the presence of 100 nM ANF indicated a twofold increase in thyroglobulin mRNA content compared with control. These findings suggest that the ANF-R-1 receptor, preferentially expressed in FRTL-5 cells and regulated by TSH, might play a role in regulating thyroid hormone production.

1994

9/3,AB/124 (Item 55 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09309359 BIOSIS NO.: 199497317729
Measurement of blood-brain barrier GLUT1 glucose transporter and actin mRNA by a quantitative polymerase chain reaction assay.
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JOURNAL: Journal of Neurochemistry 62 (6):p2085-2090 1994
ISSN: 0022-3042
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The expression of the blood-brain barrier GLUT1 glucose transporter is down-regulated in brain capillary endothelial cells in tissue culture. Consequently, the study of the regulation of this low-abundance transcript requires the isolation of **poly(A)+** mRNA from relatively large numbers of brain endothelial cells in culture (apprx 10⁻⁷). Therefore, in order to facilitate studies with smaller amounts of cells, we describe here a quantitative polymerase chain

reaction (PCR) assay to measure the mRNA of GLUT1 and the mRNA of the housekeeping gene, actin, which is used as standard control. Bovine brain endothelial cells were grown as either a primary culture (EP cells) or as a brain endothelial cell line (ECL cells) in 25-mm 6-well cluster dishes, and total or **poly(A)**+ RNA was isolated. Following synthesis of cDNA with AMV reverse transcriptase and oligo(dT)-18 primer, PCR was performed with sense and antisense primers for bovine GLUT1 and gamma-actin, respectively. Reactions were performed in the presence of 2.5 mu-Ci of (alpha-32P)dCTP, and products were resolved in agarose gels and quantified by scanning densitometry of autoradiograms. A direct relationship between RNA-cDNA and PCR products was observed for GLUT1 after 30 cycles, and for actin after 15 PCR cycles. The method was reproducible within specified ranges of starting RNA-derived cDNA, and the intraassay coefficient of variation averaged 7.2 +/- 1.8%. The GLUT1/actin mRNA ratio was as follows: brain capillaries mchgt EP **gt** ECL. In addition, it is demonstrated that tumor necrosis factor-alpha induced a three- to fourfold increase in the GLUT1/actin mRNA ratio in ECL cells. This method provides a 100-200-fold increase in the sensitivity of detection of blood-brain barrier GLUT1 transcript in bovine brain capillary endothelial cells in tissue culture compared with the conventional northern blotting technique using **poly(A)**+ mRNA.

1994

9/3,AB/125 (Item 56 from file: 5)
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09304457 BIOSIS NO.: 199497312827
Molecular cloning of the gene encoding the mouse parathyroid hormone/parathyroid hormone-related peptide receptor.
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AUTHOR ADDRESS: (a)Dep. Physiol., McGill Univ., McIntyre Med. Sci. Build.,
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JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 91 (11):p5051-5055 1994
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The parathyroid hormone/parathyroid hormone-related peptide receptor (PTHr) is a G-protein-coupled receptor containing seven predicted transmembrane domains. We have isolated and characterized recombinant bacteriophage lambda-EMBL3 genomic clones containing the mouse PTHR gene, including 10 kilobases of the promoter region. The gene spans **gt** 32 kilobases and is divided into 15 exons, 8 of which contain the transmembrane domains. The PTHR exons containing the predicted membrane-spanning domains are heterogeneous in length and three of the exon-intron boundaries fail within putative transmembrane sequences, suggesting that the exons did not arise from duplication events. This arrangement is closely related to that of the growth hormone releasing factor receptor gene, particularly in the transmembrane region, providing strong evidence that the two genes evolved from a common precursor. Transcription is initiated principally at a series of sites over a 15-base-pair region. The proximal promoter region is highly (G+C)-rich and lacks an apparent TATA box or initiator element homologies but does contain CCGCCC motifs. The presumptive amino acid sequence of the encoded receptor is 99%, 91%, and 76% identical to those of the rat, human, and opossum receptors, respectively. There is no consensus polyadenylation signal in the 3' untranslated region. The **poly(A)** tail of the PTHR transcript begins 32 bases downstream of a

35-base-long A-rich sequence, suggesting that this region directs polyadenylation.

1994

9/3,AB/126 (Item 57 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09278428 BIOSIS NO.: 199497286798

Functional expression of the nitrobenzylthioinosine-sensitive nucleoside transporter of human choriocarcinoma (BeWo) cells in isolated oocytes of *Xenopus laevis*.

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JOURNAL: Biochemical Journal 299 (3):p769-773 1994

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ABSTRACT: Cultured human choriocarcinoma (BeWo) cells have previously been shown to exhibit, in comparison with other cultured cell types, elevated nitrobenzylthioinosine (NBMPR)-sensitive transport activity and large numbers (gt 10⁷/cell) of high-affinity NBMPR-binding sites (Boumah, Hogue and Cass (1992) Biochem. J. 288, 987-996). The present study investigates whether NBMPR-sensitive nucleoside transport activity could be induced in *Xenopus laevis* oocytes by microinjection of poly(A)⁺ RNA isolated from proliferating cultures of BeWo cells. Expression of uridine transport activity was assayed by comparing rates of uptake (22 degree C) of 100 mu-M (3H)uridine by RNA-injected oocytes with uptake by water-injected or uninjected oocytes. A 4-fold stimulation of uridine uptake (2.0 versus 0.5 pmol/90 min per oocyte) was seen when oocytes were injected with 50 ng of BeWo poly(A)⁺ RNA, and this stimulation was abolished when the RNA-injected oocytes were assayed in the presence of 10 mu-M NBMPR. The expressed uridine transport activity in oocytes was highly sensitive to NBMPR, with a 50% reduction seen at 1.1 nM NBMPR (IC-50 value). The IC-50 value for NBMPR inhibition of uptake of 100 mu-M (3H)uridine by intact BeWo cells was 1.4 nM. Inward fluxes of (3H)uridine in the RNA-injected oocytes were greatly reduced in the presence of high concentrations (2 mM) of non-radioactive nucleosides (adenosine, thymidine, inosine) that are known permeants of NBMPR-sensitive nucleoside transport processes. These results establish that the abundance of NBMPR-sensitive nucleoside transporter mRNA in poly(A)⁺ RNA preparations from BeWo cells is sufficient to achieve production of functionally active transporter protein in *Xenopus* oocytes and that, when expressed in *Xenopus* oocytes, the transporters exhibit NBMPR sensitivity and permeant selectivity similar to that of the native transporters.

1994

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09269858 BIOSIS NO.: 199497278228

Primary structure and functional properties of an epithelial K channel.

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JOURNAL: American Journal of Physiology 266 (3 PART 1):pC809-C824

1994

ISSN: 0002-9513

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RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Expression cloning in *Xenopus* oocytes was used to identify a clone for a renal K channel. The clone, named ROMK2, was obtained from a cDNA library constructed in the plasmid vector pSPORT using size-selected **poly(A)+** RNA from whole rat kidney. ROMK2 consists of 1,837 nucleotides, with an open reading frame of 1,116 bases predicted to code for a 372-amino acid peptide. The clone appears to be a splice variant of a recently reported K channel (ROMK1) from rat renal outer medulla (Ho, K. H., C. G. Nichols, W. J. Lederer, J. Lytton, P. M. Vassilev, M. V. Kanazirska, and S. C. Hebert. *Nature Lond.* 362: 31-37, 1993). Northern blot analysis indicates that ROMK2 is expressed in renal cortex, medulla, and papilla. Expression in other tissues appears to be much lower. The functional properties of the channel as measured in *Xenopus* oocytes indicate its close relationship to ROMK1 and more distant relationship to the inward rectifier K channel (IRKI) (Kubo, Y, T. J. Baldwin, Y. N. Jan, and L. Y. Jan. *Nature Lond.* 362: 127-133, 1993). The inward conductance of the channel is a saturable function of external K, with a half-maximal conductance at 10^{-5} M. The selectivity sequence for ion permeability based on reversal potential measurements was K **gt** Rb **gt** NH-4 **gt** Na, Li. The conductance to Rb was only one-half that to K. Extracellular Ba-2+ and Cs+ blocked the channel in a voltage-dependent manner. The high sensitivity of Cs+ block to voltage is consistent with the channel's operating as a multi-ion pore. The channel was blocked by high concentrations (100 μ M) of glybenclamide. It did not appear to be blocked by extracellular Na+ or tetraethylammonium ion. Patch-clamp measurements indicated a single-channel conductance of 30 pS in the presence of 110 mM K and high open probability that was weakly dependent on voltage. This channel may be involved in maintaining the membrane potential of renal cells and/or mediating renal K secretion.

1994

9/3,AB/128 (Item 59 from file: 5)

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09176367 BIOSIS NO.: 199497184737

Properties of protein kinase C isoforms (beta-11, epsilon, and zeta) in a macrophage cell line (J774) and their roles in LPS-induced nitric oxide production.

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JOURNAL: Journal of Immunology 152 (4):p1898-1906 1994

ISSN: 0022-1767

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Northern analysis of **poly(A)+** RNA extracted from J774 cells (a mouse macrophage cell line) showed that this cell line constitutively expresses mRNAs specific for protein kinase C (PKC)-beta-I, -beta-II, -epsilon and -zeta, but not those for PKC-alpha, -gamma or -delta. Western analysis of the total cell lysate showed that J774 cells express PKC-beta-II, -epsilon and -zeta isoenzymes, but failed to show the expression of PKC-beta-I. The exposure of J774 cells to **gt** 10 nM PMA led to a loss of immunoreactive PKC-beta-II in 4 h.

The down-regulation of immunoreactive PKC-E required more than 8 h of the exposure to **gt** 100 nM PMA. Immunoreactive PKC-zeta was most resistant to PMA treatment and was not significantly reduced after the exposure to 300 to 600 nM PMA for 24 h. PMA-mediated, persistent down-regulation of PKC-beta-II is probably a result of the inhibition of PKC-beta-II biosynthesis at the posttranscriptional level, because PMA-exposed cells were found to gradually increase the expression of PKC-beta-II specific mRNA. PMA-pretreated cells responded to a low dose (10 ng/ml), but not to a high dose (1 μ -g/ml), of LPS by significantly lower expression of mRNA specific for the inducible nitric oxide synthase (i-NOS) gene and production of nitric oxide (NO) than the control cells did. Thus, PKC could be a part of the signal transduction apparatus involved in LPS-induced inducible nitric oxide synthase gene activation.

1994

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09175639 BIOSIS NO.: 199497184009

Preparation of cyclic 2',3'-monophosphates of oligoadenylates (A2'p)-nA
gt p and A3'p(A2'p)-n-1A **gt** p.

AUTHOR: Budowsky Edward I(a); Kayushina Elena N; Tarasov Andrew K; Orlenko
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JOURNAL: European Journal of Biochemistry 220 (1):p97-104 1994

ISSN: 0014-2956

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The action of the guanylyl-preferring RNase from *Bacillus intermedius* (binase) on a mixture of oligoadenylates with randomly distributed 2'-5' and 3'-5' internucleotide bonds ((A2'/3'p)-n) under conditions sufficient for complete hydrolysis of **poly(A)** results in a mixture containing a single circular oligoadenylate and two series of linear oligoadenylates ending in cyclic 2',3'-phosphate. Individual compounds formed upon digestion of (A2'/3'p)-n with binase have been isolated. Their structure was determined on the basis of their chemical and enzymatic conversions and confirmed by 1H-, 13C- and 31P-NMR spectra. According to these data, the circular triadenylate contains one 2'-5' and two 3'-5' internucleotide bonds, linear oligoadenylates of one series contain exclusively 2'-5' internucleotide bonds ((A2'p)-nA **gt** p), while each compound of the other series contains a single 3'-5' internucleotide bond connecting the 5'-ultimate nucleotide residue with the penultimate one (A3'p(A2'p)-n-1A **gt** p). The incubation of compounds of the former series A3'p(A2'p)-n **gt** p at pH 1.0 and the subsequent action of phosphatase results in successive formation of compounds of two other new series: A3'p(A2'p)-nA2'(3')p and A3'p(A2'p)-nA.

1994

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09173857 BIOSIS NO.: 199497182227

Halide-catalyzed cis product formation in the hydrolysis of
anti-benzo(a)pyrene diol epoxide and its alkylation of **poly(A)**

).
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JOURNAL: Chemical Research in Toxicology 7 (1):p110-119 1994
ISSN: 0893-228X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The carcinogen
7-r,8-t-dihydroxy-9-t,10-t-epoxy-7,8,9,10-tetrahydrobenzo(alpha)pyrene
(antiBPDE) forms diastereomeric cis and trans. products in its reactions
with nucleic acids and water (adducts and tetrols, respectively). The
effects of salts, buffers, and DNA on the hydrolysis product ratio were
tested. Halide ions increase the cis-tetrol/trans-tetrol ratio, with the
order of effectiveness being I > Br > Cl > F. No cation
effect was apparent. Non-halide salts of strong acids increase the ratio
to a small degree. Buffers decrease the ratio, with phosphate being more
effective than cacodylate. DNA also reduces the ratio, with denatured DNA
being more potent than native DNA. Halide ions appear to catalyze
cis-tetrol formation via trans halohydrin intermediates. At the lowest
halide concentrations which significantly raise the product ratio, and at
all levels of chloride ion, the rate of anti-BPDE hydrolysis is not
greatly increased, indicating that the halide ions are reacting primarily
with the BPDE carbocation formed in the rate-determining step. At higher
concentrations, iodide ion and, to a lesser degree, bromide ion
significantly accelerate hydrolysis, indicating that BPDE undergoes S-N2
attack by these ions. Chloride ion was also found to increase the
proportion of cis adducts formed between anti-BPDE and poly(A
) . The cis adduct/trans adduct ratio was quadrupled by 0.5 M NaCl. This
suggests that chlorohydrins can be intermediates in the alkylation of
nucleic acids by epoxides of polycyclic aromatic hydrocarbons.

1994

9/3,AB/131 (Item 62 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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09172824 BIOSIS NO.: 199497181194
Changes in expression of inhibin/activin alpha, beta-A and beta-B subunit
messenger ribonucleic acids following increases in size and during
different stages of differentiation or atresia of non-ovulatory follicles
in cows.
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AUTHOR ADDRESS: (a)Mol. Reprod. Endocrinol. Lab., Dep. Anim. Sci., Mich.
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JOURNAL: Biology of Reproduction 50 (3):p492-501 1994
ISSN: 0006-3363
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Northern and slot blot analyses were used to examine the sizes,
variability, and changes in amounts of alpha, beta-A and beta-B inhibin/
activin subunit mRNAs following increases in size and during different
stages of differentiation or atresia of bovine nonovulatory follicles. In
Study I, a major 1.3-kb band and minor 2.2-, 3.3- and 6.4-kb bands of
alpha mRNA; a major 6.4-kb band and minor 2.6 and 4.0-kb bands of beta-A;
and major 3.5- and 4.6-kb bands of beta-B mRNA were detected in total
and/or poly(A)+ RNA isolated from pools of small (1-5 mm),
medium (6-10 mm), or large (> 10 mm) follicles. In Study II, 18

of 19 follicles had a 1,3-kb alpha mRNA, and amounts of 1.3 kb alpha mRNA increased with follicle size. However, 0 of 19, 9 of 19, and 3 of 19 follicles had 2.2-, 3.3-, and 6.4-kb alpha mRNA bands. In Study III, the ratio of estradiol (E) to progesterone (P) in follicular fluid (FF) was used to separate follicles into the following three stages of differentiation and atresia: estrogen-active (EA; E \geq P in FF), atretic (P:E = 1-100), and highly atretic (P:E \geq 100). Total amounts of alpha and beta-A mRNAs were 2.4- and 5.8-fold greater in EA follicles compared with small follicles. Alpha and beta-A mRNAs and concentration of total inhibin immunoactivity were 4.4-, 9.8- and 1.8-fold lower in highly atretic follicles compared with EA follicles. Changes in amounts of follicular alpha and beta-A mRNAs were highly positively correlated with intrafollicular concentrations of E, ratio of E to P, and total inhibin immunoactivity, but negatively correlated with P. Ratio of amounts of alpha to beta-A mRNAs was 3.9- and 6.5-fold greater in small and highly atretic follicles compared with EA follicles. Amounts of beta-B subunit mRNAs were unchanged during follicular development and unrelated to changes in follicular concentrations of E, P, or total inhibin immunoactivity. On the basis of these results, we concluded that 1) multiple forms of each inhibin/activin subunit mRNA are expressed in follicular tissue; 2) alpha and beta-A subunit mRNAs and inhibin transiently increase; 3) alpha and beta mRNAs are not co-regulated similarly; and 4) beta-B mRNA is constitutively expressed during differentiation and atresia of nonovulatory follicles.

1994

9/3,AB/132 (Item 63 from file: 5)
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09125238 BIOSIS NO.: 199497133608

Striking similarities between the nucleotide sequence and genome organization of citrus tatter leaf and apple stem grooving capilloviruses.

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JOURNAL: Journal of General Virology 74 (12):p2743-2747 1993

ISSN: 0022-1317

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RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The sequence of the 3'-terminal 2956 nucleotides, excluding the **poly(A)** tail, of the citrus tatter leaf virus (CTLV) genome was determined and compared with that of the apple stem grooving virus (ASGV) genome. The sequence of the 3'-terminal region of CTLV contains two overlapping open reading frames (ORFs) and a 3'-terminal non-coding region of 142 nucleotides. The long, incomplete ORF1 ends at UAG (position 2812) and encodes a protein with at least 938 amino acids (M-r \geq 108703). This protein contains the GDD motif associated with the RNA polymerase. ORF2, in a different frame within ORF1, starts at AUG (position 1248) and stops at UGA (position 2208) encoding a protein with an M-r of 36179 (36K). Partial homologies were found among the 36K protein of CTLV, the 50K protein of apple chlorotic leaf spot closterovirus, the 40K protein of potato virus T and the gene 1 products of caulimoviruses. The arrangement of ORFs in the 3'-terminal region of the CTLV genome is in perfect agreement with that of the ASGV genome. The sequence of the 3'-terminal 2956 nucleotides, excluding the **poly(A)** tail, of the CTLV genome shows 86-1% identity to that of the ASGV genome. Similarities of amino acid sequences encoded by ORF1 and ORF2 of CTLV with the corresponding regions of ASGV are 86.1% and 97.3%,

respectively. These results indicate that CTLV is a capillovirus closely related to ASGV.

1993

9/3,AB/133 (Item 64 from file: 5)
DIALOG(R)File 5:BIOSIS Previews(R)
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09064447 BIOSIS NO.: 199497072817
Overexpression of a truncated growth hormone receptor in the sex-linked dwarf chicken: Evidence for a splice mutation.
AUTHOR: Huang Ning; Cogburn Larry A; Agarwal Sunita K; Marks Henry L; Burnside Joan
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JOURNAL: Molecular Endocrinology 7 (11):p1391-1398 1993
ISSN: 0888-8809
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Sex-linked dwarfism in chickens is a form of GH resistance that resembles the Laron syndrome in humans. The dwarfism found in chickens is due to a mutant gene (dw) carried on the sex chromosome. The homozygous dwarf (dwdw) chicken is characterized by reductions in stature and plasma insulinlike growth factor-I (IGF-I) levels. Despite the absence of hepatic GH-binding activity, Southern blot analysis shows that there is no gross structural change in the gene for the GH receptor (GHR) in this strain of dw dw chicken. GH-dependent IGF-I production can be restored in cultured dw dw hepatocytes after transfection and transient expression of a chicken GHR (cGHR) cDNA, indicating that other factors that participate in GH-mediated IGF-I synthesis are intact. Northern blot analysis of liver, muscle, fat, and pituitary RNA from normal (DwDw) chickens shows a major transcript of 4.3 kilobases (kb) and three minor transcripts (0.8, 1.7, and 3.2 kb), which correspond to the cGHR. In contrast, the 0.8-kb transcript is the major cGHR transcript expressed in these tissues from dw dw chickens. Northern blot analysis with domain-specific probes shows that the 0.8-kb transcript in DwDw and dw dw liver contains only a small portion of the extracellular domain of the cGHR. A cDNA clone encoding this transcript has been isolated from a liver library prepared from a normal chicken. The 0.8-kb transcript corresponds to the first 325 nucleotides of the coding region of the cGHR, followed by a poly(A) tail. The presence of the poly(A) tail in the 0.8-kb transcript of both DwDw and dw dw birds was confirmed by an RNase H protection assay. Sequence analysis of the intron immediately downstream of this cleavage-polyadenylation site shows a T to C mutation of the GT in the 5'-splice donor site. These results suggest that the GHR deficiency of the sex-linked dwarf chicken is due to inappropriate splicing and destabilization of the full-length transcript, which would account for the absence of a functional GHR in these dwarfs.

1993

9/3,AB/134 (Item 65 from file: 5)
DIALOG(R)File 5:BIOSIS Previews(R)
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09062591 BIOSIS NO.: 199497070961
Induction of GLUT1 mRNA in response to inhibition of oxidative phosphorylation.
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JOURNAL: American Journal of Physiology 265 (5 PART 1):pC1224-C1229
1993
ISSN: 0002-9513
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: In previous studies, we have shown that inhibition of oxidative phosphorylation in Clone 9 cells (a nontransformed rat liver cell line) by 5 mM azide results in a marked biphasic stimulation of glucose transport that is mediated by GLUT1 (M. Shetty, J. N. Loeb, and F. Ismail-Beige. Am. J. Physiol. 262 (Cell Physiol. 31): C527-C532, 1992). The late phase of the response (at 8-24 h) is associated with a doubling of cell GLUT1 content and an 8- to 10-fold increment in GLUT1 mRNA abundance. To investigate the mechanisms mediating GLUT1 mRNA induction, we have examined the effect of incubation in the presence of azide on GLUT1 gene transcription. In nuclear run-on assays, the rate of GLUT1 gene transcription was increased 2.5 +/- 0.3-fold in nuclei from cells exposed to azide for 4 h. Additionally, GLUT1 mRNA turnover was decreased in cells treated with azide: upon inhibition of RNA synthesis by actinomycin D, GLUT1 mRNA content decreased with half-lives of 2.3 +/- 0.3 and 8.0 +/- 0.5 h in control cells and cells treated with azide for 4 h, respectively. GLUT1 mRNA half-life was most prolonged (gt 12 h) when azide was added subsequent to the addition of actinomycin D, and the half-life continued to be prolonged (6.5 +/- 0.5 h) in cells exposed to azide for 16 h. Pulse-chase experiments employing (3H)uridine revealed that the half-life of poly(A)+ RNA was the same (apprx 12 h) in control and azide-treated cells, suggesting that, in contrast to the stabilization of GLUT1 mRNA, a generalized stabilization of cell mRNAs does not result from exposure to azide. These results indicate that the increase in GLUT1 mRNA content in response to exposure to azide is mediated by an enhancement of GLUT1 gene transcription as well as a specific stabilization of GLUT1 mRNA.

1993

9/3,AB/135 (Item 66 from file: 5)
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09021830 BIOSIS NO.: 199497030200
Cloning and structural analysis of four genes encoding interferon-omega in rabbit.
AUTHOR: Charlier Madia(a); L'Haridon Rene; Boissard Monique; Martal Jacques
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JOURNAL: Journal of Interferon Research 13 (5):p313-322 1993
ISSN: 0197-8357
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: By using an ovine interferon-tau (IFN-tau) cDNA probe, four recombinant phages were isolated from a rabbit genomic library and sequenced from nucleotides -450 to 1,300 relative to the CAP site. Each of the four rabbit genes contains an open reading frame of 595 nucleotides and code for proteins that exhibit structural characteristics of the interferon-omega (IFN-omega) family. They display more than 98% identity in their coding regions. The deduced amino acid sequences share gt 96% sequence similarity. In contrast, the 5' and 3' noncoding

regions have diverged considerably (approx 50% identity). Amino acid comparisons of rabbit IFN-omega with IFN-omega of other species reveal the highest degree of identity with human (72%), followed by porcine (68%) IFN-omega. Rabbit IFN-omega displays only 57% sequence similarity with ovine IFN-tau. The coding regions of the four genes subcloned in a cytomegalovirus eukaryotic expression vector and transfected in monkey COS-7 cells direct the production of proteins that protect bovine and rabbit cells against vesicular stomatitis virus infection, thus demonstrating that these genes encode fully active IFN proteins. The expression of these genes was studied in Sendai-induced rabbit leukocytes. A single band of **poly(A)**+RNA hybridized with a rabbit IFN-omega probe under stringent conditions, whereas no IFN-omega transcript was detected with RNA isolated from uninduced leukocytes. Southern blot analyses suggest the existence of at least eight IFN-omega genes or pseudogenes in the rabbit genome.

1993

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09004610 BIOSIS NO.: 199497012980
 Energetics of arginine-4 substitution mutants in the N-terminal cooperativity domain of T4 gene 32 protein.
 AUTHOR: Villemain Jana L; Giedroc David P(a)
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 JOURNAL: Biochemistry 32 (41):p11235-11246 1993
 ISSN: 0006-2960
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: Gene 32 protein (gp32) from bacteriophage T4 is a sequence-nonspecific single-strand (ss) nucleic acid binding protein which binds highly cooperatively to ss nucleic acids. The N-terminal "B" or basic domain (residues 1-21) is known to be required for highly cooperative binding by gp32 (where $K_{app} = K_{int} \cdot \omega$, ω gtoreq 500), since its removal results in a protein which binds ss nucleic acids noncooperatively ($\omega = 1$). In this paper, we probe the molecular details of cooperative binding by gp32 by physicochemical characterization of a set of four single amino acid substitution mutants of Arg-4: Lys-4 (R4K gp32), Gln-4 (R4Q gp32), Thr-4 (R4T gp32), and Gly-4 (R4G gp32). The qualitative ranking of binding affinities to **poly(A)** is wild-type gtoreq R4K gt R4Q gt R4T gt R4G gt gp32-B (gp32 lacking the first 21 amino acids). The occluded site size is $n_{pp} = 7.5 \pm 0.5$ for all gp32s. Resolution of K_{int} and ω for wild-type, R4K, R4Q, and R4T gp32s was estimated under conditions of low lattice saturation (v ltoreq 0.011) using multiple reverse fluorescence titrations collected at 10 mM Tris-HCl, pH 8.1, 20 degree C, and a NaCl concentration where K_{app} was (2-4) times 10^{-6} M-1 for each gp32 on the ribohomopolymer **poly(A)**. Binding parameters for all gp32s were obtained directly or compared by conservative extrapolation of the (NaCl) dependence of K_{app} to 0.20 M NaCl, 20 degree C, pH 8.1. The magnitude of ω was then assumed not to vary with (NaCl) (shown for R4T gp32), allowing estimation of K_{int} at 0.20 M NaCl. We find that R4K gp32 binds to **poly(A)** with an overall affinity (K_{app}) which is 2-3-fold lower than wild-type gp32, while ω for each molecule seems indistinguishable (wild-type gp32, ω apprxeq 800-1300; R4K gp32, ω apprxeq 600-1200). Surprisingly, R4Q gp32 is characterized by an ω also not readily distinguishable from the wild-type and R4K proteins (ω apprxeq 800-4400), while K_{app}

is reduced about 10-fold. This mutant also shows a significantly reduced (NaCl) dependence of the binding to poly(A). R4T gp32 binds about 10-fold weaker than the Q mutant. It exhibits an omega ranging from 300 to 700 and a substantially reduced (NaCl) dependence ($\Delta \log K_{int}/\Delta \log (NaCl) = -1.4$ from 0.10 to 0.20 M NaCl), indicative of significant perturbations in both K_{int} and w terms. R4G gp32 binds with a K_{app} about 20-fold reduced from R4T gp32, with most of this difference at 0.20 M NaCl apparently residing in the omega term (omega approx 5-35 from multiple titrations). Finally, gp32-B appears to bind with a approx 10-fold lower affinity than R4G gp32, consistent with the finding of residual cooperativity in R4G gp32. The overall trend in equilibrium affinities of mutant gp32s for poly(A) parallels their relative helix-destabilizing activities as measured with the partially double-stranded alternating DNA copolymer poly(d(A-T)). We conclude that the positive charge of Arg-4 is critical for maintenance of cooperative binding and helix-destabilizing activity of gp32 in a manner which is dependent upon the nature of the substitution. Further, these substitutions appear to give rise to a more deleterious effect on the (NaCl) dependence and overall affinity of gp32 for single-stranded nucleic acids than might have been anticipated from the loss of a single side chain in the N-terminal domain.

1993

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08993140 BIOSIS NO.: 199497001510

Aortic smooth muscle contains guanylate-cyclase-coupled 130-kDa atrial natriuretic factor receptor as predominant receptor form: Spontaneous switching to 60-kDa C-receptor upon cell culturing.

AUTHOR: Abe Tetsuaki; Nishiyama Kozo; Snajdar Rudolf; He Xiaolan; Misono Kunio S(a)

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JOURNAL: European Journal of Biochemistry 217 (1):p295-304 1993

ISSN: 0014-2956

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Photoaffinity labeling of atrial natriuretic factor (ANF) receptor in the plasma membranes from bovine aortic smooth muscle tissue using N-alpha-5-(4-azidobenzoyl)-ANF-(5-28)-peptide labeled with ¹²⁵I yielded a 130-kDa band. However, when smooth muscle cells from the same bovine aorta were placed in culture, the 130-kDa receptor quickly disappeared and a 60-kDa band began to appear at high density. After three passages, essentially no 130-kDa band was found and only the 60-kDa band was strongly labeled. The primary structures of the two receptor forms were compared by radiochemical peptide mapping after endoprotease Glu-C digestion of photoaffinity-labeled and detergent-solubilized 130-kDa receptor from the aorta or the 60-kDa receptor from the cultured cells. The peptide mapping showed courses of digestion that were significantly different from each other, suggesting difference in their primary structures. The basal guanylate cyclase activity in the aortic membranes was 1.0 pmol cGMP produced cntdot min⁻¹ cntdot mg protein⁻¹ at 37 degree C using Mn-2+-GTP as substrate. The corresponding activity in the membranes from the cultured cells was 20 fmol cGMP cntdot min⁻¹ cntdot mg protein⁻¹. Binding studies gave a density of binding sites (B-max) of 82 fmol/mg protein for the aortic membranes and 850 fmol/mg protein for the cultured cell membranes. These data suggest that the major form of ANF receptor in the cultured cells, namely the 60-kDa

receptor, lacked guanylate cyclase activity. Northern blot analysis of poly(A)-RNA extracted from bovine thoracic aorta or adrenal cortex gave a single 3.6-kb band when 32P-labeled human A-type ANF receptor cDNA was used as a hybridization probe. However, no band was detected when C-receptor cDNA was used as a probe. In addition to the major 130-kDa band, extended SDS/PAGE revealed two additional faint bands with estimated molecular masses of 126 kDa and 135 kDa. Treatment with endoglycosidase H resulted in disappearance of the 126-kDa band and appearance of a 100-kDa band. The 130-kDa and 135-kDa bands were unchanged. Treatment by endoglycosidase F or glycopeptidase F reduced all three bands to a single 100-kDa band. These results suggest that the slight difference in mobility is due to different states of glycosylation. Competitive protection experiments showed binding specificity in the order of ANF > BNP > mchgt > CNP, AP-I for all three bands, indicating that the state of glycosylation had no effect on the ligand specificity. Photoaffinity labeling of bovine adrenal cortex membranes gave a single 130-kDa band. The same experiment with lung membranes yielded a 130-kDa band and a 60-kDa band at about 1:1 ratio. The data presented in this report indicate that the vascular smooth muscle contains predominantly the 130-kDa guanylate-cyclase-coupled ANF receptor in vivo, and that C-receptors found in cultured vascular smooth muscle cells have been induced artificially from cell culturing.

1993

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08992656 BIOSIS NO.: 199497001026
Thermodynamics of single-stranded RNA and DNA interactions with oligolysines containing tryptophan: Effects of base composition.
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JOURNAL: Biochemistry 32 (40):p10568-10579 1993
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RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have examined the thermodynamics of binding of a series of oligolysines (net charge $z = +2$ to $+10$) containing one, two, or three tryptophans to several single-stranded (ss) homo-polynucleotides (poly(A), poly(C), poly(I), poly(dU), poly(dT)) and duplex (ds) DNA in order to investigate the effects of peptide charge, tryptophan content, and polynucleotide base and sugar type. Equilibrium association constants, K -obs, were measured as a function of monovalent salt concentration (KCH-3CO-2) and temperature by monitoring the quenching of the peptide tryptophan fluorescence upon interaction with the polynucleotides, from which the dependence of DELTA-G degree obs, DELTA-H degree obs, and DELTA-S degree obs, on (KCH-3CO-2) was obtained. As observed previously with poly(U) (Mascotti, D. P., & Lohman, T. M. (1992) Biochemistry 31, 8932), the dependence of AG degree obs on (K+) for peptide binding to each polynucleotide is entirely entropic in origin (i.e., DELTA-H degree obs is independent of (K+)), consistent with the conclusion that K -obs, increases with decreasing salt concentration due to the favorable increase in entropy resulting from the displacement of bound cations (K+) from the nucleic acid upon formation of the complex. For each ss polynucleotide, we find that significantly less than one potassium ion is released thermodynamically per net positive peptide charge, as determined from the value of $v\Delta \log K\text{-obs}/v\Delta \log(K+)$. Interestingly, $(-v\Delta \log K\text{-obs}/v\Delta \log(K+))/z$ decreases with

increasing peptide charge for **poly(A)**, **poly(C)**, and **poly(dT)**, contrary to the behavior observed with **poly(U)** and ds-DNA, which may reflect a significant release of bound water upon formation of peptide complexes with these ss homo-polynucleotides or an increased binding of K⁺ to the ss polynucleotide with increasing (K⁺). Alternatively, there may be conformational differences between the bound states of oligolysines of low charge, relative to oligolysines of higher charge. However, in all cases, peptides with z lt +4 display different thermodynamics of binding than peptides with z **gt** +4. The presence of tryptophan (Trp) within these peptides does not influence the salt dependence of K-obs for binding to **poly(A)**, **poly(C)**, or **poly(dT)**. However, the Trp content of the peptide does contribute significantly to the thermodynamics of these interactions: Trp interactions result in a favorable contribution to DELTA-H degree obs, but an unfavorable contribution to DELTA-S degree obs, with little effect on DELTA-G degree obs, due to entropy-enthalpy compensations. Oligolysines containing Trp also display a small, but significant, dependence of K-obs, on base composition, with K-obs decreasing in the order **poly(I)** mchgt **poly(dT)** appr **poly(U)** appr **poly(A)** mchgt **poly(C)**.

1993

9/3,AB/139 (Item 70 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08932186 BIOSIS NO.: 199396083687

The A-3 adenosine receptor is the unique adenosine receptor which facilitates release of allergic mediators in mast cells.

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JOURNAL: Journal of Biological Chemistry 268 (23):p16887-16890 1993

ISSN: 0021-9258

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Mast cells release the mediators of the immediate hypersensitivity reaction. Adenosine is known to modulate this process, but the receptor responsible for this is not the classical A-1 or A-2 adenosine receptors. This study was undertaken to determine whether the unique adenosine receptor (AR) previously postulated in a cultured mast cell line (RBL-2H3 cells) is the recently cloned A-3AR. The receptors were quantitated by the agonist 1211-labeled APNEA (aminophenylethyladenosine), an A-3AR agonist, which yielded B-max. and K-d values of 826 fmol/mg protein and 34 nm, respectively. A variety of adenosine analogs competed for 125I-APNEA binding sites with the following potency series: (R)-phenylisopropyladenosine = 5'-N-ethylcarboxamide adenosine **gt** (S)-phenylisopropyladenosine. 125I-APNEA binding was relatively insensitive to the xanthine amine congener (XAC, 1 mu-m), a selective antagonist for the AAR. Functionally, activation of these A-3AR stimulated the production of inositol 1,4,5-triphosphate, leading to an increase in the level of intracellular Ca-2+. Furthermore, while activation of these receptors alone produced little secretory response in RBL-2H3 cells, it enhanced antigen-induced secretion by 2-2.5-fold. Northern blotting studies using **poly(A)** RNA from RBL-2H3 cells detected two transcripts of 2.0 and 3.5 kilobases, which hybridized to an A-3AR cDNA but not to the A-1 or A-2AR cDNA probes. These data indicate that the unique AR that potentiates the secretory response to antigen in RBL-2H3 cells is exclusively the A-3AR.

1993

9/3,AB/140 (Item 71 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08899867 BIOSIS NO.: 199396051368

Transcriptional regulation by lovastatin and 25-hydroxycholesterol in HepG2 cells and molecular cloning and expression of the cDNA for the human hepatic squalene synthase.

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JOURNAL: Journal of Biological Chemistry 268 (17):p12818-12824 1993

ISSN: 0021-9258

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Primers, based on the cDNA nucleotide sequences for rat hepatic squalene synthase (EC 2.5.1.21) (McKenzie, T. L., Jiang, G., Straubhaar, J. R., Conrad, D., and Shechter, 1. (1992) J. Biol. Chem. 267,21368-21374), were synthesized and used for the amplification and sequencing of a 1672-base pair (bp) cDNA for the human hepatic squalene synthase (HSS) from human hepatic RNA. An open reading frame of 1251 bp encoding 417 amino acids (M_r = 48,200) was detected for HSS. We have constructed a pHSS 1286 expression vector by molecular cloning of a 1286-bp cDNA, that includes sequences of the entire coding region for HSS, into pBluescript. Expression in Escherichia coli of a functional, full-length HSS was confirmed by immunoblot analysis and enzymatic activity. Northern blot analyses of poly(A⁺) RNA obtained from the human hepatoma cell line HepG2 show three distinct size classes of mRNA for HSS. 1.4-, 1.6- and 2.1-kilobase mRNA were observed. The relative abundance is in the order 1.6 **gt** 1.4 **gt** 2.1 and did not change when the cells were grown in the presence of 25-hydroxycholesterol or lovastatin. The ratio between the level of HSS mRNA in cells grown in the absence and presence of 5 μ -g/ml 25-hydroxycholesterol varies between 8- and 16-fold. This lowering of the mRNA level was observed when the cells were grown in 10% of either full serum or lipid-depleted serum. A 2.7- and 4.0-fold increase of HSS mRNA was observed when HepG2 cells were grown in the presence of 5 μ -g/ml lovastatin in lipid-depleted or full serum, respectively. These studies show that HSS exhibit a relatively high level of transcriptional regulation in response to 25-hydroxycholesterol regardless of the presence of cholesterol in the growth media.

1993

9/3,AB/141 (Item 72 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08899616 BIOSIS NO.: 199396051117

Cloning and expression of a rabbit cDNA encoding a serum-activated ethylisopropylamiloride-resistant epithelial sodium/proton exchanger isoform (NHE-2).

AUTHOR: Tse Chung-Ming(a); Levine Susan A; Yun C H Chris; Montrose Marshall H; Little Peter J; Pouyssegur Jacques; Donowitz Mark

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JOURNAL: Journal of Biological Chemistry 268 (16):p11917-11924 1993

ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A unique Na⁺/H⁺ exchanger isoform, NHE-2, was cloned and characterized. NHE-2 is a protein of 809 amino acids with a calculated size of 90,787. It exhibits overall amino acid identity of 50, 44, and 60% with other cloned mammalian Na⁺/H⁺ exchangers NHE-1, NHE-3, and NHE-4, respectively. Northern blot analysis of **poly(A)** RNA isolated from rabbit ileum, kidney cortex, and kidney medulla using NHE-2 cDNA as a probe revealed messages of 5.2, 4.2, and 3.2 kilobases with relative abundance (in descending order) kidney medulla **gt** kidney cortex **gt** ileum. More detailed tissue distribution of message was performed by ribonuclease protection assay. NHE-2 was predominantly expressed in kidney, intestine, and adrenal gland with a small amount in skeletal muscle and trachea. Stable expression of NHE-2 in PS120 fibroblasts confirmed that NHE-2 is a functional Na⁺/H⁺ exchanger which is defined by amiloride-sensitive Na⁺-dependent alkalization of acid-loaded cells. NHE-2 has the same K_i for amiloride inhibition as NHE-1 (1 μ M) but is 25-fold more resistant to ethylisopropylamiloride inhibition than is NHE-1 (500 versus 20 nM). Like NHE-1, NHE-2 can be activated by serum. Expression of NHE-2 in a polarized human intestinal epithelial cell line, Caco2 cells, results in functional expression of NHE-2 in the apical membrane. Thus, we conclude that NHE-2 is a candidate to be an apical membrane Na⁺/H⁺ exchanger in intestinal and renal epithelial cells.

1993

9/3,AB/142 (Item 73 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08841284 BIOSIS NO.: 199395130635
Purification and characterization of the major 50-kDa repressor protein from cytoplasmic mRNP of rabbit reticulocytes.
AUTHOR: Minich Waldemar B; Maidebura Igor P; Ovchinnikov Lev P(a)
AUTHOR ADDRESS: (a)Inst. Protein Res., Russian Academy Sciences, 142292 Pushchino, Moscow Region**Russia
JOURNAL: European Journal of Biochemistry 212 (3):p633-638 1993
ISSN: 0014-2956
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A 50-kDa protein has been purified to homogeneity from free mRNP of rabbit reticulocytes. This protein, designated as p50, is present within both free mRNP (approximately 4 mol protein/mol globin mRNA) and polyribosomal mRNP (approximately 2 mol protein/mol globin mRNA). p50 is a basic protein (pI approx 9.5) and is characterized by a high glycine content of approximately 20%. Nitrocellulose-filter analysis has shown that p50 interacts with globin mRNA with an association constant of approximately 2.5 times 10⁻⁸ M⁻¹ (100 mM KAc, 4 degree C). Various RNA and polyribonucleotides have the following relative affinity for p50; **poly(G)** **gt** **poly(U)** **gt** globin mRNA approx 16S rRNA **gt** **poly(A)** **gt** **poly(C)**. p50 can be phosphorylated both in vitro and in vivo.

1993

9/3,AB/143 (Item 74 from file: 5)

08835033 BIOSIS NO.: 199395124384

Differential screening in a cDNA-library from spruce for clones associated with forest decline reveals accumulation of ribulose-1,5-bisphosphate carboxylase small subunit mRNA.

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JOURNAL: Journal of Phytopathology (Berlin) 137 (4):p317-343 1993

ISSN: 0931-1785

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English; German

ABSTRACT: In this work we identified mRNA species in spruce (*Picea abies* L., Karst), which are expressed in altered concentration if the symptoms of forest decline are present. A cDNA library was constructed and 'damage-associated' clones were identified by differential screening. A procedure for polyA⁺-RNA preparation from needles of spruce was established which yielded a RNA fraction of sufficient purity for gel electrophoresis, hybridization and most importantly, for reverse transcription and the consecutive steps of molecular cloning. RNA isolated from a symptomless and a damaged tree was combined and a cDNA library in phage lambda gt 10 was constructed. Three series of differential screening were carried out in the first series radioactively labeled cDNA samples were prepared from poly A⁺-RNA from a symptomless tree and a damaged tree. Differential hybridization of 10,000 cDNA clones with the two different samples yielded 37 cDNAs with different levels of hybridization signals. In a second series samples for hybridization tests were prepared from a symptomless and from a damaged tree at three different seasons, July, September, and December. These six different samples were used to search for significant hybridization differences in 2,000 clones. Five clones could be identified which showed hybridization differences independent of the annual season. In a third series, we tried to differentiate between genetic variations of individual trees and differences solely induced by the damage. Two mixed samples were prepared, one from an ensemble of 10 symptomless and one of 10 damaged trees. Six cDNA clones could be identified, which exerted clear differences with the mixed probes from the symptomless ensemble and the damage ensemble, respectively. In Northern hybridizations the cDNA clones could be attributed to mRNAs of well defined length. After sequence analysis of the cDNA clones and homology search in a gene data bank two sequences could be identified. One clone codes for the small subunit of ribulose-1,5-bisphosphate carboxylase (Rubisco SS) and another for the subunit II of photosystem I. By quantitative Northern hybridization a threefold higher concentration of Rubisco SS mRNA could be shown in damaged trees. This is discussed in terms of a higher turnover of this protein in damaged trees because no change (WEIDNER and KRAUS 1987, *Physiol. Plantarum* 70, 664-672) or even a decline of Rubisco activity without a decrease in enzyme concentration (SCHMIEDEN-KOMPALLA et al. 1989, *Photosynth. Res.* 21, 161-169) was found in damaged spruce. The results show that the technique of cDNA cloning and differential hybridization could be established for conifers and that 'damage-associated' cDNA clones could be identified. The features of those clones are discussed in respect to their use in basic research and diagnosis of forest decline.

1993

DIALOG(R)File 5:Biosis Previews(R)
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08807343 BIOSIS NO.: 199395096694

Application of oligo(dT)-30-latex for rapid purification of **poly(A)** positive mRNA and for hybrid subtraction with the in situ reverse transcribed cDNA.

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JOURNAL: Biochimica et Biophysica Acta 1156 (2):p204-212 1993

ISSN: 0006-3002

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The carboxyl groups on the surface of latex beads were linked to amino moiety of cytidine residue of oligo(dC)-10(dT)-30. The resultant latex beads-(dC)-10(dT)-30 showed a very stable suspension and yet is precipitable to a small pellet by centrifugation. These properties merits the oligomer-linked beads to be applied for experiments in which **poly(A)**+ mRNAs are involved. An efficient (gt 95%) hybridization to **poly(A)**+ mRNA occurred in a short reaction period (10 min), and more than 95% of bound mRNAs were recovered from the beads by heating (65 degree C, 5 min) followed by centrifugation. Interestingly, the **poly(A)**+ mRNAs could be transcribed to cDNAs in situ by reverse transcriptase, with the covalently linked oligo(dT)-30 as primers. These properties allowed the oligo(dT)-30-latex to prepare the cDNA covalently bound to latex which was used for mRNA hybrid subtraction. In a model experiment with the mixture of vaccinia virus and HeLa mRNAs, about 200-fold enrichment of vaccinia mRNA species was obtained after four cycles of hybrid subtraction with HeLa cDNA-latex.

1993

9/3,AB/145 (Item 76 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08799090 BIOSIS NO.: 199395088441

Developmental modulation of blood-brain barrier and choroid plexus GLUT1 glucose transporter messenger ribonucleic acid and immunoreactive protein in rabbits.

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AUTHOR ADDRESS: (a)c/o Dr. William M. Pardridge, Dep. Med., Univ.
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JOURNAL: Endocrinology 132 (2):p558-565 1993

ISSN: 0013-7227

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The transport of glucose across the brain capillary endothelium, which makes up the blood-brain barrier (BBB) in vivo, is developmentally up-regulated in the postnatal period, as the brain switches from combustion of circulating ketone bodies to glucose. The principle transporter mediating the uptake of circulating glucose across the BBB is the GLUT1 isoform. To further define molecular mechanisms underlying developmental modulation of the BBB GLUT1 transporter, the amounts of brain microvessel GLUT1 mRNA and immunoreactive protein were quantitated.

In addition, an immunocytochemical analysis of GLUT1 expression at the choroid plexus in developing brain was performed, since this transporter isoform is selectively expressed at the choroid plexus epithelium basolateral membrane. Quantitative Western blotting employing purified human erythrocyte glucose transporter as an assay standard showed that the concentration of immunoreactive GLUT1 protein in 70-day-old rabbit brain microvessels (111 \pm 3 pmol/mg protein) was not significantly different from the concentration of D-glucose-displaceable cytochalasin-B-binding sites (102 \pm 25 pmol/mg protein). Thus, GLUT1 is the principle isoform mediating glucose transport across the developing BBB. Quantitative Western blotting was performed on microvessels isolated from brains of rabbits on postnatal days 1, 14, 28, and 70. The concentrations of immunoreactive microvessel GLUT1 at these four stages of development were 13 \pm 2, 4 \pm 1, 49 \pm 2, and 111 \pm 3 pmol/mg protein, respectively. Capillary depletion analysis showed that essentially all of brain GLUT1 mRNA arises from the microvascular fraction, and Northern analysis of 10 μ -g poly(A)⁺ RNA from brains of rabbits 1, 14, 28, and 70 days postnatally showed a preferential stabilization of the GLUT1 mRNA compared to mRNA for two cytoskeletal proteins, actin and tubulin. Immunocytochemical analysis of immunoreactive GLUT1 in choroid plexus epithelia showed the following developmental modulation of the transporter protein: 1 day lt 14 days lt 28 days gt 70 days. The concentration of immunoreactive GLUT1 at the basolateral membrane of choroid plexus epithelium at 28 days was much greater than the immunostaining of rabbit brain microvessels at the corresponding age. In conclusion, these studies show that immunoreactive GLUT1 protein initially undergoes down-regulation between birth and 14 days and then undergoes marked up-regulation between 14 and 70 days. Conversely, the concentration of GLUT1 mRNA is virtually unchanged in brain of rabbits at 70 vs. 14 days postnatally. These combined data suggest that a principle mechanism underlying the developmental regulation of GLUT1 at the BBB may be posttranscriptional.

1993

9/3,AB/146 (Item 77 from file: 5)
 DIALOG(R)File 5:BIOSIS Previews(R)
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08798931 BIOSIS NO.: 199395088282
 Sensitivity of Xenopus oocytes to changes in extracellular pH: Possible relevance to proposed expression of atypical mammalian GABA-B receptors.
 AUTHOR: Woodward R M(a); Miledi R
 AUTHOR ADDRESS: (a)Dep. Psychobiol., U.C.I, Irvine, CA 92717-4550**USA
 JOURNAL: Molecular Brain Research 16 (3-4):p204-210 1992
 ISSN: 0169-328X
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: Electrical recordings were made to characterize the sensitivity of Xenopus oocytes to changes in extracellular pH, and to determine whether rat cerebral cortex poly(A)⁺ RNA (mRNA) expressed GABA-B receptors with atypical electrical properties. All oocytes showed some sensitivity to changes in pH, and those from a small fraction (lt 10%) of frogs were found to be highly responsive to acidification of bathing Ringer. In these oocytes, reduction in extracellular pH elicited membrane current responses with two components: (1) Smooth, maintained currents, primarily associated with a decrease in K⁺ conductance. (2) Oscillatory Cl⁻ currents, elicited through activation of the phosphoinositide/Ca-2⁺ messenger pathway. Oocytes with highest levels of sensitivity responded to decreases as low as 0.1 pH unit (Ringer pH 7.0 lowered to pH 6.9). Rat cortex mRNA consistently showed strong expression

of membrane current responses mediated by GABA-A, glutamate, kainate, serotonin and acetylcholine (muscarinic) receptors, together with responses mediated by a variety of neuropeptide receptors. In these oocytes, enantiomers of the GABA-B receptor agonist baclofen, at concentrations ranging between 1 μ M and 10 mM (pH 7.0), activated no significant membrane current responses. However, at concentrations **gt** 0.1 mM hydrochloride salts of baclofen caused appreciable acidification of Ringer solutions; for example, 1 mM baclofen lowered pH from 7.0 to 6.0. Thus, when assaying oocytes with high sensitivity to pH, failure to make the necessary re-adjustment could result in apparent baclofen responses that, in reality, are simply due to pH effects alone. Our experiments highlight the need for careful monitoring of pH when assaying oocytes for expression of exogenous receptors, and raise the possibility that previously reported expression of atypical mammalian GABA-B receptors might be unjustified.

1992

9/3,AB/147 (Item 78 from file: 5)
DIALOG(R) File 5:Biosis Previews(R)
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08784358 BIOSIS NO.: 199395073709

Conservation of a 23-kDa human transplantation antigen in mammalian species.

AUTHOR: Price S Russ; Nightingale Maria S; Bobak David A; Tsuchiya Mikako; Moss Joel(a); Vaughan Martha

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JOURNAL: Genomics 14 (4):p959-964 1992

ISSN: 0888-7543

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: A group of transplantation antigens, referred to as tum-antigens, were identified in mouse tumor cells that had been mutagenized to produce variant cells and were recognized by cloned cytolytic T lymphocytes (CTL). Alterations in these variant cells that were recognized by CTL resulted from point mutations in the genes of specific proteins. We have isolated human and bovine cDNA clones that encode the homologs of the mouse tum- antigen P198. This 23.6-kDa protein is highly basic with a predicted pI of 11.55. p23/P198 is highly conserved across mammalian species, with **gt** 94% identity (97% including conservative substitutions) among the human, bovine, and mouse deduced amino acid sequences. The nucleotide sequences of both the coding and 5'- and 3'-untranslated regions from human, bovine, and mouse are also highly conserved with **gt** 88% identity in the coding regions. Hybridization of **poly(A)**+ mRNA from various mammalian sources with cDNA and oligonucleotides specific for the coding region identified two mRNAs of 1.2 and 0.8 kb, whereas probes specific for the 3'-untranslated region between two consensus polyadenylation signals hybridized with the 1.2-kb, but not the 0.8-kb, mRNA. The abundance of the 1.2-kb mRNA relative to that of the 0.8-kb species varied depending upon the cell type. A single predominant transcription initiation site was mapped by primer extension. These studies indicate that this highly basic 23.6-kDa protein is encoded by two major mRNA species that differ only in the length of their 3'-untranslated regions and that the mechanism that gives rises to these two mRNAs, utilization of alternative polyadenylation sites, is conserved across species. Moreover, it appears that the protein product of the p23/P198 gene is under considerable evolutionary pressure to maintain its structural features.

1992

9/3,AB/148 (Item 79 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08772291 BIOSIS NO.: 199395061642
Characterization of the mouse beta-maj globin transcription termination region: A spacing sequence is required between the **poly(A)** signal sequence and multiple downstream termination elements.
AUTHOR: Tantravahi Jogiraju; Alvira Mauricio; Falck-Pedersen Erik(a)
AUTHOR ADDRESS: (a)Dep. Microbiol., W. Randolph Hearst Found., Cornell Univ. Med. Coll., 1300 York Ave., New York,
JOURNAL: Molecular and Cellular Biology 13 (1):p578-587 1993
ISSN: 0270-7306
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: For the majority of mRNA encoding eukaryotic transcription units, there is little or no knowledge of the elements responsible for transcription termination or how they may interact with RNA polymerase. In this report, we have used recombinant adenovirus reporter vectors to characterize the mouse beta-maj globin sequence elements that cause transcription termination. Within the globin 3' termination region, we have identified at least three sequence elements which induce significant levels of transcription termination (gt 50%). The smallest functionally active element (64% termination) is 69 bp in length. The natural arrangement of these elements results in a cumulative termination which is greater than 90%. Recognition of the termination elements by RNA polymerase II depends on the presence of a functional **poly(A)** signal sequence. We demonstrate that efficient transcription termination depends on appropriate spacing between the **poly(A)** signal sequence and the termination element.

1993

9/3,AB/149 (Item 80 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08768112 BIOSIS NO.: 199395057463
Renal hemodynamic effects of exogenously administered adenosine and polyadenylic acid.
AUTHOR: Thompson Carl I(a); Spielman William S
AUTHOR ADDRESS: (a)Dep. Physiology, New York Med. College, Valhalla, NY 10595
JOURNAL: American Journal of Physiology 263 (5 PART 2):pF816-F823
1992
ISSN: 0002-9513
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Steady-state intrarenal arterial infusion of adenosine (Ado) suggests that there may be both afferent and efferent arteriolar actions of Ado. This study attempts to further differentiate vascular sites of action of Ado during an intrarenal infusion of Ado. We measured the filtration fraction (FF) during intrarenal infusion of Ado (33.3 nmol cntdot kg-1 cntdot min-1) in anesthetized dogs to determine its transient actions on renal hemodynamics. FF remained unchanged from preinfusion levels (0.42 +/- 0.01 vs. 0.46 +/- 0.01, respectively) at a time when renal

blood flow (RBF) was significantly decreased ($52 \pm 6\%$ of control). During steady state, RBF was $96 \pm 5\%$ of control, while FF was significantly decreased from control (0.27 ± 0.02). To determine whether vasoconstriction and dilation to Ado are mediated by receptors accessible from intra- or extravascular compartments, two Ado analogues (oligoadenylic acid (oligo (A)), mol wt 5,000, and polyadenylic acid (poly (A)), mol wt **gt** 100,000) were injected into the renal artery, and RBF response was compared with that of Ado. Poly(A) produced a transient vasodilation ($42 \pm 6\%$ increase in RBF), whereas oligo(A) produced a transient vasoconstriction ($25 \pm 5\%$ decrease in RBF). Responses to steady-state infusion of poly(A) ($10 \text{ nmol cntdot kg-1 cntdot min-1}$) were determined in 11 anesthetized sodium-depleted dogs. Poly(A) produced a sustained significant increase in renal vascular resistance was blocked by an intrarenal infusion of the Ado antagonist theophylline ($0.5 \text{ mu-mol cntdot kg-1 cntdot min-1}$, 2.68 ± 0.38 vs. $2.85 \pm 0.38 \text{ ml cntdot g-1 cntdot min-1}$). Glomerular filtration rate was not significantly changed during the infusion of poly(A) (0.92 ± 0.08 vs. $0.97 \pm 0.10 \text{ ml g-1 cntdot min-1}$). Poly(A) had no effect on the basal release of renin (182 ± 64 vs. $138 \pm 53 \text{ ng angiotensin I cntdot h-1 cntdot min-1}$). We conclude that Ado produces a preglomerular vasoconstriction and a more slowly developing postglomerular vasodilation, mediated by receptors exposed to the intravascular fluid compartment.

1992

9/3,AB/150 (Item 81 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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08766873 BIOSIS NO.: 199395056224
 Chinese hamster ovary mRNA-dependent, sodium independent L-leucine transport in *Xenopus laevis* oocytes.
 AUTHOR: Su Ti-Zhi; Logsdon Craig D; Oxender Dale(a)
 AUTHOR ADDRESS: (a)Dep. Biological Chem., University Michigan, Ann Arbor, Michigan 48109**ussia
 JOURNAL: Molecular and Cellular Biology 12 (12):p5281-5287 1992
 ISSN: 0270-7306
 DOCUMENT TYPE: Article
 RECORD TYPE: Abstract
 LANGUAGE: English

ABSTRACT: In freshly prepared uninjected folliculated oocytes, Na⁺-independent leucine uptake is mediated predominantly by a system L-like transport system. Removal of follicular cells, however, results in an irreversible loss of this transport activity. When total poly(A)⁺ mRNA derived from Chinese hamster ovary (CHO) cells was injected into prophase-arrested stage V or VI *Xenopus laevis* oocytes, enhanced expression of Na⁺-independent leucine transport was observed. The injected mRNAs associated with increased levels of leucine uptake were between 2 and 3 kb in length. The newly expressed leucine transport activity exhibited important differences from the known characteristics of system L, which is the dominant Na⁺-independent leucine transporter in CHO cells as well as in freshly isolated folliculated oocytes. The CHO mRNA-dependent leucine uptake in oocytes was highly sensitive to the cationic amino acids lysine, arginine, and ornithine (**gt** 95% inhibition). As with leucine uptake, an enhanced lysine uptake was also observed in size-fractionated CHO mRNA-injected oocytes. The uptakes of leucine and lysine were mutually inhibitable, suggesting that the newly expressed transporter was responsible for uptakes of both leucine and lysine. The inhibition of uptake of lysine by leucine was Na⁺ independent, thus clearly distinguishing it from the previously reported endogenous system y⁺ activity. Furthermore, the high sensitivity to

tryptophan of the CHO mRNA-dependent leucine transport was in sharp contrast to the properties of the recently cloned leucine transport-associated gene from rat kidney tissue, although leucine transport from both sources was sensitive to cationic amino acids. Our results suggest that there may be a family of leucine transporters operative in different tissues and possibly under different conditions.

1992

9/3,AB/151 (Item 82 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07543152 BIOSIS NO.: 000091095230
OCCLUSION OF THE HIV **POLY-A** SITE
AUTHOR: WEICHS AN DER GLON C; MONKS J; PROUDFOOT N J
AUTHOR ADDRESS: SIR WILLIAM DUNN SCHOOL PATHOL., UNIV. OXFORD, OXFORD OX1 3RE, UK.
JOURNAL: GENES DEV 5 (2). 1991. 244-253. 1991
FULL JOURNAL NAME: Genes & Development
CODEN: GEDEE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: To investigate the selective use of **poly(A)** sites in the 3' long terminal repeat (LTR) but not the 5' LTR of retroviruses, we have studied the **poly(A)** site of the human immunodeficiency virus (HIV-1). Using hybrid HIV/.alpha.-globin gene constructs, we demonstrate that the HIV **poly(A)** site is inactive or occluded when adjacent to an active promoter, either the homologous HIV promoter or the .alpha.-globin gene promoter. Furthermore, this occlusion of the HIV **poly(A)** site occurs over a considerable distance of up to at least 500 bp. In contrast, two nonretroviral **poly(A)** sites [.alpha.-globin and a synthetic **poly(A)** site] are active when close to a promoter. We also show that a short fragment of .apprx.60 nucleotides containing the HIV **poly(A)** site is fully active when placed at the 3' end of the human .alpha.-globin gene or within the rabbit .beta.-globin gene. This result rules out the requirement of more distant upstream elements for the activity of the HIV **poly(A)** site, as has been suggested for other viral **poly(A)** sites. Finally, we show that the GT-rich downstream region of the HIV **poly(A)** site confers **poly(A)** site occlusion properties on a synthetic **poly(A)** site. This result focuses attention on this more variable part of a **poly(A)** site in retroviruses as a possible general signal for **poly(A)** site occlusion.

1991

9/3,AB/152 (Item 83 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07521762 BIOSIS NO.: 000091084891
GENE EXPRESSION DURING INDUCTION OF SOMATIC EMBRYOGENESIS IN CARROT CELL SUSPENSIONS
AUTHOR: ALEITH F; RICHTER G
AUTHOR ADDRESS: INST. BOT., UNIV. HANNOVER, HERRENHAEUSERSTR. 2, W-3000 HANNOVER 21, FRG.
JOURNAL: PLANTA (HEIDELB) 183 (1). 1991. 17-24. 1991
CODEN: PLANA
RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: We report the identification, via their cDNAs, of genes which are temporarily transcribed during the initiation of somatic embryogenesis in carrot (*Daucus carota* L.) cells cultured in an auxin-free medium. Their expression is roughly associated with the first morphogenetic, or globular, stage. A cDNA library (λ gt 10) was established using poly(A)⁺-rich RNAs from cells deprived of auxin for 8 d. By differential screening a number of clones corresponding to early-induced embryogenic genes were identified. For several a temporary accumulation of the specific mRNA between 6 and 16 d after induction was observed. With regard to the nucleotide sequence and the respective deduced amino-acid sequence, two glycine-rich proteins and a polypeptide with a proline-rich domain were among the products of genes activated at the onset of somatic embryogenesis.

1991

9/3,AB/153 (Item 84 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07377626 BIOSIS NO.: 000091004306
CLONING AND SEQUENCE ANALYSIS OF 3'-TERMINAL REGION OF HUMAN INSULIN
RECEPTOR GENE
AUTHOR: LEE J-H; PARK S-H; PARK J-S
AUTHOR ADDRESS: DEP. CHEM., SEOUL NATIONAL, SEOUL 151-742, KOREA.
JOURNAL: KOREAN BIOCHEM J 23 (3). 1990. 408-411. 1990
FULL JOURNAL NAME: Korean Biochemical Journal
CODEN: KBCJA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The 5 kb long 3'-terminal region of genomic DNA of Human Insulin Receptor (IR) gene was cloned. By the dry-gel hybridization, 4.5-5.5 kb long DNA of EcoRI cut human chromosomal DNA was identified and inserted into λ gt 10 vector. Constructed subgenomic library was screened with synthetic 21 mer probe corresponding to the carboxy terminal. By the partial DNA sequencing about 200 bp in 5 kb genomic DNA, we found the sequence was the same as the published result. We sequenced about 1.3 kb transcription terminal region by the ExoIII deletion method. The result of the sequence analysis showed that the IR gene has AATATA sequence 15 nucleotide upstream of poly(A) site instead of the canonical AATAAA consensus sequence and this may play a role in gene regulation and that in poly(A) downstream region the IR gene has the T-rich, G/T cluster sequence, which was proposed as a element of mRNA processing.

1990

9/3,AB/154 (Item 85 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07355519 BIOSIS NO.: 000090134427
PREDICTED STRUCTURE OF RABBIT AMINO-TERMINAL CALCITONIN AND KATACALCIN
PEPTIDES
AUTHOR: MARTIAL K; MINVIELLE S; JULLIENNE A; SEGOND N; MILHAUD G; LASMOLES
F
AUTHOR ADDRESS: U 113 INSERM, CHU ST. ANTOINE, 27 RUE CHALIGNY, 75571 PARIS
CEDEX 12, FRANCE.
JOURNAL: BIOCHEM BIOPHYS RES COMMUN 171 (3). 1990. 1111-1114. 1990

FULL JOURNAL NAME: Biochemical and Biophysical Research Communications
CODEN: BBRCA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: **Poly A** rich RNA was extracted from rabbit thyroid and cDNA obtained by the action of reverse transcriptase. The cDNA was used to construct a library in lambda **GT 11**. Screening of the library with a radio-labelled probe specific for human calcitonin allowed the isolation of a clone containing an open reading frame with a high homology with human and murine exon 4 of calcitonin/calcitonin gene-related peptide gene. This sequence codes for a typical calcitonin precursor. We deduced the amino acid sequence of rabbit N-terminal peptide, calcitonin and katacalcin.

1990

9/3,AB/155 (Item 86 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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07316863 BIOSIS NO.: 000090096762
SEQUENCE OF COMPLEMENTARY DNAs ENCODING ACTIN DEPOLYMERIZING FACTOR AND COFILIN OF EMBRYONIC CHICKEN SKELETAL MUSCLE TWO FUNCTIONALLY DISTINCT ACTIN-REGULATORY PROTEINS EXHIBIT HIGH STRUCTURAL HOMOLOGY
AUTHOR: ABE H; ENDO T; YAMAMOTO K; OBINATA T
AUTHOR ADDRESS: DEP. BIOL., CHIBA UNIV., YAYOI-CHO, CHIBA 260, JAPAN.
JOURNAL: BIOCHEMISTRY 29 (32). 1990. 7420-7425. 1990
FULL JOURNAL NAME: Biochemistry
CODEN: BICHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Two actin-regulatory proteins of 19 and 20 kDa are involved in the regulation of actin assembly in developing chicken skeletal muscle. They are homologous with actin depolymerizing factor (ADF) and cofilin, a pH-dependent actin-modulating protein, which were originally discovered in chicken and mammalian brain, respectively. In this study, full-length cDNA clones were isolated by screening a .lambda.**gt 11** cDNA library constructed from **poly(A+)** RNA of embryonic chicken skeletal muscle with the antibodies specific for each protein, and their complete sequences were drained. The chicken cofilin cDNA encoded a protein of 166 amino acids, the sequence of which had over 80% identity with that of porcine brain cofilin. The amino acid sequence of the ADF was 165 amino acids and showed about 70% identity with either chicken or mammalian cofilin, in spite of the fact that ADF and cofilin are functionally distinct. Like chicken and mammalian cofilin, ADF contained a sequence similar to the nuclear transport signal sequence of SV40 large T antigen. ADF and cofilin shared a hexapeptide identical with the amino-terminal sequence of tropomyosin as well as the regions homologous to other actin-regulatory proteins, including depactin, gelsolin, and profilin. The overall nucleotide sequences and Southern blot analysis of genomic DNA, however, indicated that the two proteins were derived from different genes.

1990

9/3,AB/156 (Item 87 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

06970818 BIOSIS NO.: 000089082577

MOLECULAR CLONING OF THE JAPANESE QUAIL ALPHA A GLOBIN COMPLEMENTARY DNA
AUTHOR: OSHIRO M; EGUCHI Y; TODA T; TAKEI H; NAKASHIMA Y
AUTHOR ADDRESS: DEP. BIOCHEM., UNIV. RYUKYUS, FAC. MED., OKINAWA, JPN.
JOURNAL: ACTA MED NAGASAKI 34 (2-4). 1989. 18-23. 1989
FULL JOURNAL NAME: Acta Medica Nagasakiensia
CODEN: AMNKA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Double stranded cDNA was synthesized using the poly(A)+ RNA of the Japanese quail reticulocytes and ligated into the EcoRI site of .lambda.gt 10 phage DNA. A recombinant phage, .lambda.Q.alpha.G1 was selected by plaque hybridization using a 30 mer synthetic oligonucleotide probe specific to the .alpha. globin gene. The size of the cDNA insert in the recombinant phage DNA was 0.53kb and the restriction map was similar to that of the chicken .alpha. A globin gene. Nucleotide sequencing of the cDNA insert indicated that it contained the entire coding information for the .alpha. A globin.

1989

9/3,AB/157 (Item 88 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06925787 BIOSIS NO.: 000089059180
THE COMPLEMENTARY DNA SEQUENCE OF MOUSE PGP-1 AND HOMOLOGY OF HUMAN CD-44
CELL SURFACE ANTIGEN AND PROTEOGLYCAN CORE-LINK PROTEINS
AUTHOR: WOLFFE E J; GAUSE W C; PELFREY C M; HOLLAND S M; STEINBERG A D;
AUGUST J T
AUTHOR ADDRESS: DEP. PHARMACOL. AND MOL. SCI., JOHNS HOPKINS UNIV. SCH. OF
MED., 725 N. WOLFE ST., BALTIMORE, MD. 21205.
JOURNAL: J BIOL CHEM 265 (1). 1990. 341-347. 1990
FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We describe the isolation and sequencing of a cDNA encoding mouse Pgp-1. An oligonucleotide probe corresponding to the NH2-terminal sequence of the purified protein was synthesized by the polymerase chain reaction and used to screen a mouse macrophage .lambda. gt 11 library. A cDNA clone with an insert of 1.2 kilobases was selected and sequenced. In northern blot analysis, only cells expressing Pgp-1 contained mRNA species that hybridized with this Pgp-1 cDNA. The nucleotide sequence of the cDNA has a single open reading frame that yields a protein-coding sequence of 1076 base pairs followed by a 132-base pair 3'-untranslated sequence that includes a putative polyadenylation signal but no poly(A) tail. The translated sequence comprises a 13-amino acid signal peptide followed by a polypeptide core of 345 residues corresponding to an Mr of 37,800. Portions of the deduced amino acid sequence were identical to those obtained by amino acid sequence analysis from the purified glycoprotein, confirming that the cDNA encodes Pgp-1. The predicted structure of Pgp-1 includes an NH2-terminal extracellular domain (residues 14-265), a transmembrane domain (residues 266-286), and a cytoplasmic tail (residues 287-358). Portions of the mouse Pgp-1 sequence are highly similar to that of the human CD44 cell surface glycoprotein implicated in cell adhesion. The protein also shows sequence similarity to the proteoglycan tandem repeat sequences found in cartilage link protein and cartilage proteoglycan core protein which are thought to be involved in binding to hyaluronic acid.

1990

9/3,AB/158 (Item 89 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06844542 BIOSIS NO.: 000089003734
CHICKEN EGG WHITE CYSTATIN MOLECULAR CLONING NUCLEOTIDE SEQUENCE AND TISSUE
DISTRIBUTION
AUTHOR: COLELLA R; SAKAGUCHI Y; NAGASE H; BIRD J W C
AUTHOR ADDRESS: BUREAU OF BIOL. RES., RUTGERS UNIV., PISCATAWAY, NEW JERSEY
08855.
JOURNAL: J BIOL CHEM 264 (29). 1989. 17164-17169. 1989
FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A .lambda.gt 11 chicken oviduct cDNA library was screened with a mixed synthetic oligonucleotide corresponding to amino acid residues 81-90 of chicken egg white cystatin, a cysteine proteinase inhibitor. Two initial cDNA clones of 367 and 431 bases were isolated. Both clones contained coding sequences for cystatin from amino acid residue 82 to the carboxyl end plus 3'-untranslated region and a poly(A)+ tail. The two clones utilized different polyadenylation signals located 55 nucleotides apart. Further screening of the library yielded a full-length cystatin cDNA. Sequence analysis indicated that cystatin contains an NH2-terminal extension of 23 amino acids which is probably a signal sequence. The cystatin cDNA hybridized to an mRNA of approximately 0.95 kilobase and was present in varying amounts in all chicken tissues examined. The highest concentration was found in the lung. Gizzard, brain, and heart contained lesser amounts of cystatin mRNA but considerably higher than oviduct. Among a limited number of embryonic tissues examined, significantly higher levels of the mRNA were found in liver and heart tissues when compared with the corresponding adult tissues. These results suggested that the expression of the chicken cystatin gene is tissue-dependent and under developmental control.

1989

9/3,AB/159 (Item 90 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

06764101 BIOSIS NO.: 000088073534
DEFINITION OF AN EFFICIENT SYNTHETIC POLYADENYLIC ACID SITE
AUTHOR: LEVITT N; BRIGGS D; GIL A; PROUDFOOT N J
AUTHOR ADDRESS: SIR WM. DUNN SCH. PATHOL., UNIV. OXFORD, OXFORD, OX1 3RE
UK.
JOURNAL: GENES DEV 3 (7). 1989. 1019-1025. 1989
FULL JOURNAL NAME: Genes & Development
CODEN: GEDEE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We constructed and analyzed a synthetic poly(A) (SPA) site that was based on the highly efficient poly(A) signal of the rabbit .beta.-globin gene. By use of the SPA, we demonstrate that the minimum sequences required for efficient polyadenylation are the AATAAA sequence and a GT/T-rich sequence with the correct spacing of 22-23 nucleotides between them. When placed downstream of the poly(

A) site of the human .alpha.2-globin gene, the SPA is used exclusively. We predict that the SPA, with its more extensive GT/T-rich sequence, is a more efficient poly(A) site than .alpha.-globin. Also, we compared the use of the SPA when it is placed either in the exon 3 or intron 2 of the rabbit .beta.-globin gene. When in the exonic position, SPA is used 10-fold more than the regular poly(A) site of rabbit .beta.-globin. In contrast, when it is in the intronic location, no detectable use of SPA is observed; however, the deletion of the donor site of intron 2 reactivates the intronic positioned SPA. These results indicate that the splicing of intron 2 in the rabbit .beta.-globin gene occurs ahead of polyadenylation and have important implications for termination of transcription. Polyadenylation, although required for termination of transcription, is not sufficient; therefore, additional termination signals for RNA polymerase II must exist.

1989

9/3,AB/160 (Item 91 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06736209 BIOSIS NO.: 000088045638
MOLECULAR ANALYSIS OF PLECKSTRIN THE MAJOR PROTEIN KINASE C SUBSTRATE OF PLATELETS
AUTHOR: TYERS M; HASLAM R J; RACHUBINSKI R A; HARLEY C B
AUTHOR ADDRESS: DEP. BIOCHEM., MCMASTER UNIV., HAMILTON, ONTARIO, CAN. L8N 3Z5.
JOURNAL: J CELL BIOCHEM 40 (2). 1989. 133-146. 1989
FULL JOURNAL NAME: Journal of Cellular Biochemistry
CODEN: JCEBD
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Activation of protein kinase C (PKC) in platelets causes the immediate phosphorylation of pleckstrin, an apparent Mr 40-47,000 protein previously called 40K or P47. Pleckstrin presumably plays an important but as yet unknown role in mediating cellular responses evoked by agonist-induced phosphoinositide turnover. We have cloned the cDNA for pleckstrin from the HL-60 human promyelocytic leukemia cell line by immunological screening of a .lambda.gt 11 expression library (Tyers et al.: Nature 333:470-473, 1988) and now report further analysis of the pleckstrin sequence. Pleckstrin has a deduced Mr of 40,087 and is encoded by a 1,050-bp open reading frame which is preceded by a short open reading frame that terminates before the correct initiator methionine. A single polymorphic site was found in the coding region. An unusual pattern of sequence heterogeneity occurred about a poly(A) tract in the 3' untranslated region. The 3.0-kb pleckstrin mRNA induced upon differentiation of HL-60 cells apparently has heterogeneous 5' ends which undergo differential regulation during HL-60 cell maturation. Analysis by multiple sequence alignment with known PKC substrates identified a strong candidate site for phosphorylation by PKC and a potential Ca2+-binding Ef-hand motif. No other similarities to protein in current databases were found.

1989

9/3,AB/161 (Item 92 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06650466 BIOSIS NO.: 000087092643

RAT LIVER MITOCHONDRIAL AND CYTOSOLIC FUMARASES WITH IDENTICAL AMINO ACID SEQUENCES ARE ENCODED FROM A SINGLE GENE
AUTHOR: SUZUKI T; SATO M; YOSHIDA T; TUBOI S
AUTHOR ADDRESS: DEP. BIOCHEM., YAMAGATA UNIV. SCH. MED., YAMAGATA, 990-23, JAPAN.
JOURNAL: J BIOL CHEM 264 (5). 1989. 2581-2586. 1989
FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: By use of anti-cytosolic fumarase antibody, a cDNA clone was isolated from a rat liver cDNA library in the expression vector .lambda. gt 11 and in the pBR 322 vector. A clone with an insert of about 1.7 kilobases was isolated. Nucleotide sequence analysis of the insert revealed that the cDNA contained a 5'-noncoding region of 25 nucleotides, the coding region of 1,521 nucleotides, and a 3'-nontranslated region of 43 nucleotides followed by a poly(A)+ tail. The open reading frame encoded a polypeptide of 507-amino acid residues (predicted Mr = 54,462), which contained an additional sequence of 41-amino acid residues on the NH2 terminus of the mitochondrial mature fumarase (the presequence). Thus, this reading frame was concluded to encode the precursor of mitochondrial fumarase. The amino acid sequence predicted from the nucleotide sequence contained all the amino acid sequences of 12 proteolytic polypeptides produced by digestion of purified mitochondrial fumarase with V8 protease. The total amino acid sequence of the mitochondrial fumarase also contained all the sequences of 14 proteolytic peptides obtained from the cytosolic fumarase, indicating that the amino acid sequences of these two isozymes are identical. Furthermore, the results obtained by hybrid-selected translation, Northern and Southern blot, and primer-extension analyses using appropriate cDNA segments prepared with fumarase cDNA (1.7 kilobases) as a probe or primer suggested that the mitochondrial and cytosolic fumarases with identical amino acid sequences are encoded from a single gene and a possibility that the precursors of both these fumarases were synthesized by one species of mRNA having a base sequence coding the presequence of the mitochondrial fumarase by some unknown post-transcriptional mechanisms(s).

1989

9/3,AB/162 (Item 93 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06578674 BIOSIS NO.: 000087020835
REDUCTION OF TURGOR INDUCES RAPID CHANGES IN LEAF TRANSLATABLE RNA
AUTHOR: GUERRERO F D; MULLET J E
AUTHOR ADDRESS: DEP. BIOCHEM. AND BIOPHYSICS, TEXAS A AND M UNIV., COLLEGE STATION, TEX. 77843-2128.
JOURNAL: PLANT PHYSIOL (BETHESDA) 88 (2). 1988. 401-408. 1988
FULL JOURNAL NAME: Plant Physiology (Bethesda)
CODEN: PLPHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The turgor of pea (*Pisum sativum*) leaves was reduced by exposing excised pea shoots in a stream of 23.degree.C air for 20 min. Poly(A)+ RNA was isolated from control and wilted shoots, translated in vitro and radiolabeled translation products separated by electrophoresis on two-dimensional (isoelectric focusing-sodium dodecyl sulfate) polyacrylamide gels. This analysis showed that the levels of several poly(A)+ RNAs increased in wilted plants. Most of the

poly(A)+ RNAs induced in wilted plants did not accumulate in response to heat shock or exogenously applied ABA even though endogenous ABA levels were found to increase in shoots 30 min after wilting and by 4 h increased 50-fold (1 versus 0.02 microgram per gram fresh weight). A **.lambda.gt** 10 cDNA library was constructed using **poly(A)**+ RNA from wilted shoots which had been incubated for 4 hours. Differential screening of the library identified four clones corresponding to **poly(A)**+ RNAs which are induced in wilted shoots.

1988

9/3,AB/163 (Item 94 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06268126 BIOSIS NO.: 000086102309
A NEW FAMILY OF TRANSPOSABLE SEQUENCES FROM DROSOPHILA-MELANOGASTER
AUTHOR: VASHAKIDZE R P; MZHAVIYA N Z; KOLCHINSKII A M; ANAN'EV E V
AUTHOR ADDRESS: INST. MOL. BIOL. BIOL. PHYS., ACAD. SCI. GEORGIAN SSR,
TBILISI 380060, USSR.
JOURNAL: MOL BIOL (MOSC) 22 (2). 1988. 362-368. 1988
FULL JOURNAL NAME: Molekulyarnaya Biologiya (Moscow)
CODEN: MOBIB
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

ABSTRACT: Clone Dm A89 was obtained upon cloning of DNA fragments coding abundant **poly(A)**+RNA's of D. melanogaster. Dm A89 was identified as a new transposable element using in situ hybridization with polytene chromosomes of two independent highly isogenic lines of D. melanogaster oregon RC and **gt** wa Dm A89 hybridizes with approximately 20 sites in each line. A portion of Dm A89 is homologous to the distal part of type I ribosomal gene insertion sequence and is highly repetitive. Two other sections of the clone have much less redundancy. The unity of the three fragments is not causal, as revealed by cloning of some other genomic sequences homologous to Dm A89. Dm A89 is actively transcribed throughout the development of D. melanogaster and produces polyadenylated RNA 1,1 kb long.

1988

9/3,AB/164 (Item 95 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06212129 BIOSIS NO.: 000086046311
RIBOSOMAL AND POLYADENYLATED RNA CONTENT OF RUBBER TREE LATEX ASSOCIATION
WITH SUCROSE LEVEL AND LATEX PH
AUTHOR: TUPY J
AUTHOR ADDRESS: INST. EXP. BOT., CZECHOSLOVAK ACAD. SCI., VLTAVSKA 17,
CS-150 00 PRAHA 5, CZECH.
JOURNAL: PLANT SCI (SHANNON) 55 (2). 1988. 137-144. 1988
FULL JOURNAL NAME: Plant Science (Shannon)
CODEN: PLSCE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: **Poly(A)** content of latex polysomes in tapped Hevea [brasiliensis] trees of different age and clonal origin varied from 0.1 .mu.g to 0.5 .mu.g ml-1 latex cytosol indicating **poly(A)**+RNA levels of 1.5 .mu.g-7.5 .mu.g ml-1 and between 3% and 7.5% in proportion

to rRNA. The level of rRNA was in the range 43 .mu.g-120 .mu.g ml⁻¹. The poly(A)+RNA exhibited a polydisperse sedimentation pattern with prominent peaks at 16 S, 20 S and 24 S, and an apparent mean size of 2270 nucleotides. Clonal differences in rRNA were significant and within different clonal trials were associated with variations in the level of latex sucrose and in latex pH suggesting an association with the activity of latex glycolysis. Level of polysomal poly(A), also in proportion to rRNA, was significantly higher in clone PB 217 than in clones GT 1 and PB 235 exhibiting much lower sucrose content of latex. Bark treatment with ethephon increasing latex pH, sucrose utilization and latex yield increased the levels of rRNA and particularly of poly(A)+RNA. This increase did not result in an increase of soluble proteins and may thus be concerned with synthesis of proteins bound to latex structures. Low levels of polysomes for cytoplasmic structure formation may be involved in association of low sucrose with latex vessel senescence.

1988

9/3,AB/165 (Item 96 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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06126783 BIOSIS NO.: 000085089935
 CLONING AND SEQUENCING OF COMPLEMENTARY DNA ENCODING ALPHA AND BETA
 SUBUNITS OF HUMAN PYRUVATE DEHYDROGENASE
 AUTHOR: KOIKE K; OHTA S; URATA Y; KAGAWA Y; KOIKE M
 AUTHOR ADDRESS: DEP. PATHOL. BIOCHEM., ATOMIC DIS. INST. NAGASAKI UNIV.
 SCH. MED., NAGASAKI 852, JPN.
 JOURNAL: PROC NATL ACAD SCI U S A 85 (1). 1988. 41-45. 1988
 FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
 United States of America
 CODEN: PNASA
 RECORD TYPE: Abstract
 LANGUAGE: ENGLISH

ABSTRACT: The cDNAs encoding fragments of the .alpha. and .beta. subunits (PDH.alpha. and PDH.beta.) of human pyruvate dehydrogenase (PDH, EC 1.2.4.1) were isolated from a HeLa cell cDNA library in the .lambda.gt11 expression vector by immunoscreening. Phage cDNA fragments were subsequently used to screen a human foreskin cDNA library by colony hybridization. Nucleotide sequence analyses of the positive plasmid clones (pHPDA and pHPDB) revealed an insert of 1.36 kilobases (kb) for PDH.alpha. and one of 1.69 kb for PDH.beta., respectively, allowing us to predict the complete amino acid sequences of the precursor and mature proteins of these two subunits. A putative leader sequence of 29 amino acid residues was identified in pHPDA, resulting in a precursor protein of 392 amino acid residues (Mr 43,414) and a mature protein of 363 residues (Mr 40,334). A similar leader sequence of 30 amino acid residues in pHPDB was also identified, resulting in a precursor protein of 359 amino acid residues (Mr 39,046) and a mature protein of 329 residues (Mr 35,911). The amino acid sequences of NH2-terminal regions of the two subunits of human PDH were highly homologous with those of mature porcine PDH. The amino acid sequences of phosphorylation sites determined in PDH.alpha. of bovine and porcine enzymes were also conserved in the human PDH.alpha.. Blot analysis of HeLa cell poly(A)+ RNA showed a single mRNA of 1.8 kb for PDH.alpha. and 1.7 kb for PDH.beta., respectively. The precursor proteins of PDH.alpha. and PDH.beta. were detected by immunoprecipitation from an 35S-labeled cell-free translation system.

1988

9/3,AB/166 (Item 97 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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05623878 BIOSIS NO.: 000083097019
CLONING OF A HUMAN LIVER MICROSOMAL UDP-GLUCURONOSYLTRANSFERASE
COMPLEMENTARY DNA
AUTHOR: JACKSON M R; MCCARTHY L R; HARDING D; WILSON S; COUGHTRIE M W H;
BURCHELL B
AUTHOR ADDRESS: DEP. BIOCHEMISTRY, UNIV. DUNDEE, DUNDEE DD1 4HN, SCOTLAND,
U.K.
JOURNAL: BIOCHEM J 242 (2). 1987. 581-588. 1987
FULL JOURNAL NAME: Biochemical Journal
CODEN: BIJOA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A cDNA clone (HLUG 25) encoding the complete sequence of a human liver UDP-glucuronosyltransferase was isolated from a .lambda.gt 11 human liver cDNA library. The library was screened by hybridization to a partial-length human UDP-glucuronosyltransferase cDNA (pHUDPGT1) identified from a human liver pEX cDNA expression library by using anti-UDP-glucuronosyltransferase antibodies. The authenticity of the cDNA clone was confirmed by hybrid-select translation and extensive sequence homology to rat liver UDP-glucuronosyltransferase cDNAs. The sequence of HLUG 25 cDNA was determined to be 2104 base-pairs long, including a poly(A) tail, and contains a long open reading frame. The possible site of translation initiation of this sequence is discussed with reference to a rat UDP-glucuronosyltransferase cDNA clone (RLUG 38).

1987

9/3,AB/167 (Item 98 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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05612635 BIOSIS NO.: 000083085776
ISOLATION AND CHARACTERIZATION OF COMPLEMENTARY DNA CLONES CONTAINING
SIMPLE SEQUENCES GT-N-CA-N OF ANIMAL GENOME
AUTHOR: TOKARSKAYA O N; DZHUMANOVA E T; KUPRIYANOVA N S; IVANOV P L; RYSKOV
A P
AUTHOR ADDRESS: INST. MOL. BIOL., ACAD. SCI. USSR, MOSCOW USSR.
JOURNAL: MOL GENET MIKROBIOL VIRUSOL 0 (9). 1986. 24-29. 1986
FULL JOURNAL NAME: Molekulyarnaya Genetika Mikrobiologiya i Virusologiya
CODEN: MGMVD
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

ABSTRACT: cDNA clones containing "simple" sequences (GT)n/(CA)n were selected from the cDNA banks of mouse liver and rat brain. Three of such clones were sequenced. In all cases (GT)n/(CA)n repeat was found to be located at the end of the insert. Northern blot hybridization experiments revealed the discrete species of cytoplasmic and polysomal poly(A)+ RNAs harbouring (GU)n and (CA)n sequences.

1986

9/3,AB/168 (Item 99 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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05133690 BIOSIS NO.: 000081091815

THE GENES OF DROSOPHILA-MELANOGASTER CODING FOR ABUNDANT POLYADENYLATED RNA SPECIES THEIR CLONING LOCALIZATION AND EXPRESSION

AUTHOR: KOLCHINSKII A M; VASHAKIDZE R P; ANAN'EV E V; KUPERT E YU; KOROCHKIN L I; MIRZABEKOV A D

AUTHOR ADDRESS: INST. MOL. BIOL., ACAD. SCI. USSR, MOSCOW, USSR.

JOURNAL: MOL BIOL (MOSC) 19 (6). 1985 (RECD. 1986). 1569-1578. 1985

FULL JOURNAL NAME: Molekulyarnaya Biologiya (Moscow)

CODEN: MOBIB

RECORD TYPE: Abstract

LANGUAGE: RUSSIAN

ABSTRACT: Polyadenylated RNA from *D. melanogaster* at different stages of development was labelled in vitro and used for the search of intensively transcribed DNA fragments in the genomic library. RNA was isolated from whole animals at 6 stages: 0-16 h embryos, I, II, III instar larvae, pupae and adults. 66 recombinant plasmids were chosen for further analysis. Fifty two clones are "unique" (less than 5 copies per genome). Thirty eight of them were localized at unique sites on polytene chromosomes. The distribution of these sites is to some extent non-random: the regions 18C-19, 69D-71F, 97, and especially 82D-85B contain a few of them each. Four clones are related to intervened ribosomal genes and hybridize to a number of pericentromeric sites. Seven clones hybridize essentially with chromocenter. Three cloned fragments belong to mobile dispersed genes (mdg). They were indentified using in situ hybridization with two independent highly isogenic *D. melanogaster* lines, designated Oregon RC and *gt wa*. This approach shows that two of our mdg's are identical to known genes Dm2068 and 101F, and the third is a member of a new family. The steady-state amount of transcripts of the clones studies was evaluated by dot-hybridization with 32P-labelled RNA from different stages. Most of the cloned fragments (not less than 62) are transcribed at a few or all stages studied. Sometimes the pattern of expression shows two peaks. We conclude that most of abundant poly(A)+RNAs are not stage-specific.

1985

9/3,AB/169 (Item 100 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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05064985 BIOSIS NO.: 000081023109

DEMONSTRATION OF TRANSTHYRETIN MESSENGER RNA IN THE BRAIN AND OTHER EXTRAHEPATIC TISSUES IN THE RAT

AUTHOR: SOPRANO D R; HERBERT J; SOPRANO K J; SCHON E A; GOODMAN D S

AUTHOR ADDRESS: DEP. OF MED., COLUMBIA UNIV., COLL. OF PHYSICIANS AND SURGEONS, NEW YORK, NY 10032.

JOURNAL: J BIOL CHEM 260 (21). 1985. 11793-11798. 1985

FULL JOURNAL NAME: Journal of Biological Chemistry

CODEN: JBCHA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Studies were conducted to ascertain if transthyretin mRNA was present in extrahepatic tissues of the rat. A transthyretin cDNA clone was isolated from a λ .gt11 human liver cDNA library by antibody screening and its identity was confirmed by nucleotide sequence analysis. This transthyretin cDNA clone was used to survey poly (A+) RNA isolated from 12 different rat tissues for transthyretin mRNA by Northern blot analysis. The liver contained the highest level of transthyretin mRNA and this level was not altered by the vitamin A status of the rat. A significant amount of transthyretin mRNA was found in the brain (30% of the level of the liver) which was localized in specific

regions of the brain. In addition, detectable levels of transthyretin mRNA (1% to 2% of that of the liver) were observed in the stomach, heart, skeletal muscle, and spleen. Translation of brain poly(A+) RNA in rabbit reticulocyte lysates and immunoprecipitation of the translation products with anti-transthyretin antiserum resulted in a protein band of the same size as liver pre-transthyretin. Liver pre-transthyretin was processed by the cotranslational addition of dog pancreas microsomal membranes to a protein that migrated coincidentally with monomeric serum transthyretin. These data suggest that transthyretin in the brain and the cerebrospinal fluid results from de novo synthesis and that transthyretin may play a significant physiological function, as yet unknown, within the nervous system.

1985

9/3,AB/170 (Item 101 from file: 5)
DIALOG(R) File 5:Biosis Previews(R)
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04746398 BIOSIS NO.: 000080049525
CLONING OF COMPLEMENTARY DNA FOR HUMAN ALDEHYDE DEHYDROGENASES 1 AND 2
EC-1.2.1.3
AUTHOR: HSU L C; TANI K; FUKIYOSHI T; KURACHI K; YOSHIDA A
AUTHOR ADDRESS: DEPARTMENT BIOCHEMICAL GENETICS, BECKMAN RESEARCH INSTITUTE
CITY HOPE, DUARTE, CALIF. 91010.
JOURNAL: PROC NATL ACAD SCI U S A 82 (11). 1985. 3771-3775. 1985
FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America
CODEN: PNASA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Partial c[complementary]DNA clones encoding human cytosolic aldehyde dehydrogenase (ALDH1) and mitochondrial aldehyde dehydrogenase (ALDH2) were isolated from a human liver cDNA library constructed in phage .lambda.gt11. The expression library was screened by using rabbit antibodies against ALDH1 and ALDH2. Positive clones thus obtained were subsequently screened with mixed synthetic oligonucleotides compatible with peptide sequences of ALDH1 and ALDH2. One of the positive clones for ALDH1 contained an insertion of 1.6 kilobase pairs (kbp). The insert encoded 340 amino acid residues and had a 3' noncoding region of 538 bp and a poly(A) segment. The amino acid sequence deduced from the cDNA sequence coincided with the reported amino acid sequence of human ALDH1, except that valine at position 161 in the previous amino acid sequence study was found to be isoleucine in the deduced sequence. Since the amino acid sequence of ALDH2 was unknown, 33 tryptic peptides of human ALDH2 were isolated and sequenced. Based on the amino acid sequence data thus obtained, a mixed oligonucleotide probe was prepared. Two positive clones, .lambda.ALDH2-21 and .lambda.ALDH2-36, contained the same insert of 1.2 kbp. Another clone, .lambda.ALDH2-22, contained an insert of 1.3 kbp. These 2 inserts contained an overlap region of 0.9 kbp. The combined cDNA contained a sequence that encodes 399 amino acid residues, a chain-termination codon, a 3' untranslated region of 403 bp, and a poly(A) segment. The deduced amino acid sequence was compatible with the amino acid sequences of the tryptic peptides. The degree of homology between human ALDH1 and ALDH2 is 66% for the coding regions of their cDNA and 69% at the protein level. No significant homology was found in their 3' untranslated regions.

1985

9/3,AB/171 (Item 102 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

04736589 BIOSIS NO.: 000080039716

ISOLATION OF A COMPLEMENTARY DNA CLONE FOR THE LIVER CELL ADHESION MOLECULE

AUTHOR: GALLIN W J; PREDIGER E A; EDELMAN G M; CUNNINGHAM B A

AUTHOR ADDRESS: ROCKEFELLER UNIVERSITY, 1230 YORK AVENUE, NEW YORK, N.Y.
10021.

JOURNAL: PROC NATL ACAD SCI U S A 82 (9). 1985. 2809-2813. 1985

FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America

CODEN: PNASA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Liver cell adhesion molecule (L-CAM) is a Ca-dependent cell adhesion molecule found in very early vertebrate embryos and on liver and other epithelial cells in adults. To describe the genes coding for the molecule and study its synthesis, c[complementary]DNA from poly(A)+ RNA of 10-day embryonic chicken liver using the .lambda.gt11 expression vector. One clone, .lambda.L301, was characterized and used in analyses of L-CAM mRNA and genomic DNA. Clone .lambda.L301 produced a fusion protein that reacted strongly with polyclonal antibodies that recognize L-CAM (MW 124,000) and its MW 1000 NH2-terminal fragment, Ftl, released from liver membranes by trypsin. .lambda.L301 may contain a cDNA insert complementary to protein coding sequence within the 2/3 of the mRNA coding region beginning at the 5' end. The 220-base-pair cDNA insert was isolated and used as a probe in hybridization experiments. RNA transfer blot analysis of poly(A)+ RNA showed a single 4-kilobase mRNA; Southern blot analysis showed multiple components consistent with the presence of 1-3 L-CAM genes. To test whether different tissues express different forms of L-CAM message, poly(A)+ RNA from 8 embryonic organs was analyzed. Only organs that expressed L-CAM protein contained poly(A)+ RNA that hybridized to the .lambda.L301 probe; in all cases a single band, with the same mobility as that in liver, was observed. The L-CAM mRNA in each tissue was present in proportions similar to those detected previously for the L-CAM protein in these tissues. The combined results suggest that any possible heterogeneity in the L-CAM genes is not reflected in the size of either the mRNA or protein.

1985

9/3,AB/172 (Item 103 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

04353918 BIOSIS NO.: 000078083462

CHARACTERIZATION OF A COMPLEMENTARY DNA CODING FOR HUMAN FACTOR X

AUTHOR: LEYTUS S P; CHUNG D W; KISIEL W; KURACHI K; DAVIE E W

AUTHOR ADDRESS: DEP. BIOCHEM., UNIV. WASH., SEATTLE, WASH. 98195.

JOURNAL: PROC NATL ACAD SCI U S A 81 (12). 1984. 3699-3702. 1984

FULL JOURNAL NAME: Proceedings of the National Academy of Sciences of the
United States of America

CODEN: PNASA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: A .lambda.gt11 c[complementary]DNA library containing DNA inserts prepared from human liver mRNA was screened with an antibody to human factor X, a plasma protein participating in the middle phase of the blood coagulation cascade. Ten positive clones were isolated from 2 x 10⁶ phage and plaque purified. The cDNA in the phage containing the largest

insert was sequenced and shown to code for human factor X. This cDNA insert contained 1137 base pairs coding for a portion of the L chain of the molecule, a connecting region, the H chain, a stop codon, a short 3' noncoding region and a **poly(A)** tail. The sequence of A-T-T-A-A-A, which functions as a potential recognition site for polyadenylation or processing, was present in the 3' end of the coding sequence and preceded the stop codon of TGA by 1 base pair and the **poly(A)** tail by 14 base pairs. The amino acid sequence deduced from the cDNA indicated that factor X is synthesized as a single-chain polypeptide containing the L and H chains connected by an Arg-Lys-Arg tripeptide. The single-chain molecule is then converted to the L and H chains by cleavage of 2 (or more) internal peptide bonds. In plasma, these 2 chains are linked together by a disulfide bond. The DNA sequence coding for the active site of human factor X showed a high degree of identity with prothrombin and factor IX, 2 other vitamin K-dependent Ser proteases that participate in blood coagulation. These data along with the protein sequence data previously published for the L chain of human factor X establish the complete amino acid sequence for the mature protein present in plasma.

1984

9/3,AB/173 (Item 104 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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04313781 BIOSIS NO.: 000078043324
SYNTHESIS OF RAT APO LIPO PROTEIN E BY ESCHERICHIA-COLI INFECTED WITH
RECOMBINANT BACTERIO PHAGE
AUTHOR: DE JONG F A; HOWLETT G; ALDRED A R; FIDGE N; SCHREIBER G
AUTHOR ADDRESS: RUSSELL GRIMWADE SCH. BIOCHEM., UNIV. MELBOURNE, MELBOURNE,
AUSTRALIA.
JOURNAL: BIOCHEM BIOPHYS RES COMMUN 119 (2). 1984. 657-662. 1984
FULL JOURNAL NAME: Biochemical and Biophysical Research Communications
CODEN: BBRCA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A c[complementary]DNA library was constructed from rat liver **poly(A)** RNA using the expression vector .lambda.-gt11-Amp3. Several clones expressing antigenic determinants for rat apolipoprotein E were identified. The cDNA insert in one clone was further characterized and found to have a sufficient length (1120 base pairs) to code for full length apolipoprotein E. Restriction mapping and nucleotide sequencing showed the clone to contain the coding region for apolipoprotein E flanked by about 120 nucleotides at the 3'-side and by about 64 nucleotides on the 5'-side. One of the proteins produced by the clone was found to be a prokaryotic/eukaryotic hybrid protein reacting with antibodies to both bacterial .beta.-galactosidase and rat apolipoprotein E.

1984

9/3,AB/174 (Item 105 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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04305447 BIOSIS NO.: 000078034990
THE CONSERVED 5S RIBOSOMAL RNA COMPLEMENT TO TRANSFER RNA IS NOT REQUIRED
FOR TRANSLATION OF NATURAL MESSENGER RNA
AUTHOR: ZAGORSKA L; VAN DUIN J; NOLLER H F; PACE B; JOHNSON K D; PACE N R
AUTHOR ADDRESS: INST. BIOCHEMISTRY BIOPHYSICS, POLISH ACAD. SCI., WARSAW,

POL.
JOURNAL: J BIOL CHEM 259 (5). 1984. 2798-2802. 1984
FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A putative base-paired interaction between the conserved GT .psi.C sequence of tRNA and the conserved GAAC47 sequence of 5 S ribosomal RNA was tested by in vitro protein synthesis using ribosomes containing deletions in this region of 5 S rRNA. Ribosomes reconstituted with 5 S rRNA possessing a single break between residues 41 and 42, deletion of residues 42-46 or deletion of residues 42-52 were tested for their ability to translate phage MS2 RNA. Initiator tRNA binding, aminoacyl-tRNA binding, ppGpp synthesis and miscoding were also tested. All of the measured functions could be carried out by ribosomes carrying the deleted 5 S rRNA. The sizes and relative amounts of the polypeptides synthesized by MS2 RNA-programmed ribosomes were identical whether or not the 5 S RNA contained deletions. Aminoacyl-tRNA binding and miscoding were essentially unaffected. Significant reduction in ApUpG (but not poly(A,U,G) or MS2RNA)-directed fMet-tRNA binding and ppGpp synthesis were observed, particularly in the case of the larger (residues 42-52) deletion. If tRNA and 5 S rRNA interact in this fashion, it may not be an obligatory step in protein synthesis. [Escherichia coli was used.]

1984

9/3,AB/175 (Item 106 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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03196691 BIOSIS NO.: 000071009802
MULTIPLE DISPERSED DROSOPHILA-MELANOGASTER GENES WITH VARYING LOCALIZATION
4. THE PROPERTIES OF GENE DM-225
AUTHOR: CHURIKOV N A; IL'IN YU V
AUTHOR ADDRESS: INST. MOL. BIOL., ACAD. SCI. USSR, MOSCOW, USSR.
JOURNAL: GENETIKA 16 (3). 1980. 391-401. 1980
FULL JOURNAL NAME: Genetika
CODEN: GNKAA
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

ABSTRACT: The properties of Dm225, a 3-kb fragment of the D. melanogaster genome, was excised by EcoRI endonuclease and cloned in the .lambda. gt phage or pMB9 plasmid. The DNA hybridizes to a significant portion (0.8%) of the total polysomal poly(A)+RNA (mRNA) which is present in the fraction of heavy polysomes. Dm225 DNA fragments obtained using HaeIII endonuclease were mapped. mRNA hybridizes with all the fragments and the 3'-end of the mRNA was localized, allowing determination of the transcription direction. About 250 copies of the gene Dm225 are present in the haploid genome of D. melanogaster and all have the same size upon treatment with EcoRI endonuclease. The sequence of the genome adjacent to Dm225 DNA is different and may vary from one cell line to another, as evidenced by experiments in which D. melanogaster DNA was treated by HindIII endonuclease.

1980

9/3,AB/176 (Item 107 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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02942445 BIOSIS NO.: 000069050563

CLONING AND COMPLETE NUCLEOTIDE SEQUENCE OF MOUSE IMMUNO GLOBULIN GAMMA-1
CHAIN GENE

AUTHOR: HONJO T; OBATA M; YAMAWAKI-KATAOKA Y; KATAOKA T; KAWAKAMI T;
TAKAHASHI N; MANO Y

AUTHOR ADDRESS: DEP. PHYSIOL. CHEM. NUTR., FAC. MED., UNIV. TOKYO, TOKYO,
JPN.

JOURNAL: CELL 18 (2). 1979. 559-568. 1979

FULL JOURNAL NAME: Cell

CODEN: CELLB

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: The 6.6 kb DNA fragment coding for the immunoglobulin .gamma.1 chain was cloned from newborn mouse DNA using .lambda.gt WES .cntdot. B as the EK2 vector. The complete nucleotide sequence (1823 bases) of the .gamma.1 chain gene was determined. The cloned gene contained the entire constant region gene sequence and the poly(A) addition site, but not the variable region gene. The variable and constant region genes of immunoglobulin H chain are apparently separated in newborn mouse DNA. The constant region genes of other .gamma. chains (that is, .gamma.2a, .gamma.2b and .gamma.3) were not present in the cloned DNA fragment. The .gamma.1 chain gene is apparently interrupted by 3 intervening sequences at the junction of the domains and the hinge region, as previously shown in the .gamma.2b and .alpha. chain genes and in the .gamma.1 chain gene cloned from myeloma. The intervening sequence may have been introduced into the H chain gene before divergence of the H chain classes. The hypothesis that the splicing mechanism facilitated the evolution of eukaryotic genes by linking duplicated domains of prototype peptides not directly adjacent to one another is supported. Comparison of the nucleotide sequence of the .gamma.1 chain gene around the boundaries of the coding and intervening sequences with those of other mouse genes revealed extensive divergence, although short prevalent sequences of AGGTCAG at the 5' border of the intervening sequence and TCTGCAG-GC at the 3' border were deduced. A limited homology of nucleotide sequences was found among domains and between the hinge region and the 5' portion of the CH2 domain. Comparison of 3' untranslated sequences from the .gamma.1 and .gamma.2b chain genes and the mouse major .beta.-globin gene shows significant homology and a palindrome sequence surrounding the poly(A) addition site.

1979

9/3,AB/177 (Item 108 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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02425543 BIOSIS NO.: 000066008086

NONSPECIFIC STAINING OF A LACTOBACILLUS-PLANTARUM BY SALMONELLA FLUORESCENT
ANTIBODIES

AUTHOR: THARRINGTON G JR; ASHTON D H; HATFIELD J R; FRY F H

AUTHOR ADDRESS: HUNT-WESSION FOODS INC., 1645 W. VALENCIA DR., FULLERTON,
CALIF. 92634, USA.

JOURNAL: J FOOD SCI 43 (2). 1978 548-552. 1978

FULL JOURNAL NAME: Journal of Food Science

CODEN: JFDSA

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Salmonella fluorescent antibody (FA) positives but cultural negatives were encountered in pasta samples. Salmonella FA positives were caused by an organism identified as a L. plantarum designated strain

GT. Brilliant green incorporated into lactose broth eliminated the false positives. The organism reacted to +3 to +4 with 3 commercially prepared FA Salmonella poly antisera and with staphylococcal, streptococcal and Pseudomonas FA antisera. The organism also agglutinated in response to a variety of non-FA Salmonella polyvalent antisera (poly A-1, poly D, poly C). L. plantarum/**GT** absorption of FA Salmonella poly antiserum resulted in reduction of the false positive reaction from +4 to +1. L. planatrum/**GT** absorption of FA staphylococcal and FA streptococcal antisera resulted in reduction (+4 to +1) in false positive reaction. Fluorescein isothiocyanate (FITC) conjugated normal rabbit immunoglobulin G (IgG) strained L. plantarum/**GT** and Staphylococcus aureus +4, but S. thompson was not stained. FITC alone produced no false positive staining of the 3 test organisms. The FA false positive reaction of L. plantarum/**GT** results not from the organism possessing homologous antigens with Salmonella, but is a consequence of L. plantarum/**GT** cell surface possessing affinity for the nonantigenic region of the IgG molecule in FA antisera. The data suggest the reaction is analogous to the nonspecific affinity between S. aureus cell wall protein A and the nonantigenic Fc portion of the IgG molecule.

1978

9/3,AB/178 (Item 109 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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02344809 BIOSIS NO.: 000065001825
 SELECTION AND SOME PROPERTIES OF RECOMBINANT CLONES OF LAMBDA PHAGES
 CONTAINING STRUCTURAL GENES OF DROSOPHILA-MELANOGASTER
 AUTHOR: IL'IN YU V; CHURIKOV N A; SOLONIN A S; POLUKAROVA L G; GEORGIEV G P
 AUTHOR ADDRESS: INST. MOL. BIOL., ACAD. SCI. USSR, MOSCOW, USSR.
 JOURNAL: MOL BIOL (MOSC) 11 (3). 1977 637-645. 1977
 FULL JOURNAL NAME: Molekulyarnaya Biologiya (Moscow)
 CODEN: MOBIB
 RECORD TYPE: Abstract
 LANGUAGE: RUSSIAN

ABSTRACT: The .lambda.**gt** clones containing fragments of D. melanogaster genome were prepared and characterized by hybridization with complementary RNA synthesized on the .lambda.**gt** DNA, C fragment of .lambda.**gt** DNA and total D. melanogaster DNA, and also with mRNA and a stable cytoplasmic **poly(A)**-RNA both isolated from D. melanogaster cells grown in culture. The technique for a simple selection of hybrid clones is described. The hybridization with mRNA allows the selection of clones containing structural genes of D. melanogaster. The clone contains the structural gene and the reiterated base sequences of the D. melanogaster genome. Several clones containing D. melanogaster DNA fragments of 2-4 .times. 10⁶ daltons hybridized with a relatively large portion of mRNA were selected for further analysis. [Phages were propagated in Escherichia coli].

1977

9/3,AB/179 (Item 110 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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02200233 BIOSIS NO.: 000064042752
 CONFORMATIONAL PROPERTIES OF THE FURANOSE PHOSPHATE BACKBONE IN
 NUCLEIC-ACIDS A CARBON-13 NMR STUDY
 AUTHOR: ALDERFER J L; TS'O P O P

JOURNAL: BIOCHEMISTRY 16 (11). 1977 2410-2416. 1977
FULL JOURNAL NAME: Biochemistry
CODEN: BICHA
RECORD TYPE: Abstract

ABSTRACT: ¹³C NMR spectra of the adenylic acid and uridylic acid series (monomer, dimer and polymer) were obtained either as a function of temperature or pH value. The previous assignments of the C2' and C3' resonances in the spectra of poly(U), poly(A) and in the Np portion of UpU and ApA spectra are interchanged. In the mononucleotides studied, the rotamer distribution of .vphi. (C5'-O5') is not affected by the secondary ionization of the phosphate, but .vphi.' (C3'-O3') is affected by this ionization. The conformation of the backbone in dimers and polymers as revealed by .vphi. and .vphi.' depends both on the base unit and the temperature. Conformation analysis of .vphi. in terms of rotamer distribution was accomplished using the conventional 3-rotamer model, while .vphi.' was analyzed using a nonconventional 2-rotamer model (.vphi.' gt', .vphi.' .apprxeq. 210.degree. .dblarw. tg', .vphi.' .apprxeq. 270.degree.) in rapid equilibrium. A correlation among base-stacking interaction, furanose conformation (C2'-endo .dblarw. C3'-endo), and furanose phosphate conformation (tg' rotamer .dblarw. gt' rotamer for .vphi.'; gg rotamer .dblarw. (tg + gt) rotamer for .vphi.) is demonstrated. The data indicate that a strong base-stacking interaction in ribosyl dinucleoside monophosphates and polynucleotides elicits the C3'-endo (furanose), gt' (.vphi.), and gg (.vphi.) conformations. The observed differences in the comparative study of the uridylic acid and adenylic acid series with respect to the furanose and furanose phosphate backbone conformations clearly delineate the role and the importance of base-base stacking as a major force in determining the backbone conformation of RNA in aqueous solution.

1977

9/3,AB/180 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06966431 Genuine Article#: 109JC Number of References: 9
Title: Rapid degradation of polyadenylated oop RNA (ABSTRACT AVAILABLE)
Author(s): SzalewskaPalasz A; Wrobel B; Wegrzyn G (REPRINT)
Corporate Source: UNIV GDANSK,DEPT BIOL MOL, KLADKI 24/PL-80822
GDANSK//POLAND/ (REPRINT); UNIV GDANSK,DEPT BIOL MOL/PL-80822
GDANSK//POLAND/
Journal: FEBS LETTERS, 1998, V432, N1-2 (JUL 31), P70-72
ISSN: 0014-5793 Publication date: 19980731
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS
Language: English Document Type: ARTICLE
Abstract: The oop RNA is a short (77 nucleotides (nt)) transcript encoded by bacteriophage lambda which acts as an antisense RNA for lambda cII gene expression. Recently we demonstrated that oop RNA is specifically polyadenylated gt its 3' end by poly(A) polymerase I (PAP I), the pcnB gene product. Here we demonstrate that the half life of oop RNA is 3 times longer in the pcnB mutant relative to the pcnB(+) host, indicating that polyadenylation of this transcript causes its accelerated degradation. Although it was proposed that polyadenylation of RNAs in bacteria leads to their enhanced degradation, in most cases stabilization of these molecules was observed only when other mutations (pnp, lab and rpe) were present in the pcnB(-) strain. Therefore it seems that oop RNA may serve as a very useful model in further studies on molecular mechanisms of RNA polyadenylation and degradation in bacteria. Analysis of oop RNA and its degradation product isolated from Escherichia coli cells suggests that both polyadenylated and non-modified oop transcripts can act as antisense RNA. (C) 1998

to encode BADH by their nucleotide and deduced amino acid sequence identity to spinach BADH; these clones showed minor nucleotide sequence differences consistent with their being of two different BADH alleles. The clones averaged 1.7 kb and contained an open reading frame predicting a polypeptide of 500 amino acids with 83% identity to spinach BADH. RNA gel blot analysis of total RNA showed that salinization to 500 mM NaCl increased BADH mRNA levels four-fold in leaves and three-fold in the taproot. DNA gel blot analyses indicated the presence of at least two copies of BADH in the haploid sugar beet genome.

9/3,AB/183 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2003 Inst for Sci Info. All rts. reserv.

00800600 Genuine Article#: EX518 Number of References: 23
Title: OCCLUSION OF THE HIV **POLY(A)** SITE (Abstract Available)
Author(s): GLON CWAD; MONKS J; PROUDFOOT NJ
Corporate Source: UNIV OXFORD, SIR WILLIAM DUNN SCH PATHOL/OXFORD OX1
3RE//ENGLAND/

Journal: GENES & DEVELOPMENT, 1991, V5, N2, P244-253

Language: ENGLISH Document Type: ARTICLE

Abstract: To investigate the selective use of **poly(A)** sites in the 3' long terminal repeat (LTR) but not the 5' LTR of retroviruses, we have studied the **poly(A)** site of the human immunodeficiency virus (HIV-1). Using hybrid HIV/alpha-globin gene constructs, we demonstrate that the HIV **poly(A)** site is inactive or occluded when adjacent to an active promoter, either the homologous HIV promoter or the alpha-globin gene promoter. Furthermore, this occlusion of the HIV **poly(A)** site occurs over a considerable distance of up to at least 500 bp. In contrast, two nonretroviral **poly(A)** sites [alpha-globin and a synthetic **poly(A)** site] are active when close to a promoter. We also show that a short fragment of approximately 60 nucleotides containing the HIV **poly(A)** site is fully active when placed at the 3' end of the human alpha-globin gene or within the rabbit beta-globin gene. This result rules out the requirement of more distant upstream elements for the activity of the HIV **poly(A)** site, as has been suggested for other viral **poly(A)** sites. Finally, we show that the GT-rich downstream region of the HIV **poly(A)** site confers **poly(A)** site occlusion properties on a synthetic **poly(A)** site. This result focuses attention on this more variable part of a **poly(A)** site in retroviruses as a possible general signal for **poly(A)** site occlusion.

9/3,AB/184 (Item 1 from file: 50)
DIALOG(R)File 50:CAB Abstracts
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01948153 CAB Accession Number: 880846896
Characterization of antigens from Schistosoma mansoni and construction of a cDNA library for the study of schistosomiasis.

Bugra, K.

Univ. California, Los Angeles, CA, USA.

Dissertation Abstracts International, B (Sciences and Engineering)

vol. 47 (9): p.3614

Publication Year: 1987

Order Number: 86-29875 --

Language: English

Document Type: Thesis; Journal article

To examine the antigens of adult S. mansoni, 35S-methionine-labelled,

detergent extracted proteins were immunoprecipitated and analyzed on SDS-PAGE. Human infection serum immunoprecipitated 14 polypeptides with MW ranging from 120 000 to 20 000. 5 of the polypeptides in MW range 120 000 to 29 000 had carbohydrate moieties. Extracts of female and male *S. mansoni* were analysed by immunoprecipitation and immunoblotting. 2 polypeptides of MW 86 000 and 54 000 were found in male extracts only. Polyadenylated RNA extracted from *S. mansoni* was also examined. 9 polypeptides of MW ranging from 120 000 to 22 000 were translated and only MW 94 000 and 64 000 were observed in males. Using **poly A (+)** RNA extracts from *S. mansoni* a lambda **gt** II expression library was constructed.

9/3,AB/185 (Item 1 from file: 94)
DIALOG(R)File 94:JICST-EPlus
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01885105 JICST ACCESSION NUMBER: 93A0547560 FILE SEGMENT: JICST-E
Molecular cloning and characterization of human indoleamine 2,3-dioxygenase gene.

KADOYA AKIHIKO (1)

(1) Wakayama Medical College

Wakayama Igaku(Journal of the Wakayama Medical Society), 1993,

VOL.44,NO.1, PAGE.89-100, FIG.13, TBL.2, REF.35

JOURNAL NUMBER: F0546AAI ISSN NO: 0043-0013 CODEN: WKMIA

UNIVERSAL DECIMAL CLASSIFICATION: 577.151

LANGUAGE: Japanese

COUNTRY OF PUBLICATION: Japan

DOCUMENT TYPE: Journal

ARTICLE TYPE: Original paper

MEDIA TYPE: Printed Publication

ABSTRACT: Indoleamine 2,3-dioxygenase (IDO) is a monomeric hemoprotein that catalyzes the oxidation of an essential amino acid, tryptophan, into N-formyl kynurenine. IDO is induced dramatically (up to 100-fold) in many cultured human cell lines by interferon- γ (IFN- γ). The growth inhibition of human cells by IFN- γ is accompanied with the depletion of tryptophan in the culture medium. It suggests that IDO-catalyzed tryptophan degradation facilitates the cell growth inhibition by depleting tryptophan. In order to reveal the molecular mechanism of IDO induction by IFN- γ , the human IDO cDNAs were cloned, and IDO induction was analyzed at mRNA level, also IDO gene structure was determined. The human IDO cDNA clones were isolated from a **LAMBDA.g** II library prepared from **poly (A)+** RNA of IFN- γ -treated HEL cells (Flow 2000) with the monoclonal antibody against IDO. The predicted amino acid sequences from the cDNA sequences coincided with the partial amino acid sequences of the endopeptidic digests of purified IDO protein. The open reading frame was 1209 nucleotides in length and encoded a protein containing 403 residues (a molecular weight of 45,324). Northern hybridization analysis of RNAs in various cultured human cells indicated that IDO induction by IFN- γ occurred at the mRNA level and two species of IDO mRNA (1.7kb and 2.3kb) were transcribed from a single gene. The amount of IFN- γ mediated IDO mRNAs reached the maximum level 12h after IFN- γ administration, while the enzyme activity of IDO was at its maximum 24h after. Anisomycin inhibited the transcription of IDO mRNAs mediated by IFN- γ . (abridged author abst.)

9/3,AB/186 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
(c) 2003 The HW Wilson Co. All rts. reserv.

03262982 H.W. WILSON RECORD NUMBER: BGS196012982
The mobile genetic element Alu in the human genome.
Novick, Gabriel E

Batzer, Mark A; Deininger, Prescott L
BioScience (BioScience) v. 46 (Jan. '96) p. 32-41
SPECIAL FEATURES: bibl il ISSN: 0006-3568
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 8258

ABSTRACT: Alu elements, as well as other repetitive elements, have been found to represent a dramatic source of genetic variation. Alu sequences represent the biggest group of short interspersed repetitive elements (SINES) in humans, being present in more than 500,000 copies per haploid genome. As retrotransposons and facilitators of unequal crossing over, Alu sequences reshuffle and copy the DNA, producing an important amount of genetic variability while giving genetic flexibility and increasing the population's survival in a dynamic environment. The biology of Alu transposable elements is now being widely examined to find out the molecular basis of a growing number of identified diseases and to give new directions in genome mapping and biomedical research. Subjects discussed include the discovery and classification of repetitive elements, the distribution and structure of the Alu family, the mechanism of Alu retroposition, and the function of Alu elements. Representative examples of Alu insertions that cause human disorders are also provided.

9/3,AB/187 (Item 2 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
(c) 2003 The HW Wilson Co. All rts. reserv.

03253327 H.W. WILSON RECORD NUMBER: BGS196003327
Trinucleotide repeat expansion and human disease.
Ashley, Claude T., Jr
Warren, Stephen T
Annual Review of Genetics (Annu Rev Genet) v. 29 ('95) p. 703-28
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 12844

ABSTRACT: The expansion of trinucleotide repeats and their role in human diseases are reviewed. Small expansions--2-3 times the normal length--of the polymorphic CGG/CCG or CAG/CTG repeats have been found in genes coding for polyglutamine and are linked to neurodegenerative disorders, including spinal and bulbar muscular atrophy, spinocerebellar ataxia (type 1), Huntington's disease, dentatorubral-pallidoluysian atrophy, Machado-Joseph disease, and myotonic dystrophy. Larger expansions--10-1,000 times the normal length--are associated with chromosomal fragile sites and are isolated or located in untranslated regions of genes. Expanded alleles of the 11 human loci that are affected demonstrate meiotic instability, often lengthening upon transmission. Elongation can occur in subsequent generations.

9/3,AB/188 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal
(c) 2003 INIST/CNRS. All rts. reserv.

12557529 PASCAL No.: 96-0238285
Structure and organization of the human Neuronatin gene
DEXIAN DOU; JOSEPH R
Laboratory of Molecular Neuroscience, Education and Research Building No. 3025, Department of Neurology, Henry Ford Hospital & Health Sciences Center and Case Western Reserve University, 2799 West Grand Boulevard, Detroit, Michigan 48202, United States
Journal: Genomics : (San Diego, CA), 1996, 33 (2) 292-297

Language: English

Neuronatin is a brain-specific human gene that we recently isolated and observed to be selectively expressed during brain development. In this report, the genomic structure and organization of human neuronatin is described. The human gene spans 3973 bases and contains three exons and two introns. Based on primer extension analysis, a single cap site is located 124 bases upstream from the methionine (ATG) initiation codon, in good context, GAACCATGG. The promoter contains a modified TATA box, CATAAA (-27), and a modified CAAT box, GGCGAAT (-59). The 5'-flanking region contains putative transcription factor binding sites for SP-1, AP-2 (two sites), delta -subunit, SRE-2, NF-A1, and ETS. In addition, a 21-base sequence highly homologous to the neural restrictive silence element that governs neuron-specific gene expression is observed at -421. Furthermore, SP-1 and AP-3 binding sites are present in intron 1. All splice donor and acceptor sites conformed to the GT/AG rule. Exon 1 encodes 24 amino acids, exon 2 encodes 27 amino acids, and exon 3 encodes 30 amino acids. At the 3'-end of the gene, the poly(A) signal, AATAAA, poly(A) site, and GT cluster are observed. The neuronatin gene is expressed as two mRNA species, alpha and beta, generated by alternative splicing. The alpha -form contains all three exons, whereas in the beta -form, the middle exon has been spliced out. The third nucleotide of all frequently used codons, except threonine, of neuronatin is either G or C, consistent with codon usage expected for Homo sapiens. This information about the structure of the human neuronatin gene will help in understanding the significance of this gene in brain development and human disease.

9/3,AB/189 (Item 2 from file: 144)

DIALOG(R)File 144:Pascal

(c) 2003 INIST/CNRS. All rts. reserv.

10175462 PASCAL No.: 92-0381216

Characterization of an associated microfibril protein through recombinant DNA techniques

HORRIGAN S K; RICH C B; STREETEN B W; ZONG-YI LI; FOSTER J A

Syracuse univ., dep. biology, Syracuse NY 13244, USA

Journal: (The) Journal of biological chemistry, 1992, 267 (14)

10087-10095

Language: English

The complete primary structure of a new extracellular protein associated with elastic fiber microfibrils was determined by recombinant DNA techniques. Antiserum to insoluble bovine ocular zonule protein was used to screen a lambda gt 11 cDNA expression library constructed from whole chick embryo poly(A) SUP + RNA. The cDNAs encoding immunoreactive fusion polypeptides were then used to rescreen the library by plaque hybridization. Nucleotide sequencing of overlapping cDNA clones revealed an open translation reading frame of 1326 bases beginning at an initiation start sequence and ending at a stop codon

9/3,AB/190 (Item 3 from file: 144)

DIALOG(R)File 144:Pascal

(c) 2003 INIST/CNRS. All rts. reserv.

08532123 PASCAL No.: 89-0081003

Nucleotide sequence of cDNA clones encoding the complete precursor for the "10-kDae polypeptide of photosystem II from Spinach

LAUTNER A; KLEIN R; LJUNGBERG U; REILANDER H; BARTLING D; ANDERSSON B; REINKE H; BEYREUTHER K; HERRMANN R G

Ludwig-Maximilian univ., botanisches inst., Muenchen 8000, Federal Republic of Germany

Journal: Journal of biological Chemistry, 1988, 263 (21)

10077-10081

Language: English

Isolement de la sequence complete correspondant au precurseur du polypeptide de 10 kDa du photosysteme II par criblage d'une banque ADNC lambda gt 11 preparee a partir des ARNm poly(A SUP +) de plants d'epinard illumines (4 et 16 h). Sequencage nucleotidique et deduction de la sequence aminoacide

9/3,AB/191 (Item 4 from file: 144)
DIALOG(R)File 144:Pascal
(c) 2003 INIST/CNRS. All rts. reserv.

02013286 PASCAL No.: 78-0293920
THE INTERACTION OF ETHIDIUM WITH SYNTHETIC DOUBLE-STRANDED
POLYNUCLEOTIDES AT LOW IONIC STRENGTH.
BAGULEY B C; FALKENHAUG E-M
DEP. CELL BIOL., UNIV. AUCKLAND, AUCKLAND, NEW ZEALAND
Journal: NUCLEIC ACIDS RES., 1978, 5 (1) 161-171
Language: ENGLISH
ON DEMONTE QUE L'ETHIDIUM EST UN MARQUEUR FLUORESCENT UTILE POUR ETUDIER
LES INTERACTIONS ENTRE LES POLYNUCLEOTIDES BI-CATENAIRES ET LES AUTRES
MOLECULES.

9/3,AB/192 (Item 1 from file: 203)
DIALOG(R)File 203:AGRIS
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01398472 AGRIS No: 90-003603
Construction of cDNA library in lambda gt 11 vector from white-rot
fungus Coriolus versicolor poly (A)+RNA and the immunological
screening with anti-laccase III antiserum
Nakamura, M. (Tokyo Univ. of Agriculture and Technology, Fuchu (Japan).
Faculty of Agriculture); Katayama, Y.; Morohoshi, N.; Haraguchi, T.
Journal: Journal of the Japan Wood Research Society, Jan 1989, v. 35(1)
p. 72-74
Language: English

9/3,AB/193 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2003 Thomson Derwent & ISI. All rts. reserv.

0158554 DBR Accession No.: 94-01105 PATENT
A polypeptide and DNA encoding it - protein sequence of
galactosyltransferase and application in antibody generation
PATENT ASSIGNEE: Konishiroku-Photo 1993
PATENT NUMBER: JP 5279386 PATENT DATE: 931026 WPI ACCESSION NO.:
93-374602 (9347)
PRIORITY APPLIC. NO.: JP 91256989 APPLIC. DATE: 910909
NATIONAL APPLIC. NO.: JP 91256989 APPLIC. DATE: 910909
LANGUAGE: Japanese
ABSTRACT: A polypeptide of the following protein sequence, and DNA encoding
it, are new: Arg Asp Leu Ser Arg Leu Pro Gln Leu Val Gly Val Ser Thr
Pro Leu Gln Gly Gly Ser Asn Ser Ala Ala Ala Ile Gly Gln Ser Ser Gly Glu
Leu Arg. An anti-galactosyltransferase antibody can be prepared
efficiently using the new polypeptide as an immunogen. In an example,
galactosyltransferase (GT) was purified by alpha-albumin affinity
chromatography. Human ovary clear cell malignant cell strain RMG-1 was
cultured and poly(A)+ RNA was purified from the culture and
used to prepare a cDNA gene bank. Antigen-producing strains were
screened to give 6 cDNA clones; UG-8601, 7902, 7903, 7904 and 4806.
Total cellular RNA of RMG-1 cells was subjected to Northern blot
analysis. Each cloned cDNA was cross hybridized. Only UG-8601 showed
homology with GT. The DNA sequence of UG-8601 was determined and

plasmid pBSHGT was constructed for expression of GT in Escherichia coli as a beta-galactosidase (EC-3.2.1.23) fusion protein. (8pp)

9/3,AB/194 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2003 Thomson Derwent & ISI. All rts. reserv.

0153130 DBR Accession No.: 93-11182 PATENT
Isolating glucosyltransferase enzyme for production of saccharide compound - glycosylation method for oligosaccharide, polysaccharide, glycoprotein or glycolipid production
PATENT ASSIGNEE: Univ.Pennsylvania 1993
PATENT NUMBER: WO 9313198 PATENT DATE: 930708 WPI ACCESSION NO.: 93-227316 (9328)
PRIORITY APPLIC. NO.: US 810858 APPLIC. DATE: 911220
NATIONAL APPLIC. NO.: WO 92US10891 APPLIC. DATE: 921221
LANGUAGE: English
ABSTRACT: Glycosyltransferases (GTs) may be used in a glycosylation method, involving: contacting an immobilized acceptor with a GT mixture, to allow the GT to bind to the acceptor and form a complex; and contacting the acceptor with a saccharide unit to allow bonding of the saccharide to the acceptor and free the GT from the complex. Several GTs may be used sequentially. The carbohydrate may be a monosaccharide, disaccharide, oligosaccharide or polysaccharide. A washing step may be included between each enzyme step. The saccharide may be a saccharide nucleotide (with U, G or C phosphate). The acceptor may be a protein, glycoprotein, lipid, glycolipid, monosaccharide, disaccharide, oligosaccharide or polysaccharide. The GT may be in a cell homogenate or a purified enzyme. Specified reactions are claimed. The resulting glycosylated compounds may be used in diagnostic, therapeutic, pharmaceutical and food applications. (48pp)

9/3,AB/195 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
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0095752 DBR Accession No.: 89-13743
Cloning and expression of cDNA encoding antistasin, a leech-derived protein having anticoagulant and antimetastatic properties - Autographa californica nuclear-polyhedrosis virus vector expression in Spodoptera frugiperda Sf9 cell culture
AUTHOR: Han J H; Law S W; Keller P M; Kniskern P J; Silberklang M; +Ellis R W
CORPORATE AFFILIATE: Merck-USA
CORPORATE SOURCE: Departments of Cellular and Molecular Biology, Merck Sharp and Dohme Research Laboratories, West Point, PA 19486, USA.
JOURNAL: Gene (75, 1, 47-57) 1989
CODEN: GENED6
LANGUAGE: English
ABSTRACT: A phage lambda-gt-22 cDNA gene bank was constructed from leech (Haementaria officinalis) salivary gland poly(A)+ RNA. The gene bank was screened using 2 oligonucleotides synthesized to encode amino acid residues between 70 and 107 of the mature antistasin protein. The gene bank was also screened using rabbit antibodies prepared against antistasin. Antistasin cDNA was inserted into baculo virus expression vector plasmid pAc373 and cotransfected with Autographa californica nuclear-polyhedrosis virus DNA into Spodoptera frugiperda Sf9 cell culture by the calcium phosphate method. Biologically active, recombinant antistasin was produced. Antistasin is a potent anti Factor-Xa inhibitor, an anticoagulant and an

antimetastatic compound. Antistasin has a 17 amino acid signal peptide and exists as 2 variants. Sequence analysis of multiple cDNA clones revealed 2 additional sites of amino acid substitution. Sequence variation resulted from allelic variation rather than gene duplication as deduced from DNA blot analyses. Sequence data suggest that antistasin may have evolved from a smaller gene by duplication. (31 ref)

9/3,AB/196 (Item 4 from file: 357)
DIALOG(R) File 357:Derwent Biotech Res.
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0080819 DBR Accession No.: 88-11668

The structure of the human glutathione-S-transferase pi gene - isolation from a cosmid library

AUTHOR: Cowell I G; Dixon K H; Pemble S E; Ketterer B; Taylor J B
CORPORATE SOURCE: Cancer Research Campaign Molecular Toxicology Research Group, University College and Middlesex School of Medicine, Windeyer Building, Cleveland Street, London W1P 6DB, UK.

JOURNAL: Biochem.J. (255, 1, 79-83) 1988

CODEN: BIJOAK

LANGUAGE: English

ABSTRACT: The human glutathione-S-transferase (GST) (EC-2.5.1.18) pi gene has been isolated from a cosmid library using rat GST subunit 7 cDNA as a probe. The coding sequence of the gene displayed a high degree of homology with that of rat subunit 7. The GST-pi gene spans about 3 kb and is interrupted by 6 introns, each possessing the GT and AG splicing signals at their 5' and 3' ends respectively. The transcription initiation site was determined for RNA prepared from BEN and HeLa cells. Using an oligonucleotide primer derived from the 5'-portion of exon-2 and the last base of exon-1 of the GST-pi gene, poly(A)+ or total RNA produced bands corresponding to an initiation site between 28 and 33 bp downstream of the TATA box. There is a strong bias towards G+C residues in the region surrounding the 5' end of the gene, and the proportion of CpG dinucleotides (9.2%) is much higher than that found in the genome as a whole, and is typical of an HTF (HpaII tiny fragment) island. The promoter contains a sequence matching the phorbol ester- and ras-responsive element from the polyoma virus enhancer, which may be implicated in the tumor-specific expression of GST-pi. (36 ref)

9/3,AB/197 (Item 5 from file: 357)
DIALOG(R) File 357:Derwent Biotech Res.
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0058101 DBR Accession No.: 87-02449

Structure of the carboxyl-terminal half of human alpha-2 plasmin inhibitor deduced from that of cDNA - cloning and DNA sequence

AUTHOR: Sumi Y; Nakamura Y; Aoki N; Sakai M; Muramatsu M
CORPORATE AFFILIATE: Teijin

CORPORATE SOURCE: Department of Biochemistry, The University of Tokyo Faculty of Medicine, Bunkyo-ku, Tokyo 113, Japan.

JOURNAL: J.Biochem. (100, 5, 1399-402) 1986

CODEN: JOBIAO

LANGUAGE: English

ABSTRACT: The molecular cloning of a cDNA representing the 3' region of human alpha2PI mRNA and the deduction of the carboxyl terminal region of alpha2PI (human alpha2-plasmin inhibitor) is reported. The cDNA isolated from a human liver cDNA library was constructed in the lambda gt 10 bacteriophage vector from poly(A) plus mRNA taken from HepG2 cells. The library was screened using mixed oligo-deoxynucleotide probes and a 1.7 kb clone, pPI39, subcloned into

plasmid pUC8. pPI39 Contained 822 nucleotides encoding the carboxyl terminal 274 amino acid sequence, where the plasminogen binding site is located, a stop codon and a 3' noncoding region of 0.9 kb. This insert was calculated to correspond to about 55% of the alpha2PI molecule. The amino acid sequence shows 29-31% homology with other plasma protease-inhibitors. The reactive site peptide band was Met-Ser, the Met residue was located at the 91st position from the carboxyl end. (25 ref)

9/3,AB/198 (Item 6 from file: 357)
DIALOG(R) File 357:Derwent Biotech Res.
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0035012 DBR Accession No.: 85-05801

Genomic rearrangements of the SV40 sequences in the Chinese hamster embryo fibroblasts (CHEF/18) cells transfected by the SV40 DNA with flanking mouse sequences - mapping and comparison of stable and unstable clones (conference abstract)

AUTHOR: Tanaka K; Sager R

CORPORATE SOURCE: Dept. Med. Geriatr., Osaka Univ., Osaka, Japan. (29, 2, 169-70) 1984

CODEN: 9999Z

LANGUAGE: English

ABSTRACT: The 8.8 kb EcoRI fragment containing SV40 early sequences and their flanking mouse sequences which were cloned into lambda gt WES were transfected into CHEF/18 cells. 5 Parental clones (205SV33-4E, 205SV33-26E, 205SV21-21E, 205SV21-24E and 205SV53-2E) each contained 1 copy in SV40 DNA. Significant differences were shown in the stability of the integrated SV40 sequences; 205SV33-4E was very unstable, while 205SV33-26E and 205SV53-2E were stable, and 205SV21-24E and 21-21E were intermediate. All the parental clones made tumors in nude mice, and expressed normal sizes of large T, non-viral middle and small T antigens, but 205SV33-26E showed lower levels of the large T antigen than the other clones. Restriction enzyme analyses indicated that the flanking mouse sequences may be involved in the rearrangements in the unstable clone. A deleted 3' end region of the transcription template for early mRNA in 205SV33-26E may contain a poly(A) signal for early mRNA, the lack of which may contribute to the low expression of antigen in this clone, leading to decreased viral replication and stable integration of SV40. (0 ref)

9/3,AB/199 (Item 7 from file: 357)
DIALOG(R) File 357:Derwent Biotech Res.
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0033136 DBR Accession No.: 85-03925

Human Factor-IX clones isolated with synthetic oligomer probes - DNA sequence and comparison of normal and hemophilia H Alabama variant DNA (conference abstract)

AUTHOR: Davis L M; McGraw R A; Stafford D W

CORPORATE SOURCE: Dept. of Biology, University of North Carolina, Chapel Hill, N.C., USA. (1, Adv.Gene Technol., 150-51) 1984

CODEN: 9999Z

LANGUAGE: English

ABSTRACT: Recombinant clones containing human Factor-IX coding sequences were selected from cDNA banks and genomic libraries using a series of synthetic oligonucleotides as probes. A human liver cDNA bank was constructed in the phage vector lambda gt-10 and a partial Factor-IX cDNA of 200 bp was found. This cDNA was used to probe a 2nd cDNA bank from which 2 Factor-IX clones, of approximately 550 and 3000 bases, were found. The 550 base insert corresponded to the 3' coding sequences including the stop codon, while the 3 kb insert contained an

initiation codon at its 5' terminus and a **poly-A** tract at its 3' terminus. The primary sequence of this cDNA was determined. 2 Genomic libraries representing the DNA from 2 individuals carrying the Factor-IX Alabama variant of hemophilia B were constructed by ligating partial EcoRI digests of leukocyte DNA to the phage vector lambda **gt**-lambda-B. The nature of the difference between the normal cDNA and the Alabama genomic DNA was examined. (6 ref)

library, we isolated several clones containing overlapping inserts of a novel gene that rescues the slow-growth phenotype of the dominant negative qsr1 truncations. The suppressor of qsr1 truncation mutants, SQT1, is an essential gene, which encodes a 47.1-kDa protein containing multiple WD reports and which interacts strongly with Qsr1p in a yeast two-hybrid system. SQT1 restores growth and the 'half-mer' polysome profile of the dominant negative qsr1 mutants to normal, but it does not rescue temperature-sensitive qsr1 mutants or the original qsr1-1 missense allele. In yeast cell lysates, Sqt1p fractionates as part of an oligomeric protein complex that is loosely associated with ribosomes but is distinct from known eukaryotic initiation factor complexes. Loss of SQT1 function by down regulation from an inducible promoter results in formation of half-mer polyribosomes and decreased Qsr1p levels on free 60S subunits. Sqt1p thus appears to be involved in a late step of 60S subunit assembly or **modification** in the cytoplasm.

4/3,AB/17 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05654863 Genuine Article#: WN571 Number of References: 20
Title: Cytoplasmic detection of a novel protein containing a nuclear localization sequence by human autoantibodies (ABSTRACT AVAILABLE)
Author(s): GarciaLozano JR; GonzalezEscribano MF; Wichmann I; NunezRoldan A (REPRINT)
Corporate Source: HOSP UNIV VIRGEN ROCIO,SERV IMMUNOL, AVDA MANUEL SIUROT S-N/SEVILLE 41013//SPAIN/ (REPRINT); HOSP UNIV VIRGEN ROCIO,SERV IMMUNOL/SEVILLE 41013//SPAIN/
Journal: CLINICAL AND EXPERIMENTAL IMMUNOLOGY, 1997, V107, N3 (MAR), P501-506
ISSN: 0009-9104 Publication date: 19970300
Publisher: BLACKWELL SCIENCE LTD, OSNEY MEAD, OXFORD, OXON, ENGLAND OX2 0EL
Language: English Document Type: ARTICLE
Abstract: A great diversity of antibodies directed to cell proteins has been described in sera of patients with autoimmune diseases. Most of these sera recognize nuclear components, but some others are directed against cytoplasmic autoantigens. Some of the antibodies directed to cytoplasmic autoantigens are well characterized, such as anti-mitochondrial, anti-ribosomal, anti-microsomal and anti-Golgi complex autoantibodies, but the target of many others remains unknown. In the last 5 years we have selected 32 sera with a characteristic speckled cytoplasmic pattern in indirect immunofluorescence (IIF) assay among a total of more than 31 000 sera from patients with any kind of autoimmune manifestation who attend our Connective Tissue Disease Clinic. Using a human cDNA expression library, we have identified a new autoantibody specificity named RCD-8 in five of these sera, directed to one cytoplasmic autoantigen. Affinity-purified antibodies eluted from a positive clone reproduced the same IIF cytoplasmic staining pattern as native serum and reacted with one single band of 160 kD on an immunoblot of HeLa cell extract. The sequence was found homologous to an autoantigen recently reported named Ge-1, and contains a nuclear localization sequence (NLS), an active protein domain made by a contiguous stretch of amino acids which allows the selective entry of the protein into the nucleus. The five patients whose sera exhibited this new autoantibody specificity displayed different autoimmune pathological profiles.

4/3,AB/18 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

05353057 Genuine Article#: VT054 Number of References: 35

Title: ADDITION OF DESTABILIZING **POLY(A)**-RICH SEQUENCES TO
ENDONUCLEASE CLEAVAGE SITES DURING THE DEGRADATION OF CHLOROPLAST
MESSENGER-RNA (Abstract Available)
Author(s): LISITSKY I; KLAFF P; SCHUSTER G
Corporate Source: TECHNION ISRAEL INST TECHNOL,DEPT
BIOL/IL-32000HAIFA//ISRAEL//; TECHNION ISRAEL INST TECHNOL,DEPT
BIOL/IL-32000HAIFA//ISRAEL//; UNIV DUSSELDORF,INST PHYS BIOL/D-40225
DUSSELDORF//GERMANY/
Journal: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED
STATES OF AMERICA, 1996, V93, N23 (NOV 12), P13398-13403
ISSN: 0027-8424

Language: ENGLISH Document Type: ARTICLE

Abstract: In this work, we report the posttranscriptional addition of
poly(A)-rich sequences to mRNA in chloroplasts of higher
plants. Several sites in the coding region and the mature end of
spinach chloroplast psbA mRNA, which encodes the D1 protein of
photosystem II, are detected as polyadenylylated sites. In eukaryotic
cells, the addition of multiple adenosine residues to the 3' end of
nuclear RNA plays a key role in generating functional mRNAs and in
regulating mRNA degradation. In bacteria, the adenylation of several
RNAs greatly accelerates their decay. The **poly(A)** moiety in
the chloroplast, in contrast to that in eukaryotic nuclear encoded and
bacterial RNAs, is not a ribohomopolymer of adenosine residues, but
clusters of adenosines bounded mostly by guanosines and rarely by
cytidines and uridines; it may be as long as several hundred
nucleotides. Further analysis of the initial steps of chloroplast psbA
mRNA decay revealed specific endonuclease cleavage sites that perfectly
matched the sites where **poly(A)**-rich sequences were added.
Our results suggest a mechanism for the degradation of psbA mRNA in
which endonucleolytic cleavages are followed by the addition of
poly(A)-rich sequences to the upstream cleavage products,
which target these RNAs for rapid decay.

4/3,AB/19 (Item 4 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2002 Inst for Sci Info. All rts. reserv.

03041236 Genuine Article#: MZ261 Number of References: 17
Title: OSMOREGULATORY ALTERATIONS IN MYOINOSITOL UPTAKE BY BOVINE LENS
EPITHELIAL-CELLS .2. CLONING OF A 626-BP CDNA PORTION OF A
NA+/MYO-INOSITOL COTRANSPORTER, AN OSMOTIC SHOCK PROTEIN (Abstract
Available)

Author(s): ZHOU C; AGARWAL N; CAMMARATA PR
Corporate Source: UNIV N TEXAS,HLTH SCI CTR FT WORTH N TEXAS EYE RES
INST,DEPT ANAT & CELL BIOL/FT WORTH//TX/76107; UNIV N TEXAS,HLTH SCI
CTR FT WORTH N TEXAS EYE RES INST,DEPT ANAT & CELL BIOL/FT
WORTH//TX/76107

Journal: INVESTIGATIVE OPHTHALMOLOGY & VISUAL SCIENCE, 1994, V35, N3
(MAR), P1236-1242

ISSN: 0146-0404

Language: ENGLISH Document Type: ARTICLE

Abstract: Purpose. Bovine lens epithelial cells (BLECs) accumulate
osmotically active organic solutes (i.e., osmolytes) including
myo-inositol when exposed to hypertonic stress (osmotic shock). In
hypertonic medium, the increase in myo-inositol accumulation is
attributed to an elevation in activity of Na+/myo-inositol
cotransporter(s). The authors report the nature of the
hypertonicity-induced enhancement of myo-inositol uptake in cultured
BLECs by amplifying a 626 bp cDNA from lens cell RNA.

Methods. A portion of cDNA encoding a Na+/myo-inositol
cotransporter was isolated from cultured BLECs using PCR primers
designed from an established myo-inositol transporter from Madin-Darby

canine kidney (MDCK) cells. Using the reverse transcription-**polymerase** chain reaction, a 626 bp PCR product was amplified. Its nucleic acid sequence was determined by the dideoxynucleotide method using Sequenase kit. Na⁺/Myo-inositol cotransporter mRNA expression in the cultured cells was demonstrated under physiological and hypertonic conditions by northern analysis of **poly (A)** (+) RNA using the lens cell 626 bp cDNA as probe.

Results. The BLEC cDNA sequence was 92% identical with the Na⁺/myo-inositol cotransporter of MDCK cells. Myo-inositol transporter mRNA was demonstrated in cultured BLECs and was significantly induced by hypertonic stress.

Conclusions. These data suggest that cultured bovine lens epithelial cell adaptation to hypertonicity involves intracellular accumulation of small organic osmolytes (i.e., myo-inositol) through elevation of myo-inositol uptake activity resulting from the upregulation of transporter mRNA.

4/3,AB/20 (Item 5 from file: 34)
DIALOG(R) File 34:SciSearch(R) Cited Ref Sci
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02177095 Genuine Article#: KG400 Number of References: 51
Title: RECOMBINATION AND **POLYMERASE** ERROR FACILITATE RESTORATION OF
INFECTIVITY IN BROME MOSAIC-VIRUS (Abstract Available)
Author(s): RAO ALN; HALL TC
Corporate Source: TEXAS A&M UNIV SYST, INST DEV & MOLEC BIOL/COLL
STN//TX/77843; TEXAS A&M UNIV SYST, INST DEV & MOLEC BIOL/COLL
STN//TX/77843; TEXAS A&M UNIV SYST, DEPT BIOL/COLL STN//TX/77843
Journal: JOURNAL OF VIROLOGY, 1993, V67, N2 (FEB), P969-979
ISSN: 0022-538X
Language: ENGLISH Document Type: ARTICLE

Abstract: The tRNA-like structure present in the 3' noncoding region of each of the four virion RNAs of brome mosaic virus possesses a conserved A-67-U-A-65 (67AUA65) sequence. Four mutations in this region (67UAA65, 67GAA65, and 67CAA65, each with a double base change, and 67GUA65, containing a single point mutation), previously shown in vitro to be defective in minus-strand promoter function, were introduced into full-length genomic RNAs 2 and 3, and their replicative competence was analyzed in barley protoplasts. All four RNA 3 mutants were capable of replication, although progeny plus-sense RNA 3 accumulation was only 12 to 42% of that of the wild type. Replication of RNA 2 transcripts bearing these mutations was even more severely debilitated; the accumulation of each mutant progeny plus-strand RNA 2 was < 10% of that of the wild type. Analysis of mutant RNA 3 progeny recovered from local lesions induced in *Chenopodium hybridum* and systemic infections in barley (*Hordeum vulgare*) **plants** revealed that the mutant base at position 67 from the 3' end had in each case been **modified** to an A. These changes generated RNAs with functional pseudorevertant (67AAA65 for mutants 67UAA65, 67GAA65, and 67CAA65) or revertant (67GUA65 --> 67AUA65) sequences. In most instances, the presence of internal markers permitted discrimination between **polymerase** error and RNA recombination as the process by which sequence restoration occurred. The pseudorevertant sequence was found to be capable of persistence during subsequent propagation in **plants** when present on RNA 3 but not when present on RNA 2. These data document the fluidity of the RNA genome and reveal situations in which **polymerase** error or recombination can function preferentially to restore an optimal sequence. They also support the concept that RNA viruses frequently exist as quasispecies and have implications concerning evolutionary strategies for positive-strand RNA viruses.

4/3,AB/21 (Item 1 from file: 50)
DIALOG(R)File 50:CAB Abstracts
(c) 2002 CAB International. All rts. reserv.

03010175 CAB Accession Number: 951604833
Amplification of beta -tubulin cDNA from Camellia sinensis by PCR.
Takeuchi, A.; Matsumoto, S.; Hayatsu, M.
Department of Tea Processing Technology, National Research Institute of
Vegetables, Ornamental Plants and Tea, 2769 Kanaya, Shizuoka 428, Japan.
Bulletin of the National Research Institute of Vegetables, Ornamental
Plants and Tea. Series B (No. 7): p.13-20
Publication Year: 1994
ISSN: 0914-6652 --
Language: Japanese Summary Language: english
Document Type: Journal article
Total RNAs were extracted from leaves of the variety Yabukita by means
of the modified guanidinium and SDS-phenol procedures. The
concentration of 2-mercaptoethanol in the extraction media increased to
15%. Poly(A)+ RNAs isolated from the total RNAs showed
efficient translation activity in vitro. A cDNA library constructed from
the poly(A)+ RNA using lambda gt11 as a vector consisted of
2.9 x 10⁶ independent clones. A fragment was amplified from the
recombinant phage DNA with beta -tubulin specific primers. The sequence
was 505 bp in length, and no antisense primer sequence was detected. The
deduced amino acid sequence showed that the amplified fragment covered
about a third of the beta -tubulin coding region and revealed extensive
homology with beta -tubulin sequences from other higher plant
species. 13 ref.

4/3,AB/22 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
(c) 2002 The HW Wilson Co. All rts. reserv.

04004123 H.W. WILSON RECORD NUMBER: BGS199004123
Evolution and mechanism of translation in chloroplasts.
Sugiura, Masahiro
Hirose, Tetsuro; Sugita, Hamoru
Annual Review of Genetics (Annu Rev Genet) v. 32 ('98) p. 437-59
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 10026

ABSTRACT: The mechanisms and evolution of translation in chloroplasts are
reviewed. Chloroplast genomes of a dozen plant species have been
completely sequenced and found to contain 87-183 known genes, half of which
encode components involved in translation. These components include a
complete set of rRNAs and about 30 tRNAs, which are probably sufficient to
support translation in chloroplasts. RNA is edited in some chloroplast
transcripts: Start and stop codons are created, and codons are changed to
retain conserved amino acids. Many of the chloroplast translational
machinery components resemble those found in Escherichia coli, but only
about one-third of the chloroplast mRNAs possess Shine-Dalgarno-like
sequences at the correct positions. Multiple mechanisms for translational
initiation in chloroplasts have been demonstrated both in vitro and in
vivo.

4/3,AB/23 (Item 2 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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04004113 H.W. WILSON RECORD NUMBER: BGSI99004113
Nonsegmented negative-strand RNA viruses: genetics and manipulation of
viral genomes.
Conzelmann, Karl-Klaus
Annual Review of Genetics (Annu Rev Genet) v. 32 ('98) p. 123-62
SPECIAL FEATURES: bibl il ISSN: 0066-4197
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 19760

ABSTRACT: The genetics and manipulation of nonsegmented negative-strand RNA viruses (NSVs) are discussed. Protocols that have been developed to recover NSVs entirely from cDNA have opened up this group of viruses to detailed molecular genetic and virus biology analyses. The gene-expression strategy of nonsegmented NSVs involves the replication of ribonucleoprotein complexes and sequential synthesis of free mRNA. This strategy permits the use of NSVs to express heterologous sequences and has definite advantages in terms of easy manipulation of constructs, high capacity for foreign sequences, genetically stable expression, and the possibility of controlling the levels of expression. Furthermore, chimeric virus vectors carrying novel envelope protein genes and targeted to defined host cells offer interesting prospects for biomedical applications and transient gene therapy.

4/3,AB/24 (Item 3 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
(c) 2002 The HW Wilson Co. All rts. reserv.

03757942 H.W. WILSON RECORD NUMBER: BGSA98007942
Molecular approaches to understanding salinity adaptation of estuarine animals.
Towle, David W
American Zoologist (Am Zool) v. 37 no6 (1997) p. 575-84
SPECIAL FEATURES: bibl il ISSN: 0003-1569
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 4917

ABSTRACT: The molecular processes by which estuarine organisms adjust to salinity change are the central focus of this review, with emphasis on identifying the relevant mechanisms in euryhaline crustaceans using the techniques of molecular biology. This review is not intended to be complete with respect to ecological and physiological aspects but rather is an attempt to outline a molecular approach which other investigators may find useful as they address their own specific questions. Membrane transporters of sodium ions serve as the major focus, beginning with an examination of candidate transport systems in gill epithelial cells. Particular emphasis is placed on the recent identification and sequencing of a putative Na⁺/H⁺ antiporter cDNA from gills of the green shore crab *Carcinus maenas*. Reprinted by permission of the publisher.

4/3,AB/25 (Item 4 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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03546764 H.W. WILSON RECORD NUMBER: BGSI97046764
Target site selection in transposition.
Craig, Nancy L
Annual Review of Biochemistry (Annu Rev Biochem) v. 66 ('97) p. 437-74
SPECIAL FEATURES: bibl ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States

WORD COUNT: 18605

ABSTRACT: Transposable elements are discrete mobile DNA segments that can insert into non-homologous target sites. Diverse patterns of target site selectivity are observed: Some elements display considerable target site selectivity and others display little obvious selectivity, although none appears to be truly "random." A variety of mechanisms for target site selection are used: Some elements use direct interactions between the recombinase and target DNA whereas other elements depend upon interactions with accessory proteins that communicate both with the target DNA and the recombinase. The study of target site selectivity is useful in probing recombination mechanisms, in studying genome structure and function, and also in providing tools for genome manipulation. With permission, from the Annual Review of Biochemistry Volume 66, 1997, by Annual Reviews Inc. (<http://www.annurev.org>).

4/3,AB/26 (Item 5 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
(c) 2002 The HW Wilson Co. All rts. reserv.

03546760 H.W. WILSON RECORD NUMBER: BGSI97046760
Herpes simplex virus DNA replication.
Boehmer, Paul E
Lehman, I. R
Annual Review of Biochemistry (Annu Rev Biochem) v. 66 ('97) p. 347-84
SPECIAL FEATURES: bibl il ISSN: 0066-4154
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 17926

ABSTRACT: The Herpesviridae comprise a large class of animal viruses of considerable public health importance. Of the Herpesviridae, replication of herpes simplex virus type-1 (HSV-1) has been the most extensively studied. The linear 152-kbp HSV-1 genome contains three origins of DNA replication and approximately 75 open-reading frames. Of these frames, seven encode proteins that are required for origin-specific DNA replication. These proteins include a processive heterodimeric DNA **polymerase**, a single-strand DNA-binding protein, a heterotrimeric primosome with 5'-3' DNA helicase and primase activities, and an origin-binding protein with 3'-5' DNA helicase activity. HSV-1 also encodes a set of enzymes involved in nucleotide metabolism that are not required for viral replication in cultured cells. These enzymes include a deoxyuridine triphosphatase, a ribonucleotide reductase, a thymidine kinase, an alkaline endo-exonuclease, and a uracil-DNA glycosylase. Host enzymes, notably DNA **polymerase** a-primase, DNA ligase I, and topoisomerase II, are probably also required. Following circularization of the linear viral genome, DNA replication very likely proceeds in two phases: an initial phase of theta replication, initiated at one or more of the origins, followed by a rolling-circle mode of replication. The latter generates concatemers that are cleaved and packaged into infectious viral particles. The rolling-circle phase of HSV-1 DNA replication has been reconstituted in vitro by a complex containing several of the HSV-1 encoded DNA replication enzymes. Reconstitution of the theta phase has thus far eluded workers in the field and remains a challenge for the future. With permission, from the Annual Review of Biochemistry Volume 66, 1997, by Annual Reviews Inc. (<http://www.annurev.org>).

4/3,AB/27 (Item 6 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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03546746 H.W. WILSON RECORD NUMBER: BGSA97046746

Polyadenylation of mRNA in prokaryotes.

Sarkar, Nilima

Annual Review of Biochemistry v. 66 (1997) p. 173-97

SPECIAL FEATURES: bibl il ISSN: 0066-4154

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 10767

ABSTRACT: The 3'-ends of both prokaryotic and eukaryotic mRNA are polyadenylated, but the **poly(A)** tracts of prokaryotic mRNA are generally shorter, ranging from 15 to 60 adenylate residues and associated with only 2-60% of the molecules of a given mRNA species. The sites of polyadenylation of bacterial mRNA are diverse and include the 3'-ends of primary transcripts, the sites of endonucleolytic processing in the 3' untranslated and intercistronic regions, and sites within the coding regions of mRNA degradation products. The diversity of polyadenylation sites suggests that mRNA polyadenylation in prokaryotes is a relatively indiscriminate process that can occur at all mRNA's 3'-ends and does not require specific consensus sequences as in eukaryotes. Two **poly(A) polymerases** have been identified in *Escherichia coli*. They are encoded by unlinked genes, neither of which is essential for growth, suggesting significant functional overlap. Polyadenylation promotes the degradation of a regulatory RNA that inhibits the replication of bacterial plasmids and may play a similar role in the degradation of mRNA. However, under certain conditions, **poly(A)** tracts may lead to mRNA stabilization. Their ability to bind S1 ribosomal protein suggests that **poly(A)** tracts may also play a role in mRNA translation. With permission, from the Annual Review of Biochemistry Volume 66, 1997, by Annual Reviews Inc. (<http://www.annurev.org>).

4/3,AB/28 (Item 7 from file: 98)

DIALOG(R)File 98:General Sci Abs/Full-Text

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03506102 H.W. WILSON RECORD NUMBER: BGS197006102

Prions and RNA viruses of *Saccharomyces cerevisiae*.

Wickner, Reed B

Annual Review of Genetics (Annu Rev Genet) v. 30 ('96) p. 109-39

SPECIAL FEATURES: bibl il ISSN: 0066-4197

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 12297

ABSTRACT: The prions and L-A virus of *Saccharomyces cerevisiae* are discussed. The nonchromosomal mutations {URE3} and {PSI} appear to be the prion forms of the proteins Ure2p and Sup35p, respectively. {URE3} and {PSI} each have an N-terminal domain involved in generating the prion state and a C-terminal domain involved in the protein's normal functions--nitrogen regulation and translation termination, respectively. L-A, a single-segment dsRNA virus, is the type virus of the Totiviridae. The virus is accompanied by the killer toxin-encoding satellite M. L-A uses a ribosomal frameshift to produce a Gag-Pol fusion protein. The Gag protein decapitates cellular mRNAs to divert the host 5'-->3' exoribonuclease SKI1/XRN1 from degrading viral mRNA.

4/3,AB/29 (Item 8 from file: 98)

DIALOG(R)File 98:General Sci Abs/Full-Text

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03293635 H.W. WILSON RECORD NUMBER: BGS196043635

Molecular biology of mycoplasmas.

Dybvig, Kevin

Voelker, LeRoy L

Annual Review of Microbiology (Annu Rev Microbiol) v. 50 ('96) p. 25-57

SPECIAL FEATURES: bibl il ISSN: 0066-4227

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 15082

ABSTRACT: Although mycoplasmas lack cell walls, they are in many respects similar to the gram-positive bacteria with which they share a common ancestor. The molecular biology of mycoplasmas is intriguing because the chromosome is uniquely small (< 600 kb in some species) and extremely A-T rich (as high as 75 mol% in some species). Perhaps to accommodate DNA with a lower G + C content, most mycoplasmas do not have the "universal" genetic code. In these species, TGA is not a stop codon; instead it encodes tryptophan at a frequency 10 times greater than TGG, the usual codon for this amino acid. Because of the presence of TGA codons, the translation of mycoplasmal proteins terminates prematurely when cloned genes are expressed in other eubacteria, such as *Escherichia coli*. Many mycoplasmas possess strikingly dynamic chromosomes in which high-frequency changes result from errors in DNA repair or replication and from highly active recombination systems. Often, high-frequency changes in the mycoplasmal chromosome are associated with antigenic and phase variation, which regulate the production of factors critical to disease pathogenesis. Reprinted by permission of the publisher.

4/3,AB/30 (Item 9 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text
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03262982 H.W. WILSON RECORD NUMBER: BGS196012982

The mobile genetic element Alu in the human genome.

Novick, Gabriel E

Batzer, Mark A; Deininger, Prescott L

BioScience (BioScience) v. 46 (Jan. '96) p. 32-41

SPECIAL FEATURES: bibl il ISSN: 0006-3568

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 8258

ABSTRACT: Alu elements, as well as other repetitive elements, have been found to represent a dramatic source of genetic variation. Alu sequences represent the biggest group of short interspersed repetitive elements (SINEs) in humans, being present in more than 500,000 copies per haploid genome. As retrotransposons and facilitators of unequal crossing over, Alu sequences reshuffle and copy the DNA, producing an important amount of genetic variability while giving genetic flexibility and increasing the population's survival in a dynamic environment. The biology of Alu transposable elements is now being widely examined to find out the molecular basis of a growing number of identified diseases and to give new directions in genome mapping and biomedical research. Subjects discussed include the discovery and classification of repetitive elements, the distribution and structure of the Alu family, the mechanism of Alu retroposition, and the function of Alu elements. Representative examples of Alu insertions that cause human disorders are also provided.

4/3,AB/31 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal
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12311890 PASCAL No.: 95-0549269
Characterization of a novel **plant poly(A)**
polymerase

C

DAS GUPTA J; QINGSHUN LI; THOMSON A B; HUNT A G
Univ. Kentucky, dep. agronomy, plant physiology/biochemistry/molecular
biology program, Lexington KY 40564-0091, USA
Journal: Plant science : (Limerick), 1995, 110 (2) 215-226
Language: English

We have purified and characterized **poly(A) polymerases** (PAPs) from *Pisum sativum*, *Brassica juncea*, and *Zea mays*. Through chromatography on DEAE-Sepharose and heparin-Sepharose, these PAPs copurified as a single enzyme along with RNPs that could provide RNA substrates for the enzyme. More extensive purification by chromatography on MonoQ resulted in the resolution of the PAPs into as many as three fractions. One of these (PAP-I) contained a 43-kDa polypeptide immunologically related to the yeast PAP, and two others (PAP-II and PAP-III) contained RNAs that could serve as substrates for polyadenylation. These fractions by themselves possessed little PAP activity, but mixtures containing combinations of these displayed substantial activity. Similar PAP factors (PAP-I and PAP-III) were identified after fractionation of extracts prepared from *Brassica juncea* and *Zea mays*. The factors from one **plant** were completely interchangeable with those from different **plants**. We conclude that the **poly(A) polymerases** present in vegetative **plant** tissues consist of more than one component. In this respect, they are substantially different from other reported **plant**, mammalian, and yeast PAPs.

4/3,AB/32 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res
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0226271 DBA Accession No.: 98-07868
Purification and characterization of a mitochondrial DNA-**polymerase** from cultured tobacco cells - enzyme isolation and properties
AUTHOR: Sato K; Fukuda H
CORPORATE AFFILIATE: Univ.Tohoku-Biol.Inst.
CORPORATE SOURCE: Biological Institute, Faculty of Science, Tohoku University, Sendai 980-77, Japan.
JOURNAL: Plant Cell Physiol. (37, 7, 989-95) 1996
ISSN: 0032-0781 CODEN: PCPHA5
LANGUAGE: English
ABSTRACT: The tobacco cell line BY-2 (derived from *Nicotiana tabacum* L. cv. Bright Yellow 2) was propagated on **modified** Linsmaier-Skoog medium by shaking in a reciprocal shaker at 27 deg. Protoplasts were prepared from 300 g of 4-day cultured cells, broken and mitochondria were isolated. The mitochondrial DNA-**polymerase** (EC-2.7.7.7) was purified more than 1,200-fold by column chromatography on DEAE cellulose, phosphocellulose and Affi-Prep heparin. The enzyme was classified as a gamma-type DNA-**polymerase**, in view of the inhibition of its activity by N-ethylmaleimide and dideoxy TTP, the absence of inhibition by aphidicolin and arabinosyl CTP, the stimulation by KCl, and the ability of the enzyme to utilize **poly(A)**-(dT)12-18 in the presence of Mn²⁺ ions. The mol.wt. of the native mitochondrial DNA-**polymerase** was estimated to be 70,000-110,000 by column chromatography on Superose-12. When DNA-**polymerase** activity was analyzed after SDS-PAGE, the activity that polymerized DNA was observed as a single band of protein with a mol.wt. of about 110,000. Therefore, the tobacco mitochondrial DNA-**polymerase** appears to consist of a single subunit of 110,000. (31 ref)

4/3,AB/33 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res
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0158350 DBA Accession No.: 94-00901 PATENT

Barley-mild-mosaic virus nucleotide sequence - coat protein gene cloning
and expression in a transgenic **plant** for disease-resistance

PATENT ASSIGNEE: Unilever 1993

PATENT NUMBER: WO 9322345 PATENT DATE: 931111 WPI ACCESSION NO.:
93-368725 (9346)

PRIORITY APPLIC. NO.: GB 929669 APPLIC. DATE: 920502

NATIONAL APPLIC. NO.: WO 93GB910 APPLIC. DATE: 930430

LANGUAGE: English

ABSTRACT: A new protein sequence is encoded by a specified DNA sequence, with an in-frame ATG translation start codon, 5'-initiation consensus sequence and **poly-A** tail. The following are also new: a vector containing the DNA; a method for production of a transgenic **plant** with barley-mild-mosaic virus disease-resistance, by transforming a host **plant** or tissue with the vector containing the gene, operably linked to a promoter recognized by the host, so that the transformant produces an RNA transcript and the new protein sequence; and a transgenic **plant** engineered to have increased resistance to barley-mild-mosaic virus, produced by this method. The gene is produced from barley-mild-mosaic virus coat protein cDNA. In an example, the coat protein cDNA was amplified by the **polymerase** chain reaction using a forward DNA primer homologous to the 5'-end of the coat protein gene, and the cDNA product was used to reconstruct the full-length coat protein cDNA with a **modified** 5'-end. (34pp)

4/3,AB/34 (Item 3 from file: 357)

DIALOG(R)File 357:Derwent Biotech Res

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0048664 DBA Accession No.: 86-06512

Expression of seed storage proteins in xenopus oocytes - maize zein
chimeric gene production (conference abstract)

AUTHOR: Donaldson D; Hoffman L; Drong R; Bookland R

CORPORATE AFFILIATE: Agrigenetics

CORPORATE SOURCE: Agrigenetics Corporation, Advanced Research Division,
5649 East Buckeye Rd., Madison, WI 53716, USA.

JOURNAL: J.Cell.Biochem. (Suppl.10D, 53) 1986

CODEN: 5210J

LANGUAGE: English

ABSTRACT: Maize seed storage proteins, zeins, are a complex family of lysine-deficient polypeptides with mol.wts. of 22, 19, 15, and 10 kD. The 15 kD zein is encoded by only 1 or 2 genes and is therefore a suitable candidate for genetic engineering to improve the nutritional quality of maize seed storage protein. A chimeric, high lysine zein gene has been constructed by replacing a segment of the 15 kD zein gene with a fragment of Phaseolus vulgaris DNA which encodes a lysine rich region of the bean storage protein phaseolin. Xenopus oocytes translate total maize endosperm **poly (A)**+ RNA and package zein polypeptides into protein bodies similar to those found in maize endosperm. The wild type and **modified** 15 kD zein genes were therefore subcloned into the RNA expression plasmid pSP64 and a synthetic oligonucleotide inserted near the polyadenylation site of each gene. Use of SP6 **polymerase** in the presence of cap analog allowed transcription of ug quantities of capped 15 kD zein RNAs with or without **poly-(A)** residues. After injection into oocytes, these RNAs were translated. (0 ref)

Derwent announces file enhancements. Please see HELP NEWS 357.

File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec

(c) 1998 Inst for Sci Info

Set	Items	Description
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Processing

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8114474	PLANT?
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S2	71	S1 AND MODIF?
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? rd

>>>Duplicate detection is not supported for File 235.

>>>Duplicate detection is not supported for File 306.

>>>Records from unsupported files will be retained in the RD set.

...examined 50 records (50)

>>>Record 266:270094 ignored; incomplete bibliographic data, not retained -
in RD set

>>>Record 266:267634 ignored; incomplete bibliographic data, not retained -
in RD set

...completed examining records

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Processing

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Processing

Processed 10 of 22 files ...

Processing

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Completed processing all files

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S4	34	S3 AND PY<1999
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? t s4/3,ab/all

>>>No matching display code(s) found in file(s): 65, 235, 306

4/3,AB/1 (Item 1 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

09683626 98110157 PMID: 9448707

Molecular characterization of tobacco squalene synthase and regulation in
response to fungal elicitor.

Devarenne T P; Shin D H; Back K; Yin S; Chappell J

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>>>File 6 processing for ?AATNAA? stopped at AUTOGRESSIVE

>>>File 6 processing for ?AATANA? stopped at AUTOGRESSIVE

>>>File 6 processing for ?AATAAN? stopped at AUTOGRESSIVE

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RESEARCH IN

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RESEARCH IN

>>>File 10 processing for ?AANAAA? stopped at ANIMAL AND DAIRY SCIENCE
RESEARCH IN

>>>File 10 processing for ?AATNAA? stopped at ANIMAL AND DAIRY SCIENCE
RESEARCH IN

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RESEARCH IN

>>>File 10 processing for ?AATAAN? stopped at ANIMAL AND DAIRY SCIENCE
RESEARCH IN

>>>File 34 processing for ?NATAAA? stopped at ADJF

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>>>File 34 processing for ?AANAAA? stopped at ADJF

>>>File 34 processing for ?AATNAA? stopped at ADJF

>>>File 34 processing for ?AATANA? stopped at ADJF

>>>File 34 processing for ?AATAAN? stopped at ADJF

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>>>File 44 processing for ?AANAAA? stopped at BAJKALO

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>>>File 44 processing for ?AATANA? stopped at BAJKALO

>>>File 44 processing for ?AATAAN? stopped at BAJKALO

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>>>File 50 processing for ?AANAAA? stopped at ALTUMURA

>>>File 50 processing for ?AATNAA? stopped at ALTUMURA

>>>File 50 processing for ?AATANA? stopped at ALTUMURA

>>>File 50 processing for ?AATAAN? stopped at ALTUMURA

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>>>File 76 processing for ?AATNAA? stopped at APERTUA
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>>>File 76 processing for ?AATAAN? stopped at APERTUA
Processed 10 of 22 files ...
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>>>File 94 processing for ?AATANA? stopped at AU550
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>>>File 98 processing for ?AANAAA? stopped at BREJ
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>>>File 98 processing for ?AATANA? stopped at BREJ
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>>>File 99 processing for ?NATAAA? stopped at DECONSTRUCTIV
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>>>File 99 processing for ?AANAAA? stopped at DECONSTRUCTIV
>>>File 99 processing for ?AATNAA? stopped at DECONSTRUCTIV
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) ANION-ENT
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Processed 20 of 22 files ...

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Completed processing all files

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0 ?AATAAN?
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    OR ?AATAAN?
```

Agronomy Department, University of Kentucky, Lexington 40546-0091, USA.
Archives of biochemistry and biophysics (UNITED STATES) Jan 15
1998, 349 (2) p205-15, ISSN 0003-9861 Journal Code: 0372430

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The enzyme squalene synthase (SS) represents the first commitment of carbon from the general isoprenoid pathway toward sterol biosynthesis and is a potential point for regulation of sterol biosynthesis. The isolation and characterization of tobacco (*Nicotiana tabacum*) squalene synthase (TSS) cDNA and genomic DNA clones, as well as determination of the steady state level of TSS mRNA in response to elicitor treatment, were investigated. cDNA clones for TSS were isolated from poly (A)+ RNA using a reverse transcription/polymerase chain reaction (RT/PCR) method. A 1233-bp cDNA clone was generated that contained an open reading frame of 411 amino acids giving a predicted molecular mass of 46.9 kDa. Comparison of the TSS deduced amino acid sequence with currently described SS from different species showed the highest identity with *Nicotiana benthamiana* (97%), followed by *Glycyrrhiza glabra* (81%), *Arabidopsis thaliana* (74%), rat (40%), and yeast (37%). Expression of a soluble form of the TSS enzyme with enzymatic activity in *Escherichia coli* was achieved by truncating 24 hydrophobic amino acids at the carboxy terminus. Characterization of genomic TSS (gTSS) revealed a gene of 7.086 kb with a complex organization of small exons and large introns not typical of plant genes. Southern blot hybridization indicated only two copies of the SS gene in the tobacco genome. Treatment of tobacco cell suspension cultures with a fungal elicitor dramatically reduced TSS enzymatic activity, lowering it to zero within 24 h. Analysis of TSS mRNA levels, by RNA blot hybridization and primer extension assays, in elicitor-treated cells indicated that the transcript level remained largely unchanged over this 24-h period. These results suggest that the suppression of TSS enzyme activity in elicitor-treated cells may result from a posttranscriptional modification of TSS.

4/3,AB/2 (Item 2 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09507895 97417497 PMID: 9272870

Rapid amplification of genomic ends (RAGE) as a simple method to clone flanking genomic DNA.

Cormack R S; Somssich I E

Max-Planck-Institut für Zuchtforschung, Abteilung Biochemie, Köln, Germany.

Gene (NETHERLANDS) Jul 31 1997, 194 (2) p273-6, ISSN
0378-1119 Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

This report describes the amplification of upstream genomic sequences using the polymerase chain reaction (PCR) based solely on downstream DNA information from a cDNA clone. In this novel and rapid technique, genomic DNA (gDNA) is first incubated with a restriction enzyme that recognizes a site within the 5' end of a gene, followed by denaturation and polyadenylation of its free 3' ends with terminal transferase. The modified gDNA is then used as template for PCR using a gene-specific primer complementary to a sequence in the 3' end of its cDNA and an anchored deoxyoligothymidine primer. A second round of PCR is then performed with a second, nested gene-specific primer and the anchor sequence primer. The resulting PCR product is cloned and its sequence determined. Three independent plant genomic clones were isolated using this method that exhibited complete sequence identity to their cDNAs

and to the primers used in the amplification.

4/3,AB/3 (Item 3 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09446550 97336291 PMID: 9193067

Alternative processing of the maize Ac transcript in Arabidopsis.

Martin D J; Firek S; Moreau E; Draper J

Botany Department, University of Leicester, UK.

Plant journal : for cell and molecular biology (ENGLAND) May 1997

, 11 (5) p933-43, ISSN 0960-7412 Journal Code: 9207397

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The successful application of the maize transposable element system Ac/Ds as a genome mutagen in heterologous plant species has recently proved the versatility and power of this technique in plant molecular biology. However, the frequency of Ac/Ds transposition is considerably lower in Arabidopsis thaliana than in most other dicot plant species that have been studied. Since previous research has established that transcripts derived from monocot genes can be alternatively processed in dicot plants, we have investigated both the efficiency of intron splicing and polyadenylation of the maize Ac transposase pre-mRNA in Arabidopsis thaliana, Nicotiana tabacum, Nicotiana glauca and Zea mays. In this paper, we demonstrate that intron 4 is alternatively spliced within Arabidopsis, using cryptic 5' and 3' splice sites within the intron sequence, leading to a heterogeneous population of full length of transposase transcript. Furthermore, analysis of transposase transcript polyadenylation revealed that at least four alternative poly(A) sites were utilized between introns 2 and 3, resulting in truncated transposase transcripts. Finally, by Northern blotting, we established that the truncated transposase transcript was the most abundant form of transposase message in Arabidopsis. In contrast to these findings, the alternative splicing and premature polyadenylation of Ac message in Arabidopsis was unparalleled in the other species examined. We suggest that the poor frequency of transposition of Ac in Arabidopsis may be in part due to the low quantity of correctly processed transposase transcript available in this species.

4/3,AB/4 (Item 4 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09378518 97271384 PMID: 9126335

Characterization of a cDNA encoding Arabidopsis thaliana inositol 1,3,4-trisphosphate 5/6-kinase.

Wilson M P; Majerus P W

Division of Hematology-Oncology, Washington University School of Medicine, St. Louis, Missouri 63110, USA.

Biochemical and biophysical research communications (UNITED STATES) Mar 27 1997, 232 (3) p678-81, ISSN 0006-291X Journal Code: 0372516

Contract/Grant No.: HL 07088; HL; NHLBI; HL 16634; HL; NHLBI; HL 55672; HL; NHLBI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

We have sequenced and recombinantly expressed as a fusion protein an expressed sequence tag clone (GB Z25963) from Arabidopsis thaliana that represents the plant homologue of human inositol 1,3,4 trisphosphate 5/6-kinase. The 1365 base pair clone has an open reading frame of 960 base pairs that predicts a protein product of 36.2 kDa, with a pI of 6.1. There

is no polyadenylation signal or **poly (A)** tail, suggesting that additional 3' sequence remains to be identified. The amino acid sequence is 30% identical to the human protein. There are several short regions with particularly high degrees of identity between the human and Arabidopsis protein sequences, and these may be useful in identifying the active site of the enzyme. The expressed sequence tag was expressed as a fusion protein in *Escherichia coli*, with a carboxyl terminal deletion removing one region of high identity between the two proteins. The protein product of this construct was found to have inositol 1,3,4-trisphosphate 5/6-kinase activity. The Arabidopsis enzyme produced both inositol 1,3,4,6-tetrakisphosphate and inositol 1,3,4,5-tetrakisphosphate as products in a ratio of 1:3, in contrast with the human enzyme which gives a product ratio of 3:1.

4/3,AB/5 (Item 5 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09325468 97236504 PMID: 9118227

RNA-mediated RNA degradation and chalcone synthase A silencing in petunia.

Metzlaff M; O'Dell M; Cluster P D; Flavell R B

John Innes Centre, Norwich Research Park, Colney, United Kingdom.

Cell (UNITED STATES) Mar 21 1997, 88 (6) p845-54, ISSN

0092-8674 Journal Code: 0413066

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Transgenic *Petunia* **plants** with a *chsA* coding sequence under the control of a 35S promoter sometimes lose endogene and transgene chalcone synthase activity and purple flower pigment through posttranscriptional *chsA* RNA degradation. In these **plants**, shorter **poly(A)+** and **poly(A)-** *chsA* RNAs are found, and a 3' end-specific RNA fragment from the endogene is more resistant to degradation. The termini of this RNA fragment are located in a region of complementarity between the *chsA* 3' coding region and its 3' untranslated region. Equivalent *chsA* RNA fragments remain in the white flower tissue of a nontransgenic *Petunia* variety. We present a model involving cycles of RNA-RNA pairing between complementary sequences followed by endonucleolytic RNA cleavages to describe how RNA degradation is likely to be promoted.

4/3,AB/6 (Item 6 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

09253004 97156147 PMID: 9002607

Comparative gene expression in sexual and apomictic ovaries of *Pennisetum ciliare* (L.) Link.

Vielle-Calzada J P; Nuccio M L; Budiman M A; Thomas T L; Burson B L; Hussey M A; Wing R A

Department of Soil and Crop Sciences and Crop Biotechnology Center, Texas A&M University, College Station 77843, USA.

Plant molecular biology (NETHERLANDS) Dec 1996, 32 (6)

p1085-92, ISSN 0167-4412 Journal Code: 9106343

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Limited emphasis has been given to the molecular study of apomixis, an asexual method of reproduction where seeds are produced without fertilization. Most buffelgrass (*Pennisetum ciliare* (L.) Link syn = *Cenchrus ciliaris* L.) genotypes reproduce by obligate apomixis (apospory); however, rare sexual **plants** have been recovered. A **modified**

differential display procedure was used to compare gene expression in unpollinated ovaries containing ovules with either sexual or apomictic female gametophytes. The **modification** incorporated end-labeled **poly(A)** + anchored primers as the only isotopic source, and was a reliable and consistent approach for detecting differentially displayed transcripts. Using 20 different decamers and two anchor primers, 2268 cDNA fragments between 200 and 600 bp were displayed. From these, eight reproducible differentially displayed cDNAs were identified and cloned. Based on northern analysis, one cDNA was detected in only the sexual ovaries, two cDNAs in only apomictic ovaries and one cDNA was present in both types of ovaries. Three fragments could not be detected and one fragment was detected in ovaries, stems, and leaves. Comparison of gene expression during sexual and apomictic development in buffelgrass represents a new model system and a strategy for investigating female reproductive development in the angiosperms.

4/3,AB/7 (Item 7 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08349143 95108038 PMID: 7809117

Targeting of the polyhydroxybutyrate biosynthetic pathway to the plastids of *Arabidopsis thaliana* results in high levels of polymer accumulation.

Nawrath C; Poirier Y; Somerville C
Department of Plant Biology, Carnegie Institution of Washington,
Stanford, CA 94305.

Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Dec 20 1994, 91 (26) p12760-4, ISSN 0027-8424 Journal Code: 7505876

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

In the bacterium *Alcaligenes eutrophus*, three genes encode the enzymes necessary to catalyze the synthesis of poly[(R)-(-)-3-hydroxybutyrate] (PHB) from acetyl-CoA. In order to target these enzymes into the plastids of higher **plants**, the genes were **modified** by addition of DNA fragments encoding a pea chloroplast transit peptide, a constitutive **plant** promoter, and a **poly(A)** addition sequence. Each of the **modified** bacterial genes was introduced into *Arabidopsis thaliana* by *Agrobacterium*-mediated transformation, and **plants** containing all three genes were obtained by sexual crosses. These **plants** accumulated PHB up to 14% of the dry weight as 0.2- to 0.7-micron granules within plastids. In contrast to earlier experiments in which expression of the PHB biosynthetic pathway in the cytoplasm led to a deleterious effect on growth, expression of the PHB biosynthetic pathway in plastids had no obvious effect on the growth or fertility of the transgenic **plants** and resulted in a 100-fold increase in the amount of PHB that accumulated. We conclude that there does not appear to be any biological barrier to high-level production of PHB in higher **plants**. The high level of PHB accumulation also suggests that the synthesis of plastid acetyl-CoA is regulated by a mechanism which responds to metabolic demand.

4/3,AB/8 (Item 8 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

08071026 94221071 PMID: 1344891

Expression of *E. coli* inorganic pyrophosphatase in transgenic **plants** alters photoassimilate partitioning.

Sonnenwald U

Institut fur Genbiologische Forschung Berlin GmbH, Germany.

Plant journal : for cell and molecular biology (ENGLAND) Jul 1992

, 2 (4) p571-81, ISSN 0960-7412 Journal Code: 9207397

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Transgenic **plants** were constructed expressing a novel cytosolic inorganic pyrophosphatase in order to reduce the cytosolic pyrophosphate content. To this end the *Escherichia coli* gene *ppa* encoding inorganic pyrophosphatase was cloned between the 35S CaMV promoter and the **poly (A)** site of the octopine synthase gene and transferred into tobacco and potato **plants** by *Agrobacterium*-mediated gene transfer. Regenerated **plants** were tested for the expression of the *ppa* gene by Northern blots and activity gels. **Plants** expressing active inorganic pyrophosphatase showed a dramatic change in photoassimilate partitioning. In both transgenic tobacco and potato **plants** the ratio between soluble sugars and starch was increased by about 3-4-fold in source leaves as compared with the wild-type. However, whereas source leaves of transgenic tobacco **plants** accumulated much higher levels of glucose (up to 68-fold), fructose (up to 24-fold), sucrose (up to 12-fold) and starch (up to 8-fold) this was not observed in potato **plants** where the change in assimilate partitioning in source leaves was due to an increase of about 2-fold in sucrose and a reduction in starch content. Expression of the cytosolic inorganic pyrophosphatase in tobacco results in stunted growth of vegetatively growing **plants** due to a reduced internode distance. Upon flowering the transgenic **plants** increase their growth rate, reaching almost the same height as control **plants** at the end of the growth period. Old source leaves accumulate up to 100-fold more soluble sugars than control leaves. This increase in soluble sugars is accompanied by a reduction in chlorophyll content (up to 85%). Transgenic potato **plants** showed a less dramatic change in their growth behaviour. **Plants** were slightly reduced in size, with stems more highly branched. Tuber number increased 2-3-fold, but tuber weight was lower resulting in no net increase in fresh weight.

4/3,AB/9 (Item 9 from file: 155)
DIALOG(R) File 155:MEDLINE(R)

07199372 92118313 PMID: 1370622

Production of cyclodextrins, a novel carbohydrate, in the tubers of transgenic potato **plants**.

Oakes J V; Shewmaker C K; Stalker D M
Calgene Inc., Davis, CA 95616.

Bio/technology (Nature Publishing Company) (UNITED STATES) Oct
1991, 9 (10) p982-6, ISSN 0733-222X Journal Code: 8309273

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Cyclodextrins (CDs) are cyclic oligosaccharides containing six (alpha), seven (beta), or eight (gamma) glucose molecules, respectively. The cyclodextrin glycosyltransferases (CGT), which produce CDs from starch, are found only in bacteria and are used in batch fermentors with hydrolyzed starch to produce CDs commercially. Using a CGT gene from *Klebsiella*, we attempted to engineer the tubers of developing potatoes to produce these novel, high-value carbohydrates. A chimeric gene, consisting of (1) the patatin promoter for tuber-specific expression, (2) the small subunit of ribulose biphosphate carboxylase (SSU) transit peptide for plastid targeting, (3) the CGT structural gene from *Klebsiella* and (4) the nopaline synthase 3' region, was introduced into potatoes. Both alpha and beta CDs were produced in tubers of transgenic potatoes at levels corresponding to 0.001-0.01% of the starch being converted to CDs.

4/3,AB/10 (Item 10 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

07079670 92003661 PMID: 2577506

Deletion analysis of the polyadenylation signal of a pea ribulose-1,5-bisphosphate carboxylase small-subunit gene.

Hunt A G; MacDonald M H

Department of Agronomy, University of Kentucky, Lexington 40546-0091.

Plant molecular biology (NETHERLANDS) Aug 1989, 13 (2) p125-38

, ISSN 0167-4412 Journal Code: 9106343

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The polyadenylation signal of a pea gene for the small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcS) has been analyzed by deletion mutagenesis and Ti plasmid-mediated gene transfer. Sequences between 6 and 137 bases upstream from the normal polyadenylation sites in this gene (bases -6 to -137) are required for functioning of these sites. In addition, bases -111 to -235 can affect 3' end formation by altering the pattern of 3' termini seen in various transcription units. Sequences between 37 and 95 bases upstream from a cryptic polyadenylation site in this gene [A. G. Hunt, DNA 7: 329-336 (1988)] are necessary for mRNA 3' end formation at this site. At least two different parts of the 3' region of this rbcS gene can serve as a downstream element for polyadenylation at the normal **poly(A)** addition sites in this gene. Our studies indicate that: 1. the upstream sequences required for polyadenylation in **plants** are different from those defined in mammalian RNA **polymerase** II transcription units; 2. sequences 100 or more bases upstream and downstream from **poly(A)** addition sites in this gene can affect **poly(A)** addition site choice; and 3. there are apparently redundant downstream elements for polyadenylation in this gene.

4/3,AB/11 (Item 11 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

06548070 90244445 PMID: 2159571

Human papillomavirus type 1 produces redundant as well as polycistronic mRNAs in **plantar** warts.

Palermo-Dilts D A; Broker T R; Chow L T

Department of Biochemistry, University of Rochester School of Medicine and Dentistry, New York 14642.

Journal of virology (UNITED STATES) Jun 1990, 64 (6) p3144-9,

ISSN 0022-538X Journal Code: 0113724

Contract/Grant No.: CA 36200; CA; NCI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Human papillomavirus type 1 (HPV-1) causes **plantar** warts. On the basis of previously mapped mRNAs and sequence homologies of HPV-1 to other papillomaviruses, we designed oligonucleotide primers and employed the **polymerase** chain reaction to recover HPV-1 cDNAs from **plantar** warts. Seven spliced RNA species were characterized, including three not previously detected, and the coding potentials of each were deduced. The most abundant viral mRNA encodes an E1--E4 protein. One new species is predicted to encode the full-length E2 protein, and another can, theoretically, encode the E2-C or E1-M proteins, three products that regulate mRNA transcription and DNA replication. One RNA species originating from a novel HPV promoter in the upstream regulatory region has the potential to encode the minor capsid protein L2. A newly recognized E5a open reading frame (ORF) is contained in all mRNAs that are polyadenylated at the E-region **poly(A)** site and also in a putative L2 mRNA. Three distinct species, two of which are derived from the upstream

regulatory region promoter, have the potential to encode the L1 protein; the third species also contains the entire coding region of the Eli--E4 protein 5' to the L1 ORF. Both the Eli--E4 mRNA and the potentially bicistronic L1 mRNA are derived from a promoter located in the E7 ORF. We uncovered no evidence of alternatively spliced mRNAs that could account for the multiple, abundant E4 proteins in **plantar** warts, suggesting that posttranslational **modification** is mainly responsible for the observed protein heterogeneity.

4/3,AB/12 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11036680 BIOSIS NO.: 199799657825
Turnip yellow mosaic virus RNA-dependent RNA **polymerase**: Initiation of minus strand synthesis in vitro.
AUTHOR: Singh Ravindra N; Dreher Theo W(a)
AUTHOR ADDRESS: (a)Dep. Agric. Chem., Oregon State Univ., Corvallis, OR 97331-7301**USA
JOURNAL: Virology 233 (2):p430-439 1997
ISSN: 0042-6822
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: An RNA-dependent RNA **polymerase** (RdRp) activity was detergent-solubilized from the chloroplast membranes of Chinese cabbage leaves infected with turnip yellow mosaic virus (TYMV). The template-dependent micrococcal nuclease-treated activity synthesized full-length minus strands from TYMV RNA and 3'-fragments as short as a 28-nucleotide-long RNA comprising the amino acid acceptor stem of the 3'-tRNA-like structure (TLs). Minus strands were shown to arise by de novo initiation with the insertion of GTP opposite the penultimate (C) residue of the 3'-terminal -CCA. The TYMV RdRp activity was template specific in that **poly(A)** RNA was not copied, and alfalfa mosaic virus (AIMV) RNA, which does not contain a 3'-TLS, was a very poor template. However, other viral RNAs with a 3'-TLS and in vitro transcripts of tRNAs were copied to varying degrees. Fully **modified** tRNAs were either inactive or poorly active templates, and AIMV 3'-RNA, even when provided with a 3'-terminal -ACCA, was not copied delectably. A potential role of the acceptor stem pseudoknot as a promoter element was assessed with mutations that drastically altered the structure and sequence of the pseudoknot revealing only a twofold effect in decreasing template activity. The data show that RNAs with both a tRNA-like conformation and a -CCA 3'-terminus are potential templates for TYMV RdRp and suggest that promoter elements are not limited to the acceptor stem pseudoknot.

1997

4/3,AB/13 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10758296 BIOSIS NO.: 199799379441
Polyadenylation accelerates degradation of chloroplast mRNA.
AUTHOR: Kudla Joerg; Hayes Robert; Gruissem Wilhelm(a)
AUTHOR ADDRESS: (a)Dep. Plant Biol., Univ. California, Berkeley, CA 94720** USA
JOURNAL: EMBO (European Molecular Biology Organization) Journal 15 (24):p 7137-7146 1996
ISSN: 0261-4189
RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The expression of chloroplast genes is regulated by several mechanisms, one of which is the modulation of RNA stability. To understand how this regulatory step is controlled during chloroplast development, we have begun to define the mechanism of plastid mRNA degradation. We show here that the degradation of petD mRNA involves endonucleolytic cleavage at specific sites upstream of the 3' stem-loop structure. The endonucleolytic petD cleavage products can be polyadenylated in vitro, and similar polyadenylated RNA products are detectable in vivo. PCR analysis of the psbA and psaA-psaB-rps14 operons revealed other polyadenylated endonucleolytic cleavage products, indicating that **poly(A)** addition appears to be an integral **modification** during chloroplast mRNA degradation. Polyadenylation promotes efficient degradation of the cleaved petD RNAs by a 3'-5' exoribonuclease. Furthermore, polyadenylation also plays an important role in the degradation of the petD mRNA 3' end. Although the 3' end stem-loop is usually resistant to nucleases, adenylation renders the secondary structure susceptible to the 3'-5' exoribonuclease. Analysis of 3' ends confirms that polyadenylation occurs in vivo, and reveals that the extent of adenylation increases during the degradation of plastid mRNA in the dark. Based on these results, we propose a novel mechanism for polyadenylation in the regulation of plastid mRNA degradation.

1996

4/3,AB/14 (Item 3 from file: 5)
DIALOG(R) File 5:Biosis Previews(R)
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Isolation and evaluation of RNA from polysaccharide-rich tissues in fruit for quality by cDNA library construction and RT-PCR.

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JOURNAL: Journal of the Japanese Society for Horticultural Science 64 (4): p809-814 1996

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DOCUMENT TYPE: Article

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LANGUAGE: English

SUMMARY LANGUAGE: English; Japanese

ABSTRACT: Methods for extracting total RNA from various tissues of satsuma mandarin and kiwifruit were examined. Satisfactory yields in total RNA were obtained from tissues with the exception of the albedo tissue of satsuma mandarin, by using a **modification** of the conventional extraction method devised for fruit tissues by Lopez-Gomez and Gomez-Lim (1992). In the albedo tissue, the polysaccharides may interfere with RNA extraction but further **modification** of the extraction method improved its yield. The **modification** involved repeated back extraction, chloroform/isoamyl alcohol extraction, and increasing the volume of the aqueous phase before precipitating RNA with LiCl (3 M final concentration). From the total RNA, **poly(A)+RNA** was purified using an oligo(dT)-cellulose column. The **poly(A)+RNA** could be successfully used for Reverse Transcription-**Polymerase** Chain Reaction (RT-PCR) and the construction of a cDNA library. This **modified** protocol is applicable to other fruit tissues rich in polysaccharides.

1996

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DIALOG(R)File 5:Biosis Previews(R)
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08907805 BIOSIS NO.: 199396059306
3'-end labeling of RNA with recombinant yeast **poly(A)**
polymerase.

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JOURNAL: Nucleic Acids Research 21 (12):p2917-2920 1993
ISSN: 0305-1048
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Two commonly used methods to end-label RNA-molecules are 5'-end labeling by polynucleotide kinase and 3'-end labeling with pCp and T4 RNA ligase. We show here that RNA 3'-ends can also be labeled with the chain-terminating analogue cordycepin 5'-triphosphate (3'-deoxy-ATP) which is added by **poly(A) polymerase**. For a synthetic RNA it is shown that 40% of cordycepin becomes incorporated when the nucleotide is used at limiting concentrations and that with an excess of cordycepin 5'-triphosphate essentially all the RNA becomes **modified** at its 3'-end. The reaction is complete within minutes and the RNA product is uniform and suitable for sequence analysis. The efficiency of labeling varies with different RNA-molecules and is different from RNA ligase. **Poly(A) polymerase** preferentially labels longer RNA-molecules whereas short RNA-molecules are labeled more efficiently by T4 RNA ligase.

1993

4/3,AB/16 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06055087 Genuine Article#: XR724 Number of References: 60
Title: SQT1, which encodes an essential WD domain protein of *Saccharomyces cerevisiae*, suppresses dominant-negative mutations of the ribosomal protein gene QSR1 (ABSTRACT AVAILABLE)

Author(s): Eisinger DP; Dick FA; Denke E; Trumpower BL (REPRINT)
Corporate Source: DARTMOUTH COLL SCH MED,DEPT BIOCHEM/HANOVER//NH/03755 (REPRINT); DARTMOUTH COLL SCH MED,DEPT BIOCHEM/HANOVER//NH/03755
Journal: MOLECULAR AND CELLULAR BIOLOGY, 1997, V17, N9 (SEP), P 5146-5155

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Language: English Document Type: ARTICLE

Abstract: QSR1 is an essential *Saccharomyces cerevisiae* gene, which encodes a 60S ribosomal subunit protein required for joining of 40S and 60S subunits. Truncations of QSR1 predicted to encode C-terminally truncated forms of Qsr1p do not substitute for QSR1 but do act as dominant negative-mutations, inhibiting the growth of yeast when expressed from an inducible promoter. The dominant negative mutants exhibit a polysome profile characterized by 'half-mer' polysomes, indicative of a subunit joining defect like that seen in other qsr1 mutants (D. P. Eisinger, F. A. Dick, and B. L. Trumpoffer, Mol. Cell. Biol. 17:5136-5145, 1997.) By screening a high-copy yeast genomic